

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:46:29 ; Search time 61 Seconds  
(without alignments)  
2903.075 Million cell updates/sec

Title: US-09-673-707-1  
Perfect score: 1347  
Sequence: 1 MQVLEQSGAEVKKPGASVK.....QVYGASSYFGQGTKLERK 251

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description  |
|------------|-------|-------------|--------|-------|--------------|
| 1          | 828.5 | 61.5        | 244    | 2     | Q65ZC8_HUMAN |
| 2          | 726.5 | 53.9        | 240    | 2     | Q65ZC9_HUMAN |
| 3          | 719.5 | 53.4        | 243    | 2     | Q7TQM2_MOUSE |
| 4          | 703.5 | 52.2        | 241    | 2     | Q921A6_MOUSE |
| 5          | 703.5 | 52.2        | 255    | 2     | Q6KB05_MOUSE |
| 6          | 692.5 | 51.4        | 487    | 2     | Q65ZL2_MOUSE |
| 7          | 658   | 48.8        | 248    | 2     | Q65ZQ7_MOUSE |
| 8          | 597   | 44.3        | 218    | 2     | Q925S1_MOUSE |
| 9          | 436.5 | 32.4        | 170    | 2     | Q925S2_MOUSE |
| 10         | 435   | 32.3        | 129    | 1     | KV3L_HUMAN   |
| 11         | 434   | 32.2        | 129    | 1     | KV3M_HUMAN   |
| 12         | 431   | 32.0        | 518    | 2     | Q6N030_HUMAN |
| 13         | 427   | 31.7        | 109    | 1     | KV3B_HUMAN   |
| 14         | 426   | 31.6        | 109    | 1     | KV3E_HUMAN   |
| 15         | 424   | 31.5        | 109    | 1     | KV3D_HUMAN   |
| 16         | 422   | 31.3        | 108    | 1     | KV3A_HUMAN   |
| 17         | 422   | 31.3        | 109    | 2     | Q9UL78_HUMAN |
| 18         | 421.5 | 31.3        | 236    | 2     | Q6PJF8_HUMAN |
| 19         | 419.5 | 31.1        | 500    | 2     | Q9BRV0_HUMAN |
| 20         | 417.5 | 31.0        | 159    | 2     | Q96Q50_HUMAN |
| 21         | 417   | 31.0        | 109    | 2     | Q9UL86_HUMAN |
| 22         | 414   | 30.7        | 480    | 2     | Q6P089_HUMAN |
| 23         | 410.5 | 30.5        | 235    | 2     | Q6PJF2_HUMAN |
| 24         | 410.5 | 30.5        | 236    | 2     | Q6P558_HUMAN |
| 25         | 410.5 | 30.5        | 468    | 2     | Q6N041_HUMAN |
| 26         | 408   | 30.3        | 469    | 2     | Q7Z7P5_HUMAN |
| 27         | 406   | 30.1        | 109    | 1     | KV3G_HUMAN   |
| 28         | 406   | 30.1        | 119    | 2     | Q6GY22_MOUSE |
| 29         | 406   | 30.1        | 235    | 2     | Q6GMV9_HUMAN |
| 30         | 405   | 30.1        | 119    | 2     | Q9UL94_HUMAN |
| 31         | 404   | 30.0        | 125    | 2     | Q9UL95_HUMAN |

|    |       |      |     |   |              |        |              |
|----|-------|------|-----|---|--------------|--------|--------------|
| 32 | 403   | 29.9 | 500 | 2 | Q6N091_HUMAN | Q6N091 | homo sapien  |
| 33 | 400.5 | 29.7 | 128 | 1 | KV3K_HUMAN   | P06311 | homo sapien  |
| 34 | 400.5 | 29.7 | 147 | 1 | HV1C_HUMAN   | P01744 | homo sapien  |
| 35 | 397   | 29.5 | 475 | 2 | Q6N095_HUMAN | Q6N095 | homo sapien  |
| 36 | 395.5 | 29.4 | 124 | 2 | Q9UL92_HUMAN | Q9UL92 | homo sapien  |
| 37 | 392.5 | 29.1 | 234 | 2 | Q56919_HUMAN | Q56919 | homo sapien  |
| 38 | 392   | 29.1 | 497 | 2 | Q8WY24_HUMAN | Q8WY24 | homo sapien  |
| 39 | 389.5 | 28.9 | 613 | 2 | Q8VCX7_MOUSE | Q8VCX7 | mus musculus |
| 40 | 385.5 | 28.6 | 168 | 2 | Q8VDC9_MOUSE | Q8VDC9 | mus musculus |
| 41 | 385   | 28.6 | 465 | 2 | Q6PJB2_MOUSE | Q6PJB2 | mus musculus |
| 42 | 383.5 | 28.5 | 468 | 2 | Q505N9_MOUSE | Q505N9 | mus musculus |
| 43 | 382.5 | 28.4 | 480 | 2 | Q6PJF1_HUMAN | Q6PJF1 | homo sapien  |
| 44 | 381   | 28.3 | 100 | 1 | KV3C_HUMAN   | P01621 | homo sapien  |
| 45 | 380.5 | 28.2 | 617 | 2 | Q4KML5_MOUSE | Q4KML5 | mus musculus |

ALIGNMENTS

RESULT 1

Q65ZC8\_HUMAN

ID Q65ZC8\_HUMAN PRELIMINARY; PRT; 244 AA.

AC Q65ZC8;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE Single-chain Fv (Fragment).

GN Name=scFv;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE-97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;

RA Kontermann R.E., Wing M.G., Winter G.;

RT "Complement recruitment using bispecific diabodies.";

RL Nat. Biotechnol. 15:629-631(1997).

DR EMBL; Y13057; CAA73500.1; -; mRNA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IGv; 2.

DR PROSITE; PS50835; IG\_LIKE; 2.

FT NON\_TER 1

FT NON\_TER 244

SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 61.5%; Score 828.5; DB 2; Length 244;

Best Local Similarity 64.8%; Pred. No. 1e-57; Indels 7; Gaps 2;

Matches 162; Conservative 26; Mismatches 55;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWVRQAPGQRFQWGWINPYNGNKEF 61

Db 1 QVQLVQSGAEVKKPGDSVKVSCKASGYTFSDFHYHWVRQAPGQGLEWGWIDPNNGDRF 60

Qy 62 SAKPQDRVTFTADTSANTAYMELRSLRSADTAVYCARVGEWGWDDSPQDNYMDVWGK 121

Db 61 AQRFGQGRVTMTDTSISAAVMESVRLSDDTAVVYCAREG-----TGSATVGMVWGQG 114

Qy 122 TTVTVSSGGGGGGGGGGSDIELTQSPCTLSLSPGERATFSCRSHSRSRVAVQ 181

Db 115 TLTVTVSSGGGGGGGGGGSDIQMTQSPSTLSASIGDRVITTCRASEGI-YHWLAWYQ 173

Qy 182 HKGQAPRLVHGVSNRASGISDRFSGSGSGTDFLTITRVEPEDFALYVQCVYGASSYT 241

Db 174 QKGGKAPFLIYKASSLASAPRFPFGSGSGTDFLTITISSLPDQDFATYVCOQISNYPLT 233

Qy 242 FGQGTKLERK 251

Db 234 FGGGTKLEIK 243

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[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Balb/C;
RC MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.;
RT "scfv single chain antibody variable fragment as inverse agonist for
the beta-2 adrenergic receptor.";
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CAE00495.1; -; Genomic_DNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q7TQM2; 1-236.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
SQ SEQUENCE 243 AA; 25976 MW; BEPFF64D2DCF4F76 CRC64;

Query Match 53.4%; Score 719.5; DB 2; Length 243;
Best Local Similarity 56.0%; Pred. No. 4.4e-49;
Matches 140; Conservative 41; Mismatches 56; Indels 13; Gaps 3;

Qy 2 QVLEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFWMGWINPVGNGKEF 61
Db 1 QVQLVQSGGGLVQPGGSLRLSQAASGFTFSYGMHWVRQAPGQGLEWVAIVSDGSKNY 60
Qy 62 SAKFDQRTVFTADTSANTAYMELRLSADTAVYCARVGEWGDSPQDNYMDVWGKG 121
Db 61 DEKFKNGILTVDTSSSTAYMHLSSLASEDSAVVYCARGRG-----LDVWGAG 109
Qy 122 TTVIVSSGGSGGGGGGGSDIELTQSPGTLSPGERATFSCRSHSIRSRVAVYQ 181
Db 110 TLTIVSSGGSGGGGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGI-YRWLAWYQ 169
Qy 182 HKPQAPRLVIHGVSNRSGISDRFSGSGGTDFLTITRVEPEDEALYICQVYGASST 241
Db 169 QKPGAPKLLIYKASSLASRAPSRFSGSGGTDFLTITRVEPEDEALYICQVYGASST 227

RESULT 4
Q921A6_MOUSE PRELIMINARY; PRT; 241 AA.
ID Q921A6_MOUSE PRELIMINARY; PRT; 241 AA.
AC Q921A6_MOUSE PRELIMINARY; PRT; 241 AA.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA Stark S.E., Caton A.J.;
RT "Antibodies that are specific for a single amino acid interchange in a
protein epitope use structurally distinct variable regions.";
RL J. Exp. Med. 174:613-624(1991).
DR EMBL; U88067; AAB48044.1; -; mRNA.

[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C1q/7;
RC MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wang M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
SQ SEQUENCE 240 AA; 25569 MW; FDCPD3645F64B373 CRC64;

Query Match 53.9%; Score 726.5; DB 2; Length 240;
Best Local Similarity 56.8%; Pred. No. 1.2e-49;
Matches 142; Conservative 36; Mismatches 61; Indels 11; Gaps 3;

Qy 2 QVLEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFWMGWINPVGNGKEF 61
Db 1 QVQLVQSGGGLVQPGGSLRLSQAASGFTFSYGMHWVRQAPGQGLEWVAIVSDGSKNY 60
Qy 62 SAKFDQRTVFTADTSANTAYMELRLSADTAVYCARVGEWGDSPQDNYMDVWGKG 121
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAVYCAR-----LDPWGKG 110
Qy 122 TTVIVSSGGSGGGGGGGSDIELTQSPGTLSPGERATFSCRSHSIRSRVAVYQ 181
Db 111 TLTIVSSGGSGGGGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGI-YRWLAWYQ 169
Qy 182 HKPQAPRLVIHGVSNRSGISDRFSGSGGTDFLTITRVEPEDEALYICQVYGASST 241
Db 170 QKPGAPKLLIYKASSLASRAPSRFSGSGGTDFLTITRVEPEDEALYICQVYGASST 229

Qy 242 FGGGTLKLEIK 251
Db 230 FGGGTLKLEIK 239

RESULT 3
Q7TQM2_MOUSE PRELIMINARY; PRT; 243 AA.
ID Q7TQM2_MOUSE PRELIMINARY; PRT; 243 AA.
AC Q7TQM2_MOUSE PRELIMINARY; PRT; 243 AA.
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE scFv 6H8 protein (Fragment).
GN Name=scFv_6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSP; P01607; 1BW.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match
Best Local Similarity 52.2%; Score 703.5; DB 2; Length 241;
Matches 136; Conservative 46; Mismatches 52; Indels 21; Gaps 6;

QY 2 QVLEQSGAEVKKPKASVKVSCQASGYRFSNFTVHVWVROAQGFQRFWMGWINPYNGNKEF 61
DQ |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 QVQLQQSGDGLVKKPGGSLKVSAAAGFTFSSYGMVSRQTPDKRLLEWVATITSGGSYTY 60
QY 62 SAKFDQDRVTFADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNY-YNDVWGK 120
DQ |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 ADFFKGRFAFLETSASTAYLQINLNKNEIDATYFCAR-----KDLLRFYDWGQ 110
QY 121 GTTVIVSSGGSGGGGGGGSDIELTQSPOTLSLSPGERATFSCRSRSHSIRRRVAVY 180
DQ |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 111 GTTVIVSSGGSGGGGGGGSDIELTQSPSSLSASLGKVTITCKASQDI-NKIYAWY 169
QY 181 QHKFGQAPR----LVHGVSNRAGISDRFSGSGSGDTFTLTITRVEPEDFALYYCQVYG 236
DQ |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 170 QHKPGKGRSAHTLHY----IQGIPSRFSGSGSGRDYSPFSISNLEPDIAITYCYLHYD 225
QY 237 ASSYTFGGGTGLERK 251
DQ :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 226 -NLHTFGGTGLERK 239

RESULT 5
Q6KB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE SCFv B8E5 protein (fragment).
GN Name=scfv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT monoclonal anti-M2 receptor antibody fragments.";
RL J. Biol. Chem. 279:55697-55706(2004).
DR EMBL; AJ746180; CAG34081.1; -; Other_DNA.
DR HSP; P01837; 1KCR.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD3895DF713B CRC64;

Query Match
Best Local Similarity 52.2%; Score 703.5; DB 2; Length 255;
Matches 136; Conservative 46; Mismatches 52; Indels 21; Gaps 6;
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Best Local Similarity 52.9%; Pred. No. 8.7e-48;
Matches 135; Conservative 42; Mismatches 67; Indels 11; Gaps 2;

QY 2 QVLEQSGAEVKKPKASVKVSCQASGYRFSNFTVHVWVROAQGFQRFWMGWINPYNGNKEF 61
DQ |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 QVQLQQSGDGLVKKPGGSLKVSAAAGFTFSSYGMVSRQTPDKRLLEWVATITSGGSYTY 60
QY 62 SAKFDQDRVTFADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVWGK 121
DQ |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 PDSVKGRTISRDNKNTLYLQMSLSKSDTAMVYCARHINYRDGA-----FDYWGQ 114
QY 122 TTVIVSSGGSGGGGGGGSDIELTQSPOTLSLSPGERATFSCRSRSHSIRSR----- 176
DQ |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 115 TTVIVSSGGSGGGGGGGSDIVMAQSPSSLSVSAKEKIVMSCKSLNSRNKNY 174
QY 177 VAWYQHKGPGQAPRLVHGVSNRAGISDRFSGSGSGDTFTLTITRVEPEDFALYYCQVYG 236
DQ |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 175 LAWYQKPGQSPKLLIYGASTRESGVPDRFTFGSGSGDTFTLTISVQAEDLAVYYCONDH 234
QY 237 ASSYTFGGGTGLERK 251
DQ :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 235 SYPLTFGAGTKLEIK 249

RESULT 6
Q65ZL2_9MURI PRELIMINARY; PRT; 487 AA.
AC Q65ZL2_9MURI;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE FV/M4.
GN Name=M4-IFN- $\tau$ and>;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96272580; PubMed=8688499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT antibody secreted from myeloma cells.";
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -; mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00408; IGc2; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match
Best Local Similarity 51.4%; Score 692.5; DB 2; Length 487;
Matches 131; Conservative 48; Mismatches 56; Indels 15; Gaps 4;

QY 2 QVLEQSGAEVKKPKASVKVSCQASGYRFSNFTVHVWVROAQGFQRFWMGWINPYNGNKEF 61
DQ |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 QVQLQQSDAELVKKPGASVKISCKASGYTFDTHAIHWAKRQPEQGLEWIGYISPDNDIKY 79
QY 62 SAKFDQDRVTFADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVWGK 121
DQ |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 NERFKGKATLTADKSSSTAYWQLNSLTSEDSAVYFCKR-----SYI-GHWGQ 126
```

RESULT 8  
Q925S1 MOUSE





Ensembl; ENSG00000169769; Homo sapiens.  
GO; GO:0005576; C:extracellular region; NAS.  
GO; GO:0003823; F:antigen binding; NAS.  
GO; GO:0006955; P:immune response; NAS.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003596; Ig\_v.  
SMART; SM00406; IGV; 1.  
PROSITE; PS00835; IG\_LIKE; 1.  
Immunoglobulin domain; Immunoglobulin V region; Signal.  
SIGNAL 1 20  
CHAIN 21 129 Ig kappa chain V-III region HIC.  
REGION 21 43 Framework-1.  
REGION 44 55 Complementarity-determining-1.  
REGION 56 70 Framework-2.  
REGION 71 77 Complementarity-determining-2.  
REGION 78 109 Framework-3.  
REGION 110 118 Complementarity-determining-3.  
REGION 119 129 JKL segment.  
DISULFID 43 109 By similarity.  
NON\_TER 129 129  
SEQUENCE 129 AA; 14071 MW; 7395528EA2B74D6 CRC64;

Query Match 32.2%; Score 434; DB 1; Length 129;  
Best Local Similarity 75.0%; Pred. No. 9.5e-27;  
Matches 81; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 144 DIETQSPGTLSPGERATFSCRSSHISRVRVAVYQHKGPAPRLVIHGVSNRAGSIS 203  
DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPKGAPRLIIYGASSRATGIP 80

QY 204 DRFSGSGSGTDFTLTITRVEPEDFALYCYQVYGASSYTFGGTKLERK 251  
DB 81 DRFSGSGSGTDFTLTISRLEKPEAVYCYQVYGSSPWTFGGTKVETK 128

RESULT 12  
Q6N030 HUMAN PRELIMINARY; PRT; 518 AA.  
ID Q6N030  
AC Q6N030  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686i15212.  
DE Name=DKFZp686i15212;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
NCBI\_TaxID=9606;  
[1]  
N1  
PIR; A01892; K3HUS1.  
HSSP; P01625; 1LVE.  
DR SMR; P01620; 1-109.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region.  
FT DISULFID 23 89 By similarity.  
FT NON\_TER 109 109  
FT SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 31.7%; Score 427; DB 1; Length 109;  
Best Local Similarity 73.1%; Pred. No. 2.8e-26;  
Matches 79; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 144 DIETQSPGTLSPGERATFSCRSSHISRVRVAVYQHKGPAPRLVIHGVSNRAGSIS 203  
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPKGAPRLIIYGASSRATGIP 60

QY 204 DRFSGSGSGTDFTLTITRVEPEDFALYCYQVYGASSYTFGGTKLERK 251



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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:47:54 ; Search time 104 Seconds  
(without alignments)  
231.818 Million cell updates/sec

Title: US-09-673-707-1

Perfect score: 1347

Sequence: 1 MQVLEQSGAEVKKPGASVK.....COVYGASSYTFGQTKLERK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 443638 seqs, 96052105 residues

Total number of hits satisfying chosen parameters: 443638

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*

- 1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep.\*
- 8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                          |
|------------|-------|-------------|--------|-------|--------------------------------------|
| 1          | 949   | 70.5        | 245    | 6     | US-11-266-444-1896 Sequence 1896, Ap |
| 2          | 949   | 70.5        | 245    | 8     | US-60-735-988-1896 Sequence 1896, Ap |
| 3          | 949   | 70.5        | 245    | 8     | US-60-735-988-1896 Sequence 1896, Ap |
| 4          | 884   | 65.6        | 251    | 6     | US-11-266-444-12 Sequence 12, Appl   |
| 5          | 884   | 65.6        | 251    | 6     | US-11-266-444-26 Sequence 12, Appl   |
| 6          | 884   | 65.6        | 251    | 8     | US-60-735-988-12 Sequence 12, Appl   |
| 7          | 884   | 65.6        | 251    | 8     | US-60-735-988-26 Sequence 12, Appl   |
| 8          | 884   | 65.6        | 251    | 8     | US-60-735-988-26 Sequence 12, Appl   |
| 9          | 884   | 65.6        | 251    | 8     | US-60-735-988-26 Sequence 12, Appl   |
| 10         | 883   | 65.6        | 251    | 6     | US-11-266-444-22 Sequence 26, Appl   |
| 11         | 883   | 65.6        | 251    | 6     | US-11-266-444-28 Sequence 26, Appl   |
| 12         | 883   | 65.6        | 251    | 6     | US-11-266-444-33 Sequence 28, Appl   |
| 13         | 883   | 65.6        | 251    | 6     | US-11-266-444-43 Sequence 33, Appl   |
| 14         | 883   | 65.6        | 251    | 6     | US-11-266-444-127 Sequence 127, Appl |
| 15         | 883   | 65.6        | 251    | 8     | US-60-735-988-22 Sequence 22, Appl   |
| 16         | 883   | 65.6        | 251    | 8     | US-60-735-988-28 Sequence 28, Appl   |
| 17         | 883   | 65.6        | 251    | 8     | US-60-735-988-33 Sequence 33, Appl   |
| 18         | 883   | 65.6        | 251    | 8     | US-60-735-988-43 Sequence 43, Appl   |
| 19         | 883   | 65.6        | 251    | 8     | US-60-735-988-127 Sequence 127, Appl |
| 20         | 883   | 65.6        | 251    | 8     | US-60-735-988-127 Sequence 127, Appl |
| 21         | 883   | 65.6        | 251    | 8     | US-60-735-988-127 Sequence 127, Appl |
| 22         | 883   | 65.6        | 251    | 8     | US-60-735-988-127 Sequence 127, Appl |
| 23         | 883   | 65.6        | 251    | 8     | US-60-735-988-127 Sequence 127, Appl |
| 24         | 883   | 65.6        | 251    | 8     | US-60-735-988-127 Sequence 127, Appl |
| 25         | 882   | 65.5        | 251    | 6     | US-11-266-444-17 Sequence 17, Appl   |

|    |     |      |     |   |                                      |
|----|-----|------|-----|---|--------------------------------------|
| 26 | 882 | 65.5 | 251 | 6 | US-11-266-444-30 Sequence 30, Appl   |
| 27 | 882 | 65.5 | 251 | 6 | US-11-266-444-216 Sequence 216, Appl |
| 28 | 882 | 65.5 | 251 | 8 | US-60-735-988-17 Sequence 17, Appl   |
| 29 | 882 | 65.5 | 251 | 8 | US-60-735-988-30 Sequence 30, Appl   |
| 30 | 882 | 65.5 | 251 | 8 | US-60-735-988-216 Sequence 216, Appl |
| 31 | 882 | 65.5 | 251 | 8 | US-60-776-665-17 Sequence 17, Appl   |
| 32 | 882 | 65.5 | 251 | 8 | US-60-776-665-30 Sequence 30, Appl   |
| 33 | 882 | 65.5 | 251 | 8 | US-60-776-665-216 Sequence 216, Appl |
| 34 | 881 | 65.4 | 251 | 6 | US-11-266-444-171 Sequence 171, Appl |
| 35 | 881 | 65.4 | 251 | 6 | US-11-266-444-317 Sequence 317, Appl |
| 36 | 881 | 65.4 | 251 | 8 | US-60-735-988-171 Sequence 171, Appl |
| 37 | 881 | 65.4 | 251 | 8 | US-60-735-988-317 Sequence 317, Appl |
| 38 | 881 | 65.4 | 251 | 8 | US-60-776-665-171 Sequence 171, Appl |
| 39 | 881 | 65.4 | 251 | 8 | US-60-776-665-317 Sequence 317, Appl |
| 40 | 880 | 65.3 | 251 | 6 | US-11-266-444-27 Sequence 27, Appl   |
| 41 | 880 | 65.3 | 251 | 6 | US-11-266-444-34 Sequence 34, Appl   |
| 42 | 880 | 65.3 | 251 | 6 | US-11-266-444-102 Sequence 102, Appl |
| 43 | 880 | 65.3 | 251 | 6 | US-11-266-444-238 Sequence 238, Appl |
| 44 | 880 | 65.3 | 251 | 6 | US-11-266-444-295 Sequence 295, Appl |
| 45 | 880 | 65.3 | 251 | 8 | US-60-735-988-27 Sequence 27, Appl   |

ALIGNMENTS

RESULT 1

US-11-266-444-1896

; Sequence 1896, Application US/11266444

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimula

; FILE REFERENCE: PF523P1D1

; CURRENT APPLICATION NUMBER: US/11/266,444

; CURRENT FILING DATE: 2005-11-04

; PRIOR APPLICATION NUMBER: 09/880,746

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1896

; LENGTH: 245

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-266-444-1896

Query Match Best Local Similarity 70.5%; Score 949; DB 6; Length 245;

Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKYSQASGYRFSNFTVHVVRQAPQGRFVWGWINPYNGNKEF 61

Db 1 QVQLVQSGAEVKKPGASVKYSCKASGYTFTSYAMHVRQAPQGRLEWNGINAGNTKY 60

Qy 62 SAKFDQRTVTTADTSANTAYMELRSADTAVYVCARVGEWGDWDDSPQDNYNDVWCKG 121

Db 61 SQKPFQGVITTRDTASTAYMELSSLRSEDTAVYICAREG-----PGYYGMDVWVGQ 113

Qy 122 TTIVVSGGGSGGGSGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRHSIRSRVAV 179

Db 114 TMTVSGGGSGGGSGGGGGGSALETTLTQSPGTLSPGERATLSCRAQATGTSNYLAW 173

Qy 180 YQKPGQAPRLVHGVSNRASGISDRFSGSGGTDFLTITRVEPEDFALYYCOVYGASS 239

Db 174 YQKPGQPPSLIYLGASSRATGIPDRPSASGSGTDFLTISRLEPEDFAVYICQYQ-SS 232

QY 240 YTFGQGTCLERK 251  
Db 233 ITFGQGTCLERK 244

RESULT 2  
US-60-735-988-1896  
; Sequence 1896, Application US/60735988  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat  
; FILE REFERENCE: PF523PP9  
; CURRENT APPLICATION NUMBER: US/60/735,988  
; CURRENT FILING DATE: 2005-11-14  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1896  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-735-988-1896

Query Match 70.5%; Score 949; DB 8; Length 245;  
Best Local Similarity 73.8%; Pred. No. 2.1e-50;  
Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

QY 2 QVQLVSGGAEVKKPGASVKVSCQASGYRFSNFTVHVRQAPGORFWMGWINPYNGNKEF 61  
Db 1 QVQLVSGGAEVKKPGASVKVSCASGYTFTSYAMHWVRQAPGORLEWNGWINGNNTKY 60

QY 62 SAKFDQRTVTTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVWGK 121  
Db 61 SQKFGQRTVTTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVWGK 113

QY 122 TTVIVSSGGGGSGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSRRAV 179  
Db 114 TWVTVSSGGGGSGGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 173

QY 180 YQHPGQAPRLVHGVSNRAGISDRFSGSGSGTDFLTITRVEPEDFALYYCOVYGAS 239  
Db 174 YQQKPGQPPSLLIYGASSRATGIPDRFSASGSGTDFLTISRLEPEDFAVYYCOQY-SS 232

QY 240 YTFGQGTCLERK 251  
Db 233 ITFGQGTCLERK 244

RESULT 3  
US-60-776-665-1896  
; Sequence 1896, Application US/60776665  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat  
; FILE REFERENCE: PF523PP10  
; CURRENT APPLICATION NUMBER: US/60/776,665  
; CURRENT FILING DATE: 2006-02-27  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1896  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-776-665-1896

Query Match 70.5%; Score 949; DB 8; Length 245;  
Best Local Similarity 73.8%; Pred. No. 2.1e-50;  
Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

QY 2 QVQLVSGGAEVKKPGASVKVSCQASGYRFSNFTVHVRQAPGORFWMGWINPYNGNKEF 61  
Db 1 QVQLVSGGAEVKKPGASVKVSCASGYTFTSYAMHWVRQAPGORLEWNGWINGNNTKY 60

QY 62 SAKFDQRTVTTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVWGK 121

Db 61 SQKFGQRTVTTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVWGK 113

QY 122 TTVIVSSGGGGSGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSRRAV 179  
Db 114 TWVTVSSGGGGSGGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 173

QY 180 YQHPGQAPRLVHGVSNRAGISDRFSGSGSGTDFLTITRVEPEDFALYYCOVYGAS 239  
Db 174 YQQKPGQPPSLLIYGASSRATGIPDRFSASGSGTDFLTISRLEPEDFAVYYCOQY-SS 232

QY 240 YTFGQGTCLERK 251  
Db 233 ITFGQGTCLERK 244

RESULT 4  
US-11-266-444-12  
; Sequence 12, Application US/11266444  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat  
; FILE REFERENCE: PF523P1D1  
; CURRENT APPLICATION NUMBER: US/11/266,444  
; CURRENT FILING DATE: 2005-11-04  
; PRIOR APPLICATION NUMBER: 09/880,746  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-266-444-12

Query Match 65.6%; Score 884; DB 6; Length 251;  
Best Local Similarity 68.4%; Pred. No. 1.7e-46;  
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

QY 2 QVQLVSGGAEVKKPGASVKVSCQASGYRFSNFTVHVRQAPGORFWMGWINPYNGNKEF 61  
Db 1 QVQLVSGGAEVKKPGASVKVSCASGYTFTSYAMHWVRQAPGORLEWNGWINGNNTKY 60

QY 62 SAKFDQRTVTTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVWGK 120  
Db 61 AQPFGQRTVTTADTSANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVWGK 117

QY 121 GTTVIVSSGGGGSGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSRRAV 178  
Db 118 GTVTIVSSGGGGSGGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 177

QY 179 YQHPGQAPRLVHGVSNRAGISDRFSGSGSGTDFLTITRVEPEDFALYYCOVYGAS 238  
Db 178 YQQKPGQPPSLLIYGASSRATGIPDRFSASGSGTDFLTISRLEPEDFAVYYCOQY-SS 237

QY 239 SYTFGQGTCLERK 251  
Db 238 PRTFGQGTCLERK 250

RESULT 5  
US-11-266-444-26  
; Sequence 26, Application US/11266444  
; GENERAL INFORMATION:



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US-60-776-665-12
Query Match      65.6%; Score 884; DB 8; Length 251;
Best Local Similarity 68.4%; Pred. No. 1.7e-46;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

QY      2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHVVRQAPGQRFEMMGWINPYGNKKEF 61
DB      1 QVQLVQSGVEVKKPGASVKVSCKASGYTFNSHGISWVRQAPGQGLEWVGWISGHDSTKY 60

QY      62 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVYICARVGEWGDSPQDNY-YMDVWGK 120
DB      61 AQKFQGRVTMTADTSTAYIELRSLKSDTAVYYCARP---FYDTLTTRYVYFQFDHWGQ 117

QY      121 GTTVIVSSGGGGGGGGGGGSDIE--LTQSPGTLISLSPGERATFSCRSHSIRSRVA 178
DB      118 GTWVTVSSGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

QY      179 WYQHKPGQAPRLVIHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGAS 238
DB      178 WYQKPGQAPRLMYGASRRATGVPDFRFGSGSGTDFTLTISRLEPEDFAVYYCQVYATS 237

QY      239 SYTFGQGTKLK 251
DB      238 PRTFGQGTLEIK 250

RESULT 9
US-60-776-665-26
; Sequence 26, Application US/60776665
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523PDI
; CURRENT FILING DATE: 2006-02-27
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 26
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-776-665-26

Query Match      65.6%; Score 884; DB 8; Length 251;
Best Local Similarity 68.4%; Pred. No. 1.7e-46;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

QY      2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHVVRQAPGQRFEMMGWINPYGNKKEF 61
DB      1 QVQLVQSGVEVKKPGASVKVSCKASGYTFNSHGISWVRQAPGQGLEWVGWISGHDSTKY 60

QY      62 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVYICARVGEWGDSPQDNY-YMDVWGK 120
DB      61 AQKFQGRVTMTADTSTAYIELRSLKSDTAVYYCARP---FYDTLTTRYVYFQFDHWGQ 117

QY      121 GTTVIVSSGGGGGGGGGGGSDIE--LTQSPGTLISLSPGERATFSCRSHSIRSRVA 178
DB      118 GTWVTVSSGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

QY      179 WYQHKPGQAPRLVIHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGAS 238
DB      178 WYQKPGQAPRLMYGASRRATGVPDFRFGSGSGTDFTLTISRLEPEDFAVYYCQVYATS 237

QY      239 SYTFGQGTKLK 251
DB      238 PRTFGQGTLEIK 250

RESULT 10
US-11-266-444-22
; Sequence 22, Application US/11266444
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523PDI
; CURRENT FILING DATE: 2005-11-04
; NUMBER OF SEQ ID NOS: 3239
; SEQ ID NO 22
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-22

Query Match      65.6%; Score 883; DB 6; Length 251;
Best Local Similarity 68.4%; Pred. No. 2e-46;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

QY      2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHVVRQAPGQRFEMMGWINPYGNKKEF 61
DB      1 QVQLVQSGVEVKKPGASVKVSCKASGYTFNSHGISWVRQAPGQGLEWVGWISGHDSTKY 60

QY      62 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVYICARVGEWGDSPQDNY-YMDVWGK 120
DB      61 AQKFQGRVTMTADTSTAYIELRSLKSDTAVYYCARP---FYDTLTTRYVYFQFDHWGQ 117

QY      121 GTTVIVSSGGGGGGGGGGGSDIE--LTQSPGTLISLSPGERATFSCRSHSIRSRVA 178
DB      118 GTWVTVSSGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

QY      179 WYQHKPGQAPRLVIHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGAS 238
DB      178 WYQKPGQAPRLMYGASRRATGVPDFRFGSGSGTDFTLTISRLEPEDFAVYYCQVYATS 237

QY      239 SYTFGQGTKLK 251
DB      238 PRTFGQGTLEIK 250

RESULT 11
US-11-266-444-28
; Sequence 28, Application US/11266444
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523PDI
; CURRENT FILING DATE: 2005-11-04
; NUMBER OF SEQ ID NOS: 3239
; SEQ ID NO 28
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-28
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; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-28

Query Match      65.6%; Score 883; DB 6; Length 251;
Best Local Similarity 67.2%; Pred. No. 2e-46;
Matches 174; Conservative 27; Mismatches 40; Indels 18; Gaps 4;

Qy 2 QVLEQSGAEVKKPGASVKVSQCOASGYRFSNFTVHVVRQAPGQRFENMGWINPYNGNKEF 61
Db 1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSNHGISWVRQAPGQGLEWVGWISGDDSTKY 60
Qy 62 SAKFQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGEWGDSP---QDNY---Y 114
Db 61 AQKFGQGRVTMTADTSTAYIELSLKSDDTAVYYCAR-----PFYDILTSYVFQY 111
Qy 115 MDVWGKGTITVIVSSGGSGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSHSI 172
Db 112 FDHWGQGTMTVIVSSGGSGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSV 171
Qy 173 RSRVAVYQHKGPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYYC 232
Db 172 TRGWAVYQKPGQAPRLMTYGASRRATGVPDRFSGSGGTDFTLTISRLEPEDFAVYYC 231
Qy 233 QVYGASSYTFGQGTCLERK 251
Db 232 QQVATSPRTFGQGTLEIK 250

RESULT 12
US-11-266-444-33
; Sequence 33, Application US/11266444
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimula
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11-266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-33

Query Match      65.6%; Score 883; DB 6; Length 251;
Best Local Similarity 67.2%; Pred. No. 2e-46;
Matches 174; Conservative 27; Mismatches 40; Indels 18; Gaps 4;

Qy 2 QVLEQSGAEVKKPGASVKVSQCOASGYRFSNFTVHVVRQAPGQRFENMGWINPYNGNKEF 61
Db 1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSNHGISWVRQAPGQGLEWVGWISGDDSTKY 60
Qy 62 SAKFQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGEWGDSP---QDNY---Y 114
Db 61 AQKFGQGRVTMTADTSTAYIELSLKSDDTAVYYCAR-----PFYDILTSYVFQY 111
Qy 115 MDVWGKGTITVIVSSGGSGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSHSI 172
Db 112 FDHWGQGTMTVIVSSGGSGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSV 171
Qy 173 RSRVAVYQHKGPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYYC 232
Db 172 TRGWAVYQKPGQAPRLMTYGASRRATGVPDRFSGSGGTDFTLTISRLEPEDFAVYYC 231
Qy 233 QVYGASSYTFGQGTCLERK 251
Db 232 QQVATSPRTFGQGTLEIK 250

RESULT 13
US-11-266-444-43
; Sequence 43, Application US/11266444
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimula
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11-266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-43

Query Match      65.6%; Score 883; DB 6; Length 251;
Best Local Similarity 68.4%; Pred. No. 2e-46;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQCOASGYRFSNFTVHVVRQAPGQRFENMGWINPYNGNKEF 61
Db 1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSNHGISWVRQAPGQGLEWVGWISGDDSTKY 60
Qy 62 SAKFQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGEWGDSPQDNY-YMDVMGK 120
Db 61 AQKFGQGRVTMTADTSTAYIELSLKSDDTAVYYCARP---FYDILTYSYVFQYFDHWGQ 117
Qy 121 GTTVIVSSGGSGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSHSIRSRVA 178
Db 118 GTMTVIVSSGGSGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177
Qy 179 WYQHKPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYYCQVYAS 238
Db 178 WYQKPGQAPRLMLMYGTSRRATGVPDRFSGSGGTDFTLTISRLEPEDFAVYYCQVYAS 237
Qy 239 SYTFGQGTCLERK 251
Db 238 PRTFGQGTLEIK 250

RESULT 14
US-11-266-444-127
; Sequence 127, Application US/11266444
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimula
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11-266,444
```

```
Db 112 FDHWGQGTMTVIVSSGGSGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSV 171
Qy 173 RSRVAVYQHKGPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYYC 232
Db 172 TRGWAVYQKPGQAPRLMLMYGTSRRATGVPDRFSGSGGTDFTLTISRLEPEDFAVYYC 231
Qy 233 QVYGASSYTFGQGTCLERK 251
Db 232 QQVATSPRTFGQGTLEIK 250

RESULT 13
US-11-266-444-43
; Sequence 43, Application US/11266444
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimula
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11-266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-43

Query Match      65.6%; Score 883; DB 6; Length 251;
Best Local Similarity 68.4%; Pred. No. 2e-46;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQCOASGYRFSNFTVHVVRQAPGQRFENMGWINPYNGNKEF 61
Db 1 QVQLVQSGVEVKKPGASVKVSCKASGYTFSNHGISWVRQAPGQGLEWVGWISGDDSTKY 60
Qy 62 SAKFQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGEWGDSPQDNY-YMDVMGK 120
Db 61 AQKFGQGRVTMTADTSTAYIELSLKSDDTAVYYCARP---FYDILTYSYVFQYFDHWGQ 117
Qy 121 GTTVIVSSGGSGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSHSIRSRVA 178
Db 118 GTMTVIVSSGGSGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177
Qy 179 WYQHKPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYYCQVYAS 238
Db 178 WYQKPGQAPRLMLMYGTSRRATGVPDRFSGSGGTDFTLTISRLEPEDFAVYYCQVYAS 237
Qy 239 SYTFGQGTCLERK 251
Db 238 PRTFGQGTLEIK 250

RESULT 14
US-11-266-444-127
; Sequence 127, Application US/11266444
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimula
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11-266,444
```

Mon Mar 20 08:51:24 2006

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Qy      121 GTTIVSSGGGSGGGGGGGDIE--LTQSPGTLSLSPGERATFSCRSHSIRSRVA 178
       ||| ||||| ||||| ||||| : ||||| ||||| ||||| ||||| : |||
Db      118 GTWTVSSGGGSGGGGGGGGALETLTQSPTLSLSPGERATLSCRASQSVTRGMVA 177
       ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Qy      179 WYQHKGQAQLRVTHGVSNRASGISDRFGSSGSCTDFLTITRVEPEDFALYYCOVYGAS 238
       ||| ||||| ::||| :||| :||| :||| :||| :||| :||| :|||
Db      178 WYQQKQPQAQLRLMYGASRRATGVDRFGSSGSCTDFLTILSRLEPEDFANYCQOYATS 237
       ||| ||||| ::||| :||| :||| :||| :||| :||| :||| :|||
Qy      239 SYTFQGQTKLERK 251
       ||||| :|||
Db      238 PRTFQGTRLRK 250
       ||||| :|||

Search completed: March 20, 2006, 07:49:46
Job time : 105 secs
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; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 127
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-127

Query Match      65.6%; Score 883; DB 6; Length 251;
Best Local Similarity 68.1%; Pred. No. 2e-46;
Matches 173; Conservative 29; Mismatches 44; Indels 8; Gaps 3;

QY      2 QVQLEQSGAEVKKPGASVKVSQAQSGVRFSPNFTVHVVRQAPGQRFEMWGHNIPYNGNKEF 61
Db      1 QVQLVQSGDEVKKPGASVKYSCRASGYTFFSNHGISWVRQAPGQGLEWVGWISGHDSTKY 60

QY      62 SAKFQDRVFTADTSAANTAYMELRSLRSADTAVVYCARVGEWGWDDSPQDN--YYMDVWG 119
Db      61 AQKQFQRVMTADTSTSTAYIELRSLKSDTAVVYCAR---PPYDILTSTVVFHYDDVWG 116

QY      120 KGFTTVTVSSGGGGSGGGGGGGGGSDIE--LTQSPGTLTSLSPGERATPFCSSSHISRRV 177
Db      117 QGTMVTVTVSSGGGGSGGGGGGGGGSALETTTLTQSPDTLTSLSPGERATLSCRASQSVTRGW 176

QY      178 AWYQHKPGQAPRLVTHGVSNRACISDRFSGSGSGTDFTLTITRVEPEDEALYYCQVYGA 237
Db      177 AWYQQKPGQAPRLMLMYGTSRATGVDPDRFSGSESGTDFTLTISRLEPEDFAVYYCQYAT 236

QY      238 SSYTFQGGTKLERK 251
Db      237 SPRTFGQGTREIK 250

```

```

RESULT 15
US-60-735-988-22
; Sequence 22, Application US/60735988
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulators
; FILE REFERENCE: PF523PP9
; CURRENT APPLICATION NUMBER: US/60/735,988
; CURRENT FILING DATE: 2005-11-14
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 22
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-735-988-22

```

|    | Query Match           | 65.6%   | Score 883;       | DB 8;          | Length 251; |         |
|----|-----------------------|---|------------------|----------------|-------------|---------|
|    | Best Local Similarity | 68.4%   | Pred. No. 2e-46; | Mismatches 46; | Indels 6;   | Gaps 3; |
|    | Matches 173;          | Conservative  | 28;              |                |             |         |
| Qy | 2                     | QVQLEQSGAEYVKKPGASVKVSCQASGYRFSNFTVHVRQAPQGRFEWGWGNIYPYNGNKEF | 61               |                |             |         |
| Db | 1                     | QVQLVQSGAEYVKKPGASVKVSCQASGYRFSNFTVHVRQAPQGRFEWGWGNIYPYNGNKEF | 60               |                |             |         |
| Qy | 62                    | SAKQDRVTFTADTSANTAYMELRLSGADTAVYYCARVGEWGWDPDSQDNY - YMDVWGK  | 120              |                |             |         |
| Db | 61                    | SAKQDRVTFTADTSANTAYMELRLSGADTAVYYCARVGEWGWDPDSQDNY - YMDVWGK  | 117              |                |             |         |

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:46:30 ; Search time 16 Seconds  
(without alignments)  
1509.400 Million cell updates/sec

Title: US-09-673-707-1  
Perfect score: 1347  
Sequence: 1 MQVLEQSGAEVKKPGASVK.....QVYGASSYTFGGTKLERK 251

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID     | Description        |
|------------|-------|-------|--------|----|--------|--------------------|
| 1          | 718   | 53.3  | 249    | 2  | S41374 | single chain Fv an |
| 2          | 688.5 | 51.1  | 268    | 2  | A56446 | Ig heavy chain V r |
| 3          | 656   | 48.7  | 233    | 2  | J53322 | p53 specific singl |
| 4          | 466   | 34.6  | 129    | 2  | S36260 | Ig heavy chain V r |
| 5          | 456   | 33.9  | 129    | 2  | S46393 | Ig heavy chain V r |
| 6          | 448   | 33.3  | 109    | 2  | H30601 | Ig kappa chain V-I |
| 7          | 445   | 33.0  | 109    | 2  | G30601 | Ig kappa chain V-I |
| 8          | 444   | 33.0  | 109    | 2  | F30601 | Ig kappa chain V-I |
| 9          | 443   | 32.9  | 108    | 2  | C30608 | Ig kappa chain V-I |
| 10         | 441.5 | 32.8  | 124    | 2  | S19665 | Ig heavy chain V r |
| 11         | 441   | 32.7  | 107    | 2  | PH0965 | Ig kappa chain V r |
| 12         | 439   | 32.6  | 124    | 2  | S20633 | Ig kappa chain - h |
| 13         | 438.5 | 32.6  | 114    | 2  | S46375 | Ig kappa chain V-J |
| 14         | 437   | 32.4  | 109    | 2  | S30601 | Ig kappa chain V-I |
| 15         | 437   | 32.4  | 123    | 2  | D33548 | Ig heavy chain V-I |
| 16         | 437   | 32.4  | 129    | 2  | S49532 | anti-Sm antibody V |
| 17         | 436   | 32.4  | 109    | 2  | G30607 | Ig kappa chain V-I |
| 18         | 436   | 32.4  | 109    | 2  | D30601 | Ig kappa chain V-I |
| 19         | 435   | 32.3  | 129    | 1  | K3HUHA | Ig kappa chain pre |
| 20         | 435   | 32.3  | 129    | 2  | S46369 | Ig light chain var |
| 21         | 435   | 32.3  | 134    | 2  | S38643 | Ig kappa chain V r |
| 22         | 434   | 32.2  | 109    | 2  | C30601 | Ig kappa chain V-I |
| 23         | 434   | 32.2  | 129    | 1  | K3HUHI | Ig kappa chain pre |
| 24         | 434   | 32.2  | 130    | 2  | S20637 | Ig kappa chain V r |
| 25         | 433   | 32.1  | 109    | 2  | A30608 | Ig kappa chain V-I |
| 26         | 433   | 32.1  | 129    | 2  | A32274 | Ig kappa chain pre |
| 27         | 433   | 32.1  | 144    | 2  | B30502 | Ig heavy chain V r |
| 28         | 432   | 32.1  | 109    | 2  | F44151 | Ig kappa chain V r |
| 29         | 432   | 32.1  | 148    | 2  | S29257 | Ig heavy chain V r |

30 431.5 32.0 118 2 S36265 Ig heavy chain V r  
31 430.5 32.0 118 2 PH1666 Ig heavy chain V r  
32 430 31.9 109 2 PH0963 Ig kappa chain V r  
33 430 31.9 109 2 F30607 Ig kappa chain V-I  
34 429 31.8 109 2 S47181 Ig kappa chain - h  
35 427 31.7 109 1 K3HUSI Ig kappa chain V-I  
36 426 31.6 109 1 K3HUWL Ig kappa chain V-I  
37 426 31.6 128 2 S20636 Ig kappa chain V r  
38 425 31.6 127 2 PH0955 Ig heavy chain V r  
39 424.5 31.5 114 2 PH1667 Ig heavy chain V r  
40 424 31.5 109 1 K3HUTI Ig kappa chain V-I  
41 424 31.5 627 2 S14683 Ig mu chain precur  
42 423.5 31.4 108 2 H44151 Ig kappa chain V r  
43 423.5 31.4 136 2 S31600 Ig heavy chain V r  
44 422.5 31.4 131 2 S40346 Ig kappa chain V-J  
45 422 31.3 108 1 K3HUB6 Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S41374  
single chain Fv antibody - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: S41374  
R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A:Description: Construction and functional characterization of a single chain Fv anti  
A:Reference number: S41374  
A:Accession: S41374  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-249 <ART>  
A:Cross-references: UNIPARC:UPI000017C74A; EMBL:Z29480

Query Match 53.3%; Score 718; DB 2; Length 249;  
Best Local Similarity 55.5%; Pred No. 4,6e-47;  
Matches 142; Conservative 38; Mismatches 60; Indels 16; Gaps 3;  
Qy 2 QVLEQSGAEVKKPGASVKVSQASGRYSFTVHVRQAPQRFEMWGNIPYNGNKEF 61  
Db 1 QVQLQSGAEVLRPGASVKLSCTASGPNFKDDYIHVKQRPEKGLEWIAIPASGNVKY 60  
Qy 62 SAKQDRVTFTADTSANTAYMELSLRSADTAVYICARVGEWDDSDPDNYI--MDVWG 119  
Db 61 VPREFQDKATITADTSSNTAYLLLSLTSEDVAVYICAR-----RDTLYTSLGYWG 110  
Qy 120 KGTTVIVSSGGSGGGGGGGSDIELTQSPGTLSPGERATPFCSSHSI-----RSR 175  
Db 111 QGSTVTVSSRRGGGGGGGGSDIELTQSPVVPVPGSSVSISCRSSKSLLYSDGDS 170  
Qy 176 RVANYQHKPGQAPRLVHGVNSRASGISDRFSGSGGDTFTLTITRVPPEPFPALYQCQY 235  
Db 171 YLFWFLQPGQSPQLLYRKNLASGVPDRFSGSGGTFTLIRSRVEAEADVGVYTCMQH 230  
Qy 236 GASSYTFGGTKLERK 251  
Db 231 REYPLTFGAGTKLELK 246

RESULT 2

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/c)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C:Accession: A56446  
R:Tang, P.M.; Poltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally iden  
A:Reference number: A56446; MUID:95229583; PMID:7713873  
A:Accession: A56446

```
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-268 <TAN>
A:Cross-references: UNIPARC:UPI000017C6D0; GB:U20617
C:Keywords: heterotetramer; immunoglobulin

Query Match      51.1%; Score 688.5; DB 2; Length 268;
Best Local Similarity 53.1%; Pred. No. 8.3e-45;
Matches 135; Conservative 38; Mismatches 62; Indels 19; Gaps 3;

QY 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVVRQAPQGRFEWGMWINPYNGNKEF 61
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 3 QVKLQESGAEVKKPGASVKLSCTTSFNKIDTYMHVVKRPEQGLEWGMWINPYNGNKEF 62
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 62 SAKFQDRVTFADTTSANTAYMELRSRSDTAVVYCARVGEWGDSDSPQDNYVM---DV 117
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 63 DPKFQGRVTFADTTSANTAYMELRSRSDTAVVYCARVGEWGDSDSPQDNYVM---SYLTRYENY 109
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 118 WKGKTTVIVSGGGGGGGGGGGDIETQSPGTLSPGERATFSCRSRSHSIRSRV 177
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 110 WGGKTTVIVSGGGGGGGGGGGDIETQSPALMSASLGEKVTMSCRASSVNF--I 167
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 178 AWYQHPQAPRLVIHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYVCQYGA 237
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 168 YWYQKSDASPKLWVYVYTHLPQGPVAPRFGSGSGNSYSLTSSMEGEDAATYVCQOFTS 227
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:

QY 238 SSVTFGGGKLERK 251
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 228 SPFTFGGKLEIK 241
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:

RESULT 3
JC5322
p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950; PMID:9016757
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Cross-references: UNIPARC:UPI000017C3DE
A:Experimental source: hybridoma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match      48.7%; Score 656; DB 2; Length 233;
Best Local Similarity 54.3%; Pred. No. 2e-42;
Matches 134; Conservative 35; Mismatches 60; Indels 18; Gaps 3;

QY 6 EQSGAEVKKPGASVKVSQASGYRFSNFTVHVVRQAPQGRFEWGMWINPYNGNKEFSAKF 65
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 QESGAELVRSGASVKLSCTTSFNIDYMHVVKRPEQGLEWIGRIDPENGDADMTRSS 60
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 66 QDRVTFADTTSANTAYMELRSRSDTAVVYCARVGEWGDSDSPQDNYVMDVWGKTTVI 125
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 GVKATMTADTTSNTAYLQSLTSEDTAVVYCYC-----NAGMDYWGQGITVT 106
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 126 VSSGGGGGGGGGGGGGGDIETQSPGTLSPGERATFSCRSRSHSIRSRV---WYQH 182
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 107 VSSGGGGGGGGGGGGGGDIETQSPALVSLGORATISCRASKSVSTSGSYMHWNQ 166
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 183 KPGQAPRLVIHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYVCQYGASVTF 242
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 167 KPGQAPRLVIHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYVCQYHIRELTRSE 226
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 243 GQGTKLE 249
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 227 G-GTKLE 232
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

```
RESULT 4
S36260
Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36260
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36260
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-129 <GRI>
A:Cross-references: UNIPARC:UPI0000118DEB; EMBL:Z18851; NID:g33124; PIDN:CAA79303.1; P1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match      34.8%; Score 466; DB 2; Length 129;
Best Local Similarity 70.0%; Pred. No. 2.1e-28;
Matches 91; Conservative 12; Mismatches 23; Indels 4; Gaps 2;

QY 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVVRQAPQGRFEWGMWINPYNGNKEF 61
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISVWRQAPQGLEWGMWISAYNGNTNY 60
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 62 SAKFQDRVTFADTTSANTAYMELRSRSDTAVVYCARVGEWGDSDS---PDNYYMDVW 118
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 AQKLGKRVMTTDTSTAYMELRSRSDTAVVYCAR-DSFGYCSSTSCPYYVMDVW 119
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 119 KGKTTVIVSS 128
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 120 KGKTTVTVSS 129
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 5
S46393
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46393
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage b1
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46393
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <FIG>
A:Cross-references: UNIPARC:UPI000011663A; EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; P1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match      33.9%; Score 456; DB 2; Length 129;
Best Local Similarity 69.0%; Pred. No. 1.2e-27;
Matches 89; Conservative 10; Mismatches 28; Indels 2; Gaps 1;

QY 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVVRQAPQGRFEWGMWINPYNGNKEF 61
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGMHWVRQAPQGLEWGMWINPNSGGTNY 60
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 62 SAKFQDRVTFADTTSANTAYMELRSRSDTAVVYCARVGEWGDSDSP---QDNYVMDVWG 119
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 AQKQGVMTTDTSTISAYMELSRSDTAVVYCARSDSAYYDSSGYYSANYVMDVWG 120
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 120 KGTTIVVSS 128
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 KGTTVTVSS 129
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 6
```

C:Accession: F30601  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol  
J. Immunol. 142, 3158-3163, 1999  
A:Title: Structural and idiotypic characterization of the L chains of human IGM autoant  
A:Reference number: A30601; MUID:9215279; PMID:2496160  
A:Accession: F30601  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-109 <GON>  
A:Cross-references: UNIPARC:UPI0000176AE8  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 33.0%; Score 444; DB 2; Length 109;  
Best Local Similarity 76.9%; Pred. No. 8.1e-27;  
Matches 83; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 144 DIELTQSPGTLISLSPGERATFSCRSSHSIRRRVAVYQHKPGQAPRLVIHGVSNRAGIS 203  
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSRYLAWYQKPGQAPRLLIYGASSRATGIP 60

Qy 204 DRFGSGSGTGDTLTITRVEPEPFALYICQVYGASSYTFGGGTXLERK 251  
Db 61 DRFGSGSGTGDTLTITRVEPEPFALYICQVYGASSYTFGGGTXLERK 108

RESULT 9  
C30608  
Ig kappa chain V-III region (Pie) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: C30608  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol  
J. Immunol. 142, 3158-3163, 1999  
A:Title: Structural and idiotypic characterization of the L chains of human IGM autoant  
A:Reference number: A30601; MUID:9215279; PMID:2496160  
A:Accession: C30608  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-108 <GON>  
A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE3  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 32.9%; Score 443; DB 2; Length 108;  
Best Local Similarity 76.9%; Pred. No. 9.5e-27;  
Matches 83; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 144 DIELTQSPGTLISLSPGERATFSCRSSHSIRRRVAVYQHKPGQAPRLVIHGVSNRAGIS 203  
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSRYLAWYQKPGQAPRLLIYGASSRATGIP 60

Qy 204 DRFGSGSGTGDTLTITRVEPEPFALYICQVYGASSYTFGGGTXLERK 251  
Db 61 DRFGSGSGTGDTLTITRVEPEPFALYICQVYGASSYTFGGGTXLERK 108

RESULT 10  
S19665  
Ig heavy chain V region (alpha-phOx15) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 20-Jun-2000  
C:Accession: S19665; S24442  
R:Marks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter  
J. Mol. Biol. 222, 581-597, 1991  
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p  
A:Reference number: S19663; MUID:92085276; PMID:1748994  
A:Accession: S19665  
A:Molecule type: mRNA  
A:Residues: 1-124 <MAR>  
A:Cross-references: UNIPARC:UPI0000176B80; EMBL:X61647

Mon Mar 20 08:51:24 2006

R; Jones, P. T.  
Submitted to the EMBL Data Library, October 1991  
A; Reference number: S24442  
A; Accession: S24442  
A; Molecule type: mRNA  
A; Residues: 1-40, 'GUSGWDGSALTVMVTQSILOK', 61-118, 'T', 120-124 <JON>  
A; Cross-references: UNIPARC:UP10000115F5; EMBL: X61647; NID: G37667; PIDN: CA443828.1; PID: 10000115F5  
A; Note: the difference for residues 41-60 results from misplacement of 10 bases in the s  
A; Superfamily: immunoglobulin V region; immunoglobulin homology  
C; Keywords: heterotetramer; immunoglobulin  
P: 15-98/Domain: immunoglobulin homology <IMV>

|   | Query Match           | 32.8%  | Score 441.5;       | DB 2;  | Length 124;    |
|---|-----------------------|--|--------------------|--------|----------------|
|   | Best Local Similarity | 65.6%;   | Pred. NO. 1.4e-26; |        |                |
|   | Matches               | 86;  | Conservative       | 14;    | Mismatches 20; |
|   |                       |  |                    | Indels | 11; Gaps 2     |
| y | 2                     | QVQLQSGAEVKKPGASVKVSQCOAGYRFSNFTVHVVRRPQGRFEWGMWNPYNGNKEF  | 61                 |        |                |
| b | 1                     | QVQLVQSGAEVKKPGASVKVSQKAGYTFSTYGISWVRPQPGGLEWGMWISAYNGNTKY | 60                 |        |                |
| y | 62                    | SAKFQDRVFTADTSANTAYMELRSLRSADTAVYVCARVGEWGDSDSPOD----      | 117                |        |                |
| b | 61                    | QKLCQRYMTWTTDTSNTAYMELRSLRSDTAVYVCRL-----LPKRTATLHYHIDV    | 113                |        |                |

RESULT 11

PH0965  
IG kappa chain V region (G6+ CLL-BRA) - human (fragment)

PH0965  
C:Species: Homo sapiens (man)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: PH0965  
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291  
A:Accession: PH0965  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-107 <MAR>

A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176A2B  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-21/Region: framework 1  
F:14-89/Domain: immunoglobulin homology <IMM>  
F:22-32/Region: complementarity-determining 1  
F:33-48/Region: framework 2  
F:49-54/Region: complementarity-determining 2  
F:55-87/Region: framework 3  
F:88-95/Region: complementarity-determining 3

|     | Query Match           | 32.7%                    | Score 441;         | DB 2;          | Length 107; |
|-----|-----------------------|--------------------------|--------------------|----------------|-------------|
|     | Best Local Similarity | 78.1%                    | Pred. No. 1.3e-26; |                |             |
|     | Matches 82;           | Conservative 12;         | Mismatches 11;     | Indels 0;      | Gaps 0;     |
| 147 | LTQSPGTLSPGGERATF     | CGRSHSTRSR               | RVAMVQHKPGQAPRLV   | IHGVSNRAGISDRP | 206         |
|     |                       |                          |                    |                |             |
|     |                       |                          |                    |                |             |
|     |                       |                          |                    |                |             |
| 2   | LTQSPGTLSPGGERATL     | SCRASQSVSSYLAWYQKPGQAPRL | IYGASSRATGIPDRF    | 61             |             |
|     |                       |                          |                    |                |             |
|     |                       |                          |                    |                |             |
|     |                       |                          |                    |                |             |
| 207 | SGSGGTFDFTLTIR        | VEPEDFALYYCQVY           | GASSYTFGQGTKLERK   | 251            |             |
|     |                       |                          |                    |                |             |
|     |                       |                          |                    |                |             |
|     |                       |                          |                    |                |             |
| 62  | SGSGGTFDFTLTISR       | PEPFVAVYYCQVY            | GSSRYTFGQGTKVEIK   | 106            |             |
|     |                       |                          |                    |                |             |
|     |                       |                          |                    |                |             |
|     |                       |                          |                    |                |             |

RESULT 12  
S20633  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 22-Nov-1993 #sequence\_revision 14-Jul-1995 #text\_change 21-Jan-2000  
C:Accession: S20633

R;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.  
submitted to the EMBL Data Library, April 1992

A:Reference number: S20631

A:Accession: S20633

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-124 <LEE>

A:Cross-references: UNIPARC:UPI00001163D9; EMBL:Z11891; NID:G331

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:Keywords: heterotetramer; immunoglobulin

F:32-107/Domain: immunoglobulin homology xIMM>

|    |                       |   |                   |       |             |                      |
|----|-----------------------|---|-------------------|-------|-------------|----------------------|
|    | Query Match           | 32.6%   | Score 439;        | DB 2; | Length 124; |                      |
|    | Best Local Similarity | 77.4%;  | Pred.No. 2.2e-26; |       |             |                      |
|    | Matches               | 82;   | Conservative      | 12;   | Mismatches  | 12; Indels 0; Gaps 0 |
| Qy | 144                   | DIETQSPGTLTSLSPGERATFSCRSHSIRSRVANYQHKGPGAPRLVIHGVSNRASGIS                          | 203               |       |             |                      |
|    | :                     | : |                   |       |             |                      |
| Dd | 17                    | EIVLTQSPGTLTSLSPGERATLISCRASQSVSYILAWYQQKPKGAPRLIIYTGSRRATGP                        | 76                |       |             |                      |
|    | :                     | : |                   |       |             |                      |
| Qy | 204                   | DRFGSGSGTDFTLTITRVEDPDAFYCYCQYGASSYTFGGGTKLE  | 249               |       |             |                      |
|    | :                     | : |                   |       |             |                      |
| Dd | 77                    | DRVSGSGSGTDFTLTISRLEDPAFYCYCQYGSSSYTFGGGTKLE  | 122               |       |             |                      |
|    | :                     | : |                   |       |             |                      |

```

RESULT 13
S46375
Ig kappa chain V-J region (T33-5) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46375; S38648
R:Benshamon, C.; Chastagnet, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(DJ)
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46375
A:Molecule type: mRNA
A:Residues: 1-114 <GEN>
A:Cross-references: UNIPARC:UPI00001165A8; EMBL:Z27176; NID:9415967; PIDN:C
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:20-95/Domain: immunoglobulin homology <IMM>

```

|    |                       |   |                    |                |                   |
|----|-----------------------|---|--------------------|----------------|-------------------|
|    | Query Match           | 32.6%   | Score 438.5;       | DB 2;          | Length 114;       |
|    | Best Local Similarity | 78.0%;  | Pred. No. 2.2e-26; |                |                   |
|    | Matches               | 85;   | Conservative 11;   | Mismatches 12; | Indels 1; Gaps 1; |
| QY | 144                   | DIEITQSPGTTLSLPGERATSCSSHSIRSRVAVYQHKGQAPRLVIHGVSNRASGIS                            | 203                |                |                   |
|    | :                     | : |                    |                |                   |
| Db | 5                     | EIVLTQSPGTTLSLPGERATSLCRASQSISSSYLAWYQQKPGQAPRLIYGASSRATGP                          | 64                 |                |                   |
| QY | 204                   | DRFGSGSGDTFTTITRVBEDPALYCQVYGAS-SYTFQGCGTKLERK                                      | 251                |                |                   |
| nB | 65                    | DRFGSGSGDTFTTISRLEPEDPAVYYCOOYGSSPPYTFQGCKLEIK                                      | 113                |                |                   |

RESULT 14  
B30601  
Ig kappa chain V-III region (Glo) - human (fragment)  
C.Species: Homo sapiens (man)  
C.Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
C.Accession: B30601  
J.Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Car-  
r, J. Immunol. 142, 3158-3163, 1989  
A.Title: Structural and idiotypic characterization of the L chains of human  
A.Reference number: A30601; MUID:89215279; PMID:2496160  
A.Accession: B30601  
A.Status: preliminary  
A.Molecule type: protein  
A.Residues: 1-109 <GON>  
A.Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE7  
A.Cross-family: immunoglobulin V region; immunoglobulin homology  
C.Keywords: heterotrimer; immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

[illegible]

RESULT 15

IG heavy chain V-1 region (WIL2) - human  
 D33548  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
 C:Accession: D33548  
 R:Kipps, T. J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
 A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expressed in B-1 cells  
 A:Reference number: A33548; MUID:89345575; PMID:2503826  
 A:Accession: D33548  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-123 <KIP>  
 A:Cross-references: UNIPARC:UPI0000176909  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

|                       |        |   |                |                   |
|-----------------------|--------|---|----------------|-------------------|
| Query Match           | 32.4%  | Score 437;  | DB 2;          | Length 123;       |
| Best Local Similarity | 66.9%; | Pred. No. 3.1e-36;  |                |                   |
| Matches               | 85;    | Conservative 9;   | Mismatches 29; | Indels 4; Gaps 1; |
| QY                    | 2      | OYOLEGSGAEVKKPGASVKVSCASGYRFSNFTVTHVVRQAPGGRFEGWGMGINPYNGNKEF | 61             |                   |
| DB                    | 1      | QVQLVDSGAEVKKPGASVKVSCASGYTFTHYMHVVRQAPGGGLEWGMGINPNSGGTNY    | 60             |                   |
| QY                    | 62     | SAKFQDVRVTFATDSANTAYMELSLRLSADTAVVYCARVGEWGDSDSPQDNYTMDVYWGK  | 121            |                   |
| DB                    | 61     | AEKFGQRVITRQTSINTAYMELSLRLSDDTAVVYCARASYCGYD----              | CYFFDITWGQ     | 116               |
| QY                    | 122    | TTTVIVSS  | 128            |                   |
| DB                    | 117    | TLTVSS  | 123            |                   |

Search completed: March 20, 2006, 07:48:06  
Job time : 17 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:47:50 ; Search time 216 Seconds  
(without alignments)  
1605.883 Million cell updates/sec

Title: US-09-673-707-1

Perfect score: 1347

Sequence: 1 MQVLEQSGAEVKKPGASVK.....QVYGASSYTFQGKLERK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2\_6/ptodata/1/paa/US074\_COMB.pep.\*
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- 50: /cgn2\_6/ptodata/1/paa/US606\_COMB.pep.\*
- 51: /cgn2\_6/ptodata/1/paa/US607\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                  | Description       |
|------------|-------|-------------|--------|----|---------------------|-------------------|
| 1          | 1347  | 100.0       | 251    | 26 | US-09-673-707-1     | Sequence 1, Appli |
| 2          | 949   | 70.5        | 245    | 1  | PCT-US01-19110-1896 | Sequence 1896, Ap |
| 3          | 949   | 70.5        | 245    | 1  | PCT-US02-36496-1896 | Sequence 1896, Ap |
| 4          | 949   | 70.5        | 245    | 28 | US-09-880-748-1896  | Sequence 1896, Ap |
| 5          | 949   | 70.5        | 245    | 32 | US-10-293-418-1896  | Sequence 1896, Ap |
| 6          | 949   | 70.5        | 245    | 40 | US-11-054-515-1896  | Sequence 1896, Ap |
| 7          | 949   | 70.5        | 245    | 51 | US-60-725-626-1896  | Sequence 1896, Ap |
| 8          | 927.5 | 68.9        | 281    | 35 | US-10-535-764-1896  | Sequence 186, App |
| 9          | 910   | 67.6        | 247    | 1  | PCT-US02-40597-56   | Sequence 56, Appl |
| 10         | 910   | 67.6        | 247    | 1  | PCT-US04-13900-56   | Sequence 56, Appl |
| 11         | 910   | 67.6        | 247    | 33 | US-10-322-673-56    | Sequence 56, Appl |
| 12         | 910   | 67.6        | 247    | 39 | US-10-981-465-56    | Sequence 56, Appl |
| 13         | 910   | 67.6        | 247    | 39 | US-10-981-621-56    | Sequence 56, Appl |
| 14         | 910   | 67.6        | 247    | 39 | US-10-981-673-56    | Sequence 56, Appl |
| 15         | 910   | 67.6        | 247    | 39 | US-10-981-691-56    | Sequence 56, Appl |
| 16         | 896.5 | 66.6        | 263    | 34 | US-10-422-628-14    | Sequence 14, Appl |
| 17         | 884   | 65.6        | 251    | 1  | PCT-US01-19110-12   | Sequence 12, Appl |
| 18         | 884   | 65.6        | 251    | 1  | PCT-US01-19110-26   | Sequence 26, Appl |
| 19         | 884   | 65.6        | 251    | 1  | PCT-US02-36496-12   | Sequence 12, Appl |
| 20         | 884   | 65.6        | 251    | 1  | PCT-US02-36496-26   | Sequence 26, Appl |
| 21         | 884   | 65.6        | 251    | 28 | US-09-880-748-12    | Sequence 12, Appl |
| 22         | 884   | 65.6        | 251    | 28 | US-09-880-748-26    | Sequence 26, Appl |
| 23         | 884   | 65.6        | 251    | 32 | US-10-293-418-12    | Sequence 12, Appl |
| 24         | 884   | 65.6        | 251    | 32 | US-10-293-418-26    | Sequence 26, Appl |
| 25         | 884   | 65.6        | 251    | 40 | US-11-054-515-12    | Sequence 12, Appl |
| 26         | 884   | 65.6        | 251    | 40 | US-11-054-515-26    | Sequence 26, Appl |
| 27         | 884   | 65.6        | 251    | 51 | US-60-725-626-12    | Sequence 12, Appl |
| 28         | 884   | 65.6        | 251    | 51 | US-60-725-626-26    | Sequence 26, Appl |
| 29         | 883   | 65.6        | 251    | 1  | PCT-US01-19110-22   | Sequence 22, Appl |
| 30         | 883   | 65.6        | 251    | 1  | PCT-US01-19110-28   | Sequence 28, Appl |
| 31         | 883   | 65.6        | 251    | 1  | PCT-US01-19110-33   | Sequence 33, Appl |
| 32         | 883   | 65.6        | 251    | 1  | PCT-US01-19110-43   | Sequence 43, Appl |
| 33         | 883   | 65.6        | 251    | 1  | PCT-US01-19110-127  | Sequence 127, App |
| 34         | 883   | 65.6        | 251    | 1  | PCT-US02-36496-22   | Sequence 22, Appl |
| 35         | 883   | 65.6        | 251    | 1  | PCT-US02-36496-28   | Sequence 28, Appl |
| 36         | 883   | 65.6        | 251    | 1  | PCT-US02-36496-33   | Sequence 33, Appl |
| 37         | 883   | 65.6        | 251    | 1  | PCT-US02-36496-43   | Sequence 43, Appl |
| 38         | 883   | 65.6        | 251    | 1  | PCT-US02-36496-127  | Sequence 127, App |
| 39         | 883   | 65.6        | 251    | 28 | US-09-880-748-22    | Sequence 22, Appl |
| 40         | 883   | 65.6        | 251    | 28 | US-09-880-748-28    | Sequence 28, Appl |
| 41         | 883   | 65.6        | 251    | 28 | US-09-880-748-33    | Sequence 33, Appl |
| 42         | 883   | 65.6        | 251    | 28 | US-09-880-748-43    | Sequence 43, Appl |
| 43         | 883   | 65.6        | 251    | 28 | US-09-880-748-127   | Sequence 127, App |
| 44         | 883   | 65.6        | 251    | 32 | US-10-293-418-22    | Sequence 22, Appl |
| 45         | 883   | 65.6        | 251    | 32 | US-10-293-418-28    | Sequence 28, Appl |

ALIGNMENTS

RESULT 1  
US-09-673-707-1  
; Sequence 1, Application US/09673707  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira H.

```
; APPLICANT: Bera, Tapan K.
; APPLICANT: Kennedy, Paul E.
; APPLICANT: Berger, Edward A.
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Immunotoxin Directed Against the HIV-1
; FILE REFERENCE: 015280-356100US
; CURRENT APPLICATION NUMBER: US/09/673,707
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: WO PCT/US99/12909
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: US 60/088,860
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:3B3(Fv) amino
; OTHER INFORMATION: acid sequence
US-09-673-707-1

Query Match 100.0%; Score 1347; DB 26; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.2e-107;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQVLEQSGAEVKKPGASVKVSQAQGYRFSNFTVHVRQAPGQRFEMWGWINPYGNKE 60
Db 1 MQVLEQSGAEVKKPGASVKVSQAQGYRFSNFTVHVRQAPGQRFEMWGWINPYGNKE 60

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Db 61 FSAKFDQRTVTADTSANTAYMELSLRSADTAVYVCARVGEWGDSPQDNYMDVWGK 120

Qy 121 GTTVIVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSISRIRRVAV 180
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Qy 121 GTTVIVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSISRIRRVAV 180
Db 121 GTTVIVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSISRIRRVAV 180

Qy 181 QHKPQAPRLVIHGVSNRAGISDRFSGSGGTDFTLTITRVEPEDFALYVCQVYGASSY 240
Db 181 QHKPQAPRLVIHGVSNRAGISDRFSGSGGTDFTLTITRVEPEDFALYVCQVYGASSY 240

Qy 241 TFGQGTKLERK 251
Db 241 TFGQGTKLERK 251

RESULT 2
PCT-US01-19110-1896
; Sequence 1896, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1896
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1896

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Best Local Similarity 73.8%; Pred. No. 1.3e-72;
Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQAQGYRFSNFTVHVRQAPGQRFEMWGWINPYGNKEF 61
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Qy 62 SAKFDQRTVTADTSANTAYMELSLRSADTAVYVCARVGEWGDSPQDNYMDVWGK 121
Db 61 SQKFDQRTVTITRDTASANTAYMELSLRSEDATVYVCAREG-----PGYYGMDVWGQ 113

Qy 122 TTVIVSSGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSISRIRRVAV 179
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Qy 180 YQHKPQAPRLVIHGVSNRAGISDRFSGSGGTDFTLTITRVEPEDFALYVCQVYGASS 239
Db 174 YQKPGQPPSLIYGASSRATGIPDRFSASGSDFTLTISRLEPEDFAVYVCQYQYG-SS 232

Qy 240 YTFGQGTKLERK 251
Db 233 ITFGQGTRLRIK 244

RESULT 3
PCT-US02-36496-1896
; Sequence 1896, Application PC/TUS0236496
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/36496
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1896
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-36496-1896

Query Match 70.5%; Score 949; DB 1; Length 245;
Best Local Similarity 73.8%; Pred. No. 1.3e-72;
Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSQAQGYRFSNFTVHVRQAPGQRFEMWGWINPYGNKEF 61
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Db 61 SQKFDQRTVTITRDTASANTAYMELSLRSEDATVYVCAREG-----PGYYGMDVWGQ 113

Qy 122 TTVIVSSGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSISRIRRVAV 179
Db 114 TMVTIVSSGGGGGGGGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 173

Qy 180 YQHKPQAPRLVIHGVSNRAGISDRFSGSGGTDFTLTITRVEPEDFALYVCQVYGASS 239
Db 174 YQKPGQPPSLIYGASSRATGIPDRFSASGSDFTLTISRLEPEDFAVYVCQYQYG-SS 232

Qy 240 YTFGQGTKLERK 251
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Db 233 ITFGQGTREIK 244

RESULT 4

US-09-880-748-1896

Sequence 1896, Application US/09880748

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1896

LENGTH: 245

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1896

Query Match 70.5%; Score 949; DB 28; Length 245;

Best Local Similarity 73.8%; Pred. No. 1.3e-72;

Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

QY 2 QVLEQSGAEVKKPGASVKVSQCASGYRFSNFTVHVRQAPGQRFEMWGHPYNGNKEF 61

Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRFLEWGWINGNNTKY 60

QY 62 SAKFQDRVTFTADTSANTATMELSLRSADTAVYICARVGEWGWDDSPQDNYMDVWGK 121

Db 61 SQKFGQRTVITRDTASATAYMELSLRSEDATVYICAREG-----PGYYGMDVWGQ 113

QY 122 TTVIVSGGGSGGGSGGGGSDIE--LTQSPGTLSPGERATFSCRSRHSIRSRVAV 179

Db 114 TMTVSSGGSGGGSGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 173

QY 180 YQHPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYICQVYGASS 239

Db 174 YQKPGQPPSLIYGASSRATGIPDRFSASGSGTDFTLTISRLEPEDFAVYICQYQY-SS 232

QY 240 YTFGQGTLEIK 251

Db 233 ITFGQGTREIK 244

RESULT 5

US-10-293-418-1896

Sequence 1896, Application US/10293418

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

QY 2 QVLEQSGAEVKKPGASVKVSQCASGYRFSNFTVHVRQAPGQRFEMWGHPYNGNKEF 61

Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRFLEWGWINGNNTKY 60

QY 62 SAKFQDRVTFTADTSANTATMELSLRSADTAVYICARVGEWGWDDSPQDNYMDVWGK 121

Db 61 SQKFGQRTVITRDTASATAYMELSLRSEDATVYICAREG-----PGYYGMDVWGQ 113

QY 122 TTVIVSGGGSGGGSGGGGSDIE--LTQSPGTLSPGERATFSCRSRHSIRSRVAV 179

Db 114 TMTVSSGGSGGGSGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 173

QY 180 YQHPGQAPRLVHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYICQVYGASS 239

Db 174 YQKPGQPPSLIYGASSRATGIPDRFSASGSGTDFTLTISRLEPEDFAVYICQYQY-SS 232

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Db 233 ITFGQGTREIK 244

RESULT 6

US-11-054-515-1896

Sequence 1896, Application US/11054515

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1896

LENGTH: 245

TYPE: PRT

|   |  |   |  |
|---|--|---|--|
| ; ORGANISM: Homo sapiens  |  | ; ORGANISM: Homo sapiens  |  |
| US-11-054-515-1896  |  | US-10-535-764-186   |  |
| Query Match   |  | Query Match   |  |
| Best Local Similarity 70.5%; Score 949; DB 40; Length 245;                              |  | Best Local Similarity 70.1%; Score 927.5; DB 35; Length 281;            |  |
| Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;                         |  | Matches 178; Conservative 24; Mismatches 39; Indels 13; Gaps 2;         |  |
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| DB 1 QVQLVQSGAEVKKPGASVKVSQAQGYRFSNFTVHVRQAPGQRFWMGWINPYNNGKEF 60                       |  | DB 25 QVQLVQSGAEVKKPGASVKVSQAQGYRFSNFTVHVRQAPGQRFWMGWINPYNNGKEF 84      |  |
| QY 62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGEWGWDDSPQDNYMDVWGK 121                      |  | QY 62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGEWGWDDSPQDNYMDV 117         |  |
| DB 61 SQKFGQGRVTITRDTSASTAYMELSLRSADTAVYCARVGEWGWDDSPQDNYMDVWGK 113                     |  | DB 85 AQKFGQGRVTITRDTSASTAYMELSLRSADTAVYCARVGEWGWDDSPQDNYMDV 135        |  |
| QY 122 TTVIVSSGGSGGGSGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSIRSRVAV 179                     |  | QY 118 WKGTTVTIVSSGGSGGGGGSDIELTQSPGTLSPGERATFSCRSRSHSIRSRV 177         |  |
| DB 114 TMVTSSGGSGGGSGGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 173                       |  | DB 136 WGQGTTLTVSSGGSGGGGGSGGGGGSEIVLTQSPGTLSPGERATLSCRAQAIGSNYL 195    |  |
| QY 180 YQKPGQAPRLVTHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYVCQVYGAS 239                    |  | QY 178 AWYQKPGQAPRLVTHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYVCQVYG 237    |  |
| DB 174 YQKPGQAPRLVTHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYVCQVYG 232                      |  | DB 196 AWYQKPGQAPRLVTHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYVCQVY 255     |  |
| QY 240 YTFGQGTGLERK 251   |  | QY 238 SSTFGQGTGLERK 251  |  |
| DB 233 ITFGQGTGLERK 244   |  | DB 256 SPYTFGQGTGLERK 269   |  |
| RESULT 7  |  | RESULT 9  |  |
| US-60-725-626-1896  |  | PCT-US02-40597-56   |  |
| ; Sequence 1896, Application US/60725626  |  | ; Sequence 56, Application PC/TUS0240597                                |  |
| ; GENERAL INFORMATION:  |  | ; GENERAL INFORMATION:  |  |
| ; APPLICANT: Ruben et al.   |  | ; APPLICANT: Human Genome Sciences, Inc.                                |  |
| ; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to B Lymphocyte Stimulat |  | ; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to TRAIL |  |
| ; FILE REFERENCE: PF523PP8  |  | ; FILE REFERENCE: PF585PCT  |  |
| ; CURRENT APPLICATION NUMBER: US/60725,626  |  | ; CURRENT APPLICATION NUMBER: PCT/US02/40597                            |  |
| ; CURRENT FILING DATE: 2005-10-13   |  | ; CURRENT FILING DATE: 2002-12-18                                       |  |
| ; NUMBER OF SEQ ID NOS: 3247  |  | ; PRIOR APPLICATION NUMBER: 60/341,237                                  |  |
| ; SEQ ID NO 1896  |  | ; PRIOR FILING DATE: 2001-12-20   |  |
| ; LENGTH: 245   |  | ; PRIOR APPLICATION NUMBER: 60/369,877                                  |  |
| ; TYPE: PRT   |  | ; PRIOR FILING DATE: 2002-04-05   |  |
| ; ORGANISM: Homo sapiens  |  | ; PRIOR APPLICATION NUMBER: 60/384,828                                  |  |
| US-60-725-626-1896  |  | ; PRIOR FILING DATE: 2002-06-04   |  |
| Query Match   |  | ; PRIOR APPLICATION NUMBER: 60/396,591                                  |  |
| Best Local Similarity 73.8%; Score 949; DB 51; Length 245;                              |  | ; PRIOR FILING DATE: 2002-07-18   |  |
| Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;                         |  | ; PRIOR FILING DATE: 2002-08-15   |  |
| QY 2 QVQLVQSGAEVKKPGASVKVSQAQGYRFSNFTVHVRQAPGQRFWMGWINPYNNGKEF 61                       |  | ; PRIOR APPLICATION NUMBER: 60/425,737                                  |  |
| DB 1 QVQLVQSGAEVKKPGASVKVSQAQGYRFSNFTVHVRQAPGQRFWMGWINPYNNGKEF 60                       |  | ; NUMBER OF SEQ ID NOS: 72  |  |
| QY 62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGEWGWDDSPQDNYMDVWGK 121                      |  | ; SEQ ID NO 56  |  |
| DB 61 SQKFGQGRVTITRDTSASTAYMELSLRSADTAVYCARVGEWGWDDSPQDNYMDVWGK 113                     |  | ; LENGTH: 247   |  |
| QY 122 TTVIVSSGGSGGGSGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSIRSRVAV 179                     |  | ; TYPE: PRT   |  |
| DB 114 TMVTSSGGSGGGSGGGGGSALETTLTQSPGTLSPGERATLSCRAQAIGSNYLAW 173                       |  |   |  |
| QY 180 YQKPGQAPRLVTHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYVCQVYGAS 239                    |  |   |  |
| DB 174 YQKPGQAPRLVTHGVSNRAGISDRFSGSGSGTDFTLTITRVEPEDFALYVCQVYG 232                      |  |   |  |
| QY 240 YTFGQGTGLERK 251   |  |   |  |
| DB 233 ITFGQGTGLERK 244   |  |   |  |
| RESULT 8  |  |   |  |
| US-10-535-764-186   |  |   |  |
| ; Sequence 186, Application US/10535764   |  |   |  |
| ; GENERAL INFORMATION:  |  |   |  |



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; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
; US-10-981-621-56

Query Match          67.6%; Score 910; DB 39; Length 247;
Best Local Similarity 69.4%; Pred. No. 2.8e-69;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy 2 QVLEQSGAEVKPGASVKSCQASGYRFSNFTVHWVQAPGORFEWMGWINPVGNGKEF 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVQSGAEVKPGASVKSCRASGYTFSTYGITVWVQAPGQGLEWMGWSAYNGKTN 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 SAKFDQRTVFTADTSANTAYMELRSASADTAVVYCARVGEWGWDDSPQDNY---YMDV 118
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VQLQGRVTWTTDTSTSTVYVMELTSLRSDDTAVVYCARRG-----NNYRFGYDFW 111
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 119 GKTTTVVSGGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRHSIRSR 176
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 GQGLTVTVSGGGGGGGGGGGGSALETTLTQSPGTLSPGERATLSCRASQSISSN 171
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 177 VAWYQHKGQAPRLVHGVNRSAGISDRFSGSGSGTDFLTITRVEPEDFALVYCOV 236
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 LAWYQQKPGAPRLIYGASSRAIGIPDRFSGSGSGTDFLTITRLEAEAFVAYYCO 231
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 237 ASSVTFGGQTKLERK 251
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 SSPITFGQTRLEIK 246
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-10-981-621-56
; Sequence 56, Application US/10981621
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585P1D1
; CURRENT APPLICATION NUMBER: US/10/981,621
; PRIOR FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-12-19

```

```

; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
; US-10-981-621-56

Query Match          67.6%; Score 910; DB 39; Length 247;
Best Local Similarity 69.4%; Pred. No. 2.8e-69;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy 2 QVLEQSGAEVKPGASVKSCQASGYRFSNFTVHWVQAPGORFEWMGWINPVGNGKEF 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVQSGAEVKPGASVKSCRASGYTFSTYGITVWVQAPGQGLEWMGWSAYNGKTN 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 SAKFDQRTVFTADTSANTAYMELRSASADTAVVYCARVGEWGWDDSPQDNY---YMDV 118
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VQLQGRVTWTTDTSTSTVYVMELTSLRSDDTAVVYCARRG-----NNYRFGYDFW 111
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 119 GKTTTVVSGGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRHSIRSR 176
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 GQGLTVTVSGGGGGGGGGGGGSALETTLTQSPGTLSPGERATLSCRASQSISSN 171
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 177 VAWYQHKGQAPRLVHGVNRSAGISDRFSGSGSGTDFLTITRVEPEDFALVYCOV 236
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 LAWYQQKPGAPRLIYGASSRAIGIPDRFSGSGSGTDFLTITRLEAEAFVAYYCO 231
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 237 ASSVTFGGQTKLERK 251
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 SSPITFGQTRLEIK 246
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-10-981-673-56
; Sequence 56, Application US/10981673
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585P1D2
; CURRENT APPLICATION NUMBER: US/10/981,673
; PRIOR FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15

```

```
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-981-673-56
```

```
Query Match      67.6%; Score 910; DB 39; Length 247;
Best Local Similarity 69.4%; Pred. No. 2.8e-69;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy  2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFQFWMGWINPYNKKEF 61
Db  1 EVQLVQSGAEVKKPGASVKVSCRASGYFTFSYGITWVRQAPGQGLEWMGWISAYNGKTN 60
Qy  62 SAKFQDRVTFTADTSANTAYMELSLRSADTAIVYCARVGEWGDSDPDNY---YMDVW 118
Db  61 VQELQGRVTMTTDTSTSTVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 111
Qy  119 GKGTIVVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 176
Db  112 QGGLTVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 171
Qy  177 VAWYQHKPGQAPRLVIHGVSNRAGISDRFSGSGSGTDFTLTITRVPEDFALYYCQVYG 236
Db  172 LAWYQQKPGAPRLIIYGASSRAIGIPDRFSGSGSGTDFTLTISRLEADFAVYYCQY 231
Qy  237 ASSYTFGQGTLEIK 251
Db  232 SSPITFGQGTLEIK 246
```

## RESULT 15

```
US-10-981-691-56
; Sequence 56, Application US/10981691
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585P13
; CURRENT APPLICATION NUMBER: US/10/981,691
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
```

```
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-981-691-56

Query Match      67.6%; Score 910; DB 39; Length 247;
Best Local Similarity 69.4%; Pred. No. 2.8e-69;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy  2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFQFWMGWINPYNKKEF 61
Db  1 EVQLVQSGAEVKKPGASVKVSCRASGYFTFSYGITWVRQAPGQGLEWMGWISAYNGKTN 60
Qy  62 SAKFQDRVTFTADTSANTAYMELSLRSADTAIVYCARVGEWGDSDPDNY---YMDVW 118
Db  61 VQELQGRVTMTTDTSTSTVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 111
Qy  119 GKGTIVVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 176
Db  112 QGGLTVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 171
Qy  177 VAWYQHKPGQAPRLVIHGVSNRAGISDRFSGSGSGTDFTLTITRVPEDFALYYCQVYG 236
Db  172 LAWYQQKPGAPRLIIYGASSRAIGIPDRFSGSGSGTDFTLTISRLEADFAVYYCQY 231
Qy  237 ASSYTFGQGTLEIK 251
Db  232 SSPITFGQGTLEIK 246
```

Search completed: March 20, 2006, 07:51:34  
Job time : 217 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:48:22 ; Search time 13 Seconds  
(without alignments)  
552.642 Million cell updates/sec

Title: US-09-673-707-1  
Perfect score: 1347  
Sequence: 1 MQVLESGAEVKPGASVK.....CQVYGASSYFGQGTKLERK 251

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 949   | 70.5        | 245    | 7     | US-11-054-515-1896 |
| 2          | 884   | 65.6        | 251    | 7     | US-11-054-515-12   |
| 3          | 884   | 65.6        | 251    | 7     | US-11-054-515-26   |
| 4          | 883   | 65.6        | 251    | 7     | US-11-054-515-22   |
| 5          | 883   | 65.6        | 251    | 7     | US-11-054-515-28   |
| 6          | 883   | 65.6        | 251    | 7     | US-11-054-515-33   |
| 7          | 883   | 65.6        | 251    | 7     | US-11-054-515-43   |
| 8          | 883   | 65.6        | 251    | 7     | US-11-054-515-127  |
| 9          | 882   | 65.5        | 251    | 7     | US-11-054-515-17   |
| 10         | 882   | 65.5        | 251    | 7     | US-11-054-515-30   |
| 11         | 882   | 65.5        | 251    | 7     | US-11-054-515-216  |
| 12         | 881   | 65.4        | 251    | 7     | US-11-054-515-171  |
| 13         | 881   | 65.4        | 251    | 7     | US-11-054-515-317  |
| 14         | 880   | 65.3        | 251    | 7     | US-11-054-515-27   |
| 15         | 880   | 65.3        | 251    | 7     | US-11-054-515-34   |
| 16         | 880   | 65.3        | 251    | 7     | US-11-054-515-102  |
| 17         | 880   | 65.3        | 251    | 7     | US-11-054-515-238  |
| 18         | 880   | 65.3        | 251    | 7     | US-11-054-515-295  |
| 19         | 879   | 65.3        | 251    | 7     | US-11-054-515-23   |
| 20         | 879   | 65.3        | 251    | 7     | US-11-054-515-29   |
| 21         | 879   | 65.3        | 251    | 7     | US-11-054-515-35   |
| 22         | 879   | 65.3        | 251    | 7     | US-11-054-515-37   |
| 23         | 879   | 65.3        | 251    | 7     | US-11-054-515-96   |
| 24         | 879   | 65.3        | 251    | 7     | US-11-054-515-143  |
| 25         | 879   | 65.3        | 251    | 7     | US-11-054-515-146  |

Sequence 222, App  
Sequence 224, App  
Sequence 237, App  
Sequence 242, App  
Sequence 249, App  
Sequence 313, App  
Sequence 50, Appl  
Sequence 31, Appl  
Sequence 36, Appl  
Sequence 94, Appl  
Sequence 110, App  
Sequence 150, App  
Sequence 149, App  
Sequence 195, App  
Sequence 299, App  
Sequence 10, Appl  
Sequence 16, Appl  
Sequence 24, Appl  
Sequence 45, Appl

ALIGNMENTS

RESULT 1  
US-11-054-515-1896  
; Sequence 1896, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523p3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1896  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-1896

Query Match 70.5%; Score 949; DB 7; Length 245;  
Best Local Similarity 73.8%; Pred. No. 6.2e-59;  
Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;  
  
Qy 2 QVLESGAEVKPGASVKVSCQSGYRFSNFTVHWVRQAPGORFEWMGWINPVNGKEF 61  
Db 1 QVLESGAEVKPGASVKVSCASGTTFTSYAHHWVRQAPGORLEWMGWINAGNTKY 60  
Qy 62 SAKFQDRVTFPTADTSANTAYMELSLRSADTAVYVCARVGEMGWDDSPQDNYMDVMGKG 121



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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 10/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 22
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-22

Query Match 65.6%; Score 883; DB 7; Length 251;
Best Local Similarity 68.4%; Pred. No. 2.2e-54;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

Qy 2 QVQLQSGAEVKKPGASVKVSQCOASGYRFSNFTVHWVRQAPGQRFWMGWINPYNKKEF 61
Db 1 QVQLVQSGVEVKKPGASVKVSKAGYTFNSHGISWVRQAPGQGLEWVGWISGHDDSTKY 60
Qy 62 SAKFQDRVTFTADTSTANTAYMELSLRSADTAVYICARVGEWGWDDSPQNY-YMDVWGK 120
Db 61 AQKFGQGRVTMTADTSTAYIELSLKSDDTAVYICARP---FYDTLTSLVYVFOYDHWGQ 117
Qy 121 GTTVIVSGGGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSRVA 178
Db 118 GTMTVTSSGGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRSQSVTRGWVA 177
Qy 179 WYQHKPQAPRLVIHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYICQVYGAS 238
Db 178 WYQKPKQAPRLMYGASRRATGVDPDRFSGSGGTDFTLTISRLEPEDFAVYICQVYATS 237
Qy 239 SYTFGQGTQKLERK 251
Db 238 PRTEGQGTTRLEIK 250

RESULT 5
US-11-054-515-28
; Sequence 28, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
```

```
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 28
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-28

Query Match 65.6%; Score 883; DB 7; Length 251;
Best Local Similarity 67.2%; Pred. No. 2.2e-54;
Matches 174; Conservative 27; Mismatches 40; Indels 18; Gaps 4;

Qy 2 QVQLQSGAEVKKPGASVKVSQCOASGYRFSNFTVHWVRQAPGQRFWMGWINPYNKKEF 61
Db 1 QVQLVQSGVEVKKPGASVKVSKAGYTFNSHGISWVRQAPGQGLEWVGWISGHDDSTKY 60
Qy 62 SAKFQDRVTFTADTSTANTAYMELSLRSADTAVYICARVGEWGWDDSP---QDNY---Y 114
Db 61 AQKFGQGRVTMTADTSTAYIELSLKSDDTAVYICAR-----PFYDILTSLVYFOY 111
Qy 115 MDVWGKGTTVIVSGGGGGGGGGGGSDIE--LTQSPGTLSPGERATFSCRSRSHSI 172
Db 112 FDHWGQGTMTVTSSGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRSQSV 171
Qy 173 RSRRAVWYQHKPQAPRLVIHGVNRSAGISDRFSGSGGTDFTLTITRVEPEDFALYIC 232
Db 172 TRGWAVWYQKPKQAPRLMYGASRRATGVDPDRFSGSGGTDFTLTISRLEPEDFAVYIC 231
Qy 233 QVYTGASSYTFGQGTQKLERK 251
Db 232 QYATSPRTFGQGTTRLEIK 250

RESULT 6
US-11-054-515-33
; Sequence 33, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
```

Mon Mar 20 08:51:24 2006

```

; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 2007/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 33
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-33

Query Match      65.6%; Score 883; DB 7; Length 251;
Best Local Similarity 67.2%; Pred. No. 2.2e-54;
Matches 174; Conservative 27; Mismatches 40; Indels 18; Gaps 4

QY      2 QVQLFQSGAEVKKPKGASVKVSQASGRFRNFTVHWVRAQPGQRFQEWGMWNPYNGNKEF 61
Db      1 QVQLVQSGVEVKKPKGASVKVSCKASGYTFNHHGISWVRQAPGGLEWGMVSGHDDSTKY 60

QY      62 SAKFDQRYVTFTADTSANTAYMELSLRSADTAVYCARVGEWGDNDSP-----QDNY---Y 114
Db      61 AQKFGGRVTMTADTSTSTAYIELSLKSDDTAVYCAR-----PFYDILTSYVFOY 111

QY      115 MDVWKGKGTIVVSSGGSGSGGGGGGGSDIE--LTQSPGTLISLSPGERATFSCRSSHSI 172
Db      112 FDIHWGGGTMTVTVSSGGSGSGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSV 171

QY      173 RSRRAVWYQHKPQAPRLVIGHVGNRASIGDRFSGSGSGTDFTLTITRVEPEDFALYYC 232
Db      172 TRGVWAWYQKQKQAPRLIMVYTSRATGVDFRSGSGSGTDFTLTISRLEPEDFAVYYC 231

QY      233 QVYGASSYTFGGGTKLERK 251
Db      232 QOYATSPRTFGGGRLEIK 250

```

```

RESULT 7
US-11-054-515-43
; Sequence 43, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 43
; LENGTH: 251
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
us-11-054-515-43

Query Match      65.6%; Score 883; DB 7; Length 251;
Best Local Similarity 68.4%; Pred. NO. 2.2e-54;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

Qy      2  QVLEQSGAEVKKPGASVKVSCKASQVRFESNFTVHWVROAPGQRFEMWGWINPYGNKKEF 61
Db      1  QVQLVDSGVEVKKPGASVKVSCKASQYTFSSNHHGISWVRQAPGGQGLEWVGWISGHDDSTKY 60

Qy      62  SAKFQQRVTPTADTSTANTAYMELRSLSADTAVYCARVGEWGDSDSPQNY- YMDVWGK 120
Db      61  AQKQFGRVTMTADTSTSTAYIELRSLKSDTAVVYCARP---FYDTLTSTVFQYFDHWGQ 117

Qy      121  GTTVIVSSGGGGGGGGGGGGGGDIE--LTQSPCTLSLSPGERATFSCRSHSIRSRVA 178
Db      118  GTVWTVSSGGGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRAQSQVTRGVVA 177

Qy      179  WYQHKPGQAPRLVTHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGAS 238
Db      178  WYQKPGQAPRLLMYGTISRATGVPRFSGSGSGTDFTLTISRLEPEDFAVYCCQYVATS 237

Qy      239  SYTFGGQTGLERK 251
Db      238  PRTFGGQTRLEIK 250

```

## RESULT 8

[illegible]

|            |  |
|------------|--|
| Query      |  |
| Best Match |  |
| Matched    |  |
| Qy         |  |
| Db         |  |



Mon Mar 20 08:51:24 2006

```
; Sequence 216, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 216
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-216

Query Match 65.5%; Score 882; DB 7; Length 251;
Best Local Similarity 68.4%; Pred. No. 2.6e-54;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKPGASVKVSCQASGYRFSNFTVHVRQAPGQRFEMWGNPNYGNKEF 61
Db 1 QVQLVQSGAEVKPGASVKVSCASGYTFSNHSISWRQAPGQGLEWVGWISGHDSTKY 60

Qy 62 SAKFQDRVTFTADTSTANTAYMELRSADTAVYYCARVGEWGWDDSPQDNY-YMDVWGK 120
Db 61 AQKFGQRTVTADTSTSTAYIELRLSKSDDTAVYYCARP---FYDTLTSTYVFQYFDHWGQ 117

Qy 121 GTTVIVSSGGGGGGGGGGGGSDIE--LTQSPGTLSLSPGERATFSCRSHSRRA 178
Db 118 GTMTVTVSSGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

Qy 179 WYQHKPGQAPRLVTHGVNRSAGISDRFSGSGGTDFTLITRVEPEDFALYYCQVYGAS 238
Db 178 WYQKPGQAPRLMLYIGISRRATGVPDRFSGSESGTDFTLISRLPEDFAVYYCQVYATS 237

Qy 239 SYTFGGQTKLERK 251
Db 238 PRFTGGQTRLEIK 250

RESULT 12
US-11-054-515-171
; Sequence 171, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-03-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 216
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-171

Query Match 65.4%; Score 881; DB 7; Length 251;
Best Local Similarity 68.4%; Pred. No. 3.1e-54;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKPGASVKVSCQASGYRFSNFTVHVRQAPGQRFEMWGNPNYGNKEF 61
Db 1 QVQLVQSGAEVKPGASVKVSCASGYTFSNHSISWRQAPGQGLEWVGWISGHDSTKY 60

Qy 62 SAKFQDRVTFTADTSTANTAYMELRSADTAVYYCARVGEWGWDDSPQDNY-YMDVWGK 120
Db 61 AQKFGQRTVTADTSTSTAYIELRLSKSDDTAVYYCARP---FYDTLTSTYVFQYFDHWGQ 117

Qy 121 GTTVIVSSGGGGGGGGGGGGSDIE--LTQSPGTLSLSPGERATFSCRSHSRRA 178
Db 118 GTMTVTVSSGGGGGGGGGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

Qy 179 WYQHKPGQAPRLVTHGVNRSAGISDRFSGSGGTDFTLITRVEPEDFALYYCQVYGAS 238
Db 178 WYQKPGQAPRLMLYIGISRRATGVPDRFSGSESGTDFTLISRLPEDFAVYYCQVYATS 237

Qy 239 SYTFGGQTKLERK 251
Db 238 PRFTGGQTRLEIK 250

RESULT 13
US-11-054-515-317
; Sequence 317, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
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; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 317
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-317

Query Match          65.4%; Score 881; DB 7; Length 251;
Best Local Similarity 68.4%; Pred No. 3,1e-54;
Matches 173; Conservative 28; Mismatches 46; Indels 6; Gaps 3

Qy . 2 QVLEQSGAEYKPKGASVKVSCQASGYRFSNFTVHWVRAQPCQRFEWGWINPYNGNKEF 61
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 QVQLVQSGEVEVKPKGASVKVSCKASGYTFSNHGISWVRQAQPCQGLEWGWISGHDDSTKY 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 62 SAKTQDRVTFADTSTANTAYNELRLRSADTAVYICARVGEWGWDSDPDNY-YMDVWGK 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AQKFGQGRVTMTADTSTSTAYTELRLSKSDDTAVYICARP---FYDTLTSYVFQYFDHWGQ 117
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 121 GTTVIVSGGGSGGGGGGGGGSDLE--LTQSPGTLSPGCRATFSCRSSHSISRRA 178
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 GTMTVTVSGGGSGGGGGGGGSALETTLTQSPDLSLSPGSRATFLSCRASQSVTRGWVA 177
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 179 WYQHKPGQAPRLVIHGVNRSAGISDRFGSGSGGTDFTLTITRVPEPDFALYVCQVYGAS 238
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 WYQKPGQAPRLLMYGTISRRATGVPDFRFGSGESGTDFTLTISRLEPDFAVYICQYGTG 237
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 239 SYTFGQGTKLK 251
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 PRTEGQGRLEIK 250
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-11-054-515-27
; Sequence 27, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247

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; SEQ ID NO 27
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-27

Query Match      65.3%; Score 880; DB 7; Length 251;
Best Local Similarity 68.0%; Pred. No. 3.6e-54;
Matches 172; Conservative 30; Mismatches 45; Indels 6; Gaps 3

Qy      2 QVQLQQSGAEVKKPGASVKYSCQASGYRFSNFTVHWVRQAPGQRFENWGWINPYNGNKEP 61
Db      1 QVLUVQSGVEVKKPGASVKYSCRASGYTFNSHGISWVRQAPGQGLWVGWISGHDDSTKY 60

Qy     62 SAKFQDRVTFTADTSTANTAYMELRSLSADTAVYYCARVGEWGDSDPDNY - YMDVWGK 120
Db     61 AOKFQGRVTWTADTFTSTAYIELRSLKSDDTAVYYCARP --- FYDTLTRYYVFQYFDHWGQ 117

Qy    121 GTTVIVSSGGGGSGGGSGGGGGSDIE -- LTQSPDTLSLSPGERATFSCRSRSHSTRSRVA 178
Db    118 GTWTVVSSGGGGSGGGSGGGGSALETTLTQSPDTLSLSPGKRATLSCRASQSVTRGWA 177

Qy    179 WYQHKPGQAPRLVTHGVNRSAGISDRFSGSGSGTDFTLTTRVPEPDFALYYCOVYGAS 238
Db    178 WYQOKPGQAPRLLMYGASRRATGVPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYATS 237

Qy    239 SYTFGQGTKLERK 251
Db    238 PRTFGQGTRLLEIK 250

RESULT 15
US-11-054-515-34
; Sequence 34, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 03/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 34
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-34

```

Query Match 65.3%; Score 880; DB 7; Length 351;  
Best Local Similarity 68.0%; Pred. No. 3.6e-54;  
Matches 172; Conservative 30; Mismatches 45; Indels 6; Gaps 3;





GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:48:00 ; Search time 69 Seconds  
(without alignments)  
1519.930 Million cell updates/sec

Title: US-09-673-707-1  
Perfect score: 1347  
Sequence: 1 MQVLEQSGAEVKKPGASVK.....QVYGCASYTFGQGTGLERK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                          |
|------------|-------|-------------|--------|-------|--------------------------------------|
| 1          | 949   | 70.5        | 245    | 3     | US-09-880-748-1896 Sequence 1896, Ap |
| 2          | 949   | 70.5        | 245    | 4     | US-10-293-418-1896 Sequence 1896, Ap |
| 3          | 910   | 67.6        | 247    | 4     | US-10-322-673-56 Sequence 56, Appl   |
| 4          | 910   | 67.6        | 247    | 5     | US-10-981-465-56 Sequence 56, Appl   |
| 5          | 910   | 67.6        | 247    | 5     | US-10-981-621-56 Sequence 56, Appl   |
| 6          | 910   | 67.6        | 247    | 5     | US-10-981-673-56 Sequence 56, Appl   |
| 7          | 910   | 67.6        | 247    | 5     | US-10-981-691-56 Sequence 56, Appl   |
| 8          | 896.5 | 66.6        | 263    | 4     | US-10-422-628-14 Sequence 14, Appl   |
| 9          | 884   | 65.6        | 251    | 3     | US-09-880-748-12 Sequence 12, Appl   |
| 10         | 884   | 65.6        | 251    | 3     | US-09-880-748-26 Sequence 26, Appl   |
| 11         | 884   | 65.6        | 251    | 4     | US-10-293-418-12 Sequence 12, Appl   |
| 12         | 884   | 65.6        | 251    | 4     | US-10-293-418-26 Sequence 26, Appl   |
| 13         | 883   | 65.6        | 251    | 3     | US-09-880-748-22 Sequence 22, Appl   |
| 14         | 883   | 65.6        | 251    | 3     | US-09-880-748-28 Sequence 28, Appl   |
| 15         | 883   | 65.6        | 251    | 3     | US-09-880-748-33 Sequence 33, Appl   |
| 16         | 883   | 65.6        | 251    | 3     | US-09-880-748-43 Sequence 43, Appl   |
| 17         | 883   | 65.6        | 251    | 3     | US-09-880-748-127 Sequence 127, Appl |
| 18         | 883   | 65.6        | 251    | 4     | US-10-293-418-22 Sequence 22, Appl   |
| 19         | 883   | 65.6        | 251    | 4     | US-10-293-418-28 Sequence 28, Appl   |
| 20         | 883   | 65.6        | 251    | 4     | US-10-293-418-33 Sequence 33, Appl   |
| 21         | 883   | 65.6        | 251    | 4     | US-10-293-418-43 Sequence 43, Appl   |
| 22         | 883   | 65.6        | 251    | 4     | US-10-293-418-127 Sequence 127, Appl |
| 23         | 882   | 65.5        | 251    | 3     | US-09-880-748-17 Sequence 17, Appl   |
| 24         | 882   | 65.5        | 251    | 3     | US-09-880-748-30 Sequence 30, Appl   |
| 25         | 882   | 65.5        | 251    | 3     | US-09-880-748-216 Sequence 216, Appl |
| 26         | 882   | 65.5        | 251    | 4     | US-10-293-418-17 Sequence 17, Appl   |
| 27         | 882   | 65.5        | 251    | 4     | US-10-293-418-30 Sequence 30, Appl   |

ALIGNMENTS

RESULT 1

US-09-880-748-1896  
; Sequence 1896, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1896  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1896

|                       |     |  |                    |                |                    |
|-----------------------|-----|--|--------------------|----------------|--------------------|
| Query Match           |     | 70.5%  | Score 949;         | DB 3;          | Length 245;        |
| Best Local Similarity |     | 73.8%  | Pred. No. 6.1e-64; |                |                    |
| Matches 186;          |     | Conservative   | 21;                | Mismatches 35; | Indels 10; Gaps 3; |
| Oy                    | 2   | QVLEQSGAEVKKPGASVKVKSQASGYRFSNFTVHWVRQAPQORPEWGWINPYNGNKEF   | 61                 |                |                    |
| Db                    | 1   | QVQLVQSGAEVKKPGASVKVSKASGYTFTSYAMHWVRQAPQORLEWGWINAGNNTKY    | 60                 |                |                    |
| Oy                    | 62  | SAKFDQRYTFTADTSANTAYMELSLRSADTAVVYCARVGEWGWDDSPDNNYMDVWGKG   | 121                |                |                    |
| Db                    | 61  | SKQFGQRTVITRDTTSASTAYMELSLRSADTAVVYCARVGEWGWDDSPDNNYMDVWGQG  | 113                |                |                    |
| Oy                    | 122 | TTVIVSSGGSGSGSGSGSGSGSDIE--LTQSPGTLISLSPGERATFCSRSSHSIRSRVAV | 179                |                |                    |
| Db                    | 114 | TMVTVSSGGSGSGSGSGSGSGSALETTLTQSPGTLISLSPGERATLSCRAQASGNYLAW  | 173                |                |                    |
| Oy                    | 180 | YQKPGQAPRLIVHGVSNRSGISDRFSGSGSGDTFTLTITRVRPEDFALVYCOVYGASS   | 239                |                |                    |
| Db                    | 174 | YQKPGQPPSLITVYASGRATGIPDRFSASGSGDFTLTITRLPEDPVAVYCOQYQ-SS    | 232                |                |                    |
| Oy                    | 240 | YTFQGTGLERK 251  |                    |                |                    |

```
Db      233 ITFGQGTTRLEIK 244

RESULT 2
US-10-293-418-1896
; Sequence 1896, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1896
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1896

Query Match      70.5%; Score 949; DB 4; Length 245;
Best Local Similarity 73.8%; Pred. No. 6.1e-64;
Matches 186; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

Qy      2 QVLEQSGAEVKKPGASVKYSCKASGYRFSNFTVHHVRAQPGQRFEMWGINPNYGNKEF 61
Db      1 QVQLVQSGAEVKKPGASVKYSCKASGYRFTSYAMHWVRQAPGQRLLEWNGWINAGNGNTKY 60

Qy      62 SAKFDQRTVFTADTSTANTAYMELSLRSADTAVVYCARVGEWGDSPQDNYMDVMGKG 121
Db      61 SQKFGQRTVITRTSTASTAYMELSLRSEDATVYYCAREG-----PGYYGMDVMGQG 113

Qy      122 TTVIVSSGGGGSGGGSGGGSDIE--LTQSPGTLSPGGERATFSCRSHSIRSRVAV 179
Db      114 TMVTVSSGGGGSGGGSGGGSALETTLTQSPGTLSPGGERATLSCRASQAIGSNYLAW 173

Qy      180 YQHKGQAPRLVIHGVNRSAGISDRFSGSGGTDTLTITRVEPEDEALYYCVQYGASS 239
Db      174 YQQKGPQPPSLIYGASSRATGIPDRFSASGSGTDTLTISRLEPEDFAVYYCQYQY-SS 232

Qy      240 YTFGGGTGLERK 251
Db      233 ITFGQGTTRLEIK 244

RESULT 3
US-10-322-673-56
; Sequence 56, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF595
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237

; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-322-673-56

Query Match      67.6%; Score 910; DB 4; Length 247;
Best Local Similarity 69.4%; Pred. No. 5.5e-61;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy      2 QVLEQSGAEVKKPGASVKYSCKASGYRFSNFTVHHVRAQPGQRFEMWGINPNYGNKEF 61
Db      1 EVQLVQSGAEVKKPGASVKSCRASGYFTSYGITWVRQAPGQGLEWMGWIATNGKNTY 60

Qy      62 SAKFDQRTVFTADTSTANTAYMELSLRSADTAVVYCARVGEWGDSPQDNY---YMDVM 118
Db      61 VQELQGRVTWTTDTSTSTVYVWELTSLRSDDTAVYYCARRG-----NNYRFGYFDFW 111

Qy      119 GKTTIVSSGGGGSGGGSGGGSDIE--LTQSPGTLSPGGERATFSCRSHSIRSR 176
Db      112 GQGTIVTVSSGGGGSGGGSGGSALETTLTQSPGTLSPGGERATLSCRASQSISSN 171

Qy      177 VANYQHKGQAPRLVIHGVNRSAGISDRFSGSGGTDTLTITRVEPEDEALYYCVQYG 236
Db      172 LAMVYQKGPGRAPRLIYGASSRAIGIPDRFSGSGSGTDTLTISRLEAEDFAVYYCQYQ 231

Qy      237 ASSYTFGGGTGLERK 251
Db      232 SSPTFGQGTTRLEIK 246

RESULT 4
US-10-981-465-56
; Sequence 56, Application US/10981465
; Publication No. US20050214205A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585P1
; CURRENT APPLICATION NUMBER: US/10/981,465
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
```

```
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-981-465-56

Query Match      67.6%; Score 910; DB 5; Length 247;
Best Local Similarity 69.4%; Pred. No. 5.5e-61;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy  2 QVQLVQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFENWGWINPYNGNKEF 61
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  1 EVQLVQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFENWGWINPYNGNKEF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  62 SAKFQDRVTFADTSANTAYMELRSLSRSDTAVVYCARVGEWGDSPQDNY---YMDVW 118
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  61 VQELQGRVTMTDSTSTVYMWELTSLRSDDTAVVYCARRG-----NNYRFGYDFW 111
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  119 GKGTIVVSSGGGGGGGGGGGGGSDIE--LTQSPGTLSPGGERATFSCRSSHSIRSR 176
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  112 GQGLTVTVSSGGGGGGGGGGGGGSALETTLTQSPGTLSPGGERATLSCRASQSISSN 171
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  177 VANYQHFGQAPRLVIHGVNRSAGISDRFSGSGSGTDFTLTITRVPEDFALYYCQYVG 236
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  172 LAMTQQKPGRAPRLIYGASSRAIGIPDRFSGSGSGTDFTLTISRLEAEDFVYYCQYVG 231
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  237 ASSYTFGGQTKLERK 251
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  232 SSPITFGQGRLEIK 246
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-10-981-621-56
; Sequence 56, Application US/10981621
; Publication No. US20050214206A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585P1D1
; CURRENT APPLICATION NUMBER: US/10/981,621
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-981-673-56
```

```
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-981-621-56

Query Match      67.6%; Score 910; DB 5; Length 247;
Best Local Similarity 69.4%; Pred. No. 5.5e-61;
Matches 177; Conservative 24; Mismatches 40; Indels 14; Gaps 3;

Qy  2 QVQLVQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFENWGWINPYNGNKEF 61
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  1 EVQLVQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFENWGWINPYNGNKEF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  62 SAKFQDRVTFADTSANTAYMELRSLSRSDTAVVYCARVGEWGDSPQDNY---YMDVW 118
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  61 VQELQGRVTMTDSTSTVYMWELTSLRSDDTAVVYCARRG-----NNYRFGYDFW 111
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  119 GKGTIVVSSGGGGGGGGGGGGGSDIE--LTQSPGTLSPGGERATFSCRSSHSIRSR 176
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  112 GQGLTVTVSSGGGGGGGGGGGGGSALETTLTQSPGTLSPGGERATLSCRASQSISSN 171
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  177 VANYQHFGQAPRLVIHGVNRSAGISDRFSGSGSGTDFTLTITRVPEDFALYYCQYVG 236
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  172 LAMTQQKPGRAPRLIYGASSRAIGIPDRFSGSGSGTDFTLTISRLEAEDFVYYCQYVG 231
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy  237 ASSYTFGGQTKLERK 251
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  232 SSPITFGQGRLEIK 246
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
US-10-981-673-56
; Sequence 56, Application US/10981673
; Publication No. US20050214207A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585P1D2
; CURRENT APPLICATION NUMBER: US/10/981,673
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-981-673-56

Query Match      67.6%; Score 910; DB 5; Length 247;
```

[illegible]

RESULT 7  
US-10-981-691-56  
; Sequence 56, Application US/10981691  
; Publication No. US20050214208A1  
; GENERAL INFORMATION:  
; APPLICANT: Salcedo et al.

```

1 GENERAL INFORMATION:
2
3 APPLICANT: Salcedo et al.
4
5 TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
6
7 TITLE OF INVENTION: Receptors
8
9 FILE REFERENCE: PF585PID3
10
11 CURRENT APPLICATION NUMBER: US/10/981,691
12
13 CURRENT FILING DATE: 2004-11-05
14
15 PRIOR APPLICATION NUMBER: 60/608,386
16
17 PRIOR FILING DATE: 2004-09-10
18
19 PRIOR APPLICATION NUMBER: PCT/US04/013900
20
21 PRIOR FILING DATE: 2004-05-05
22
23 PRIOR APPLICATION NUMBER: 60/468,092
24
25 PRIOR FILING DATE: 2003-05-06
26
27 PRIOR APPLICATION NUMBER: 60/495,140
28
29 PRIOR FILING DATE: 2003-08-15
30
31 PRIOR APPLICATION NUMBER: 10/322,673
32
33 PRIOR FILING DATE: 2002-12-19
34
35 PRIOR APPLICATION NUMBER: 60/369,877
36
37 PRIOR FILING DATE: 2002-04-05
38
39 PRIOR APPLICATION NUMBER: 60/384,828
40
41 PRIOR FILING DATE: 2002-06-04
42
43 PRIOR APPLICATION NUMBER: 60/396,591
44
45 PRIOR FILING DATE: 2002-07-18
46
47 PRIOR APPLICATION NUMBER: 60/403,370
48
49 PRIOR FILING DATE: 2002-08-15
50
51 PRIOR APPLICATION NUMBER: 60/425,737
52
53 PRIOR FILING DATE: 2002-11-13
54
55 Remaining Prior Application data removed - See File Wrapper or PALM.
56 NUMBER OF SEQ ID NOS:76

```

```

; SEQ ID NO 56
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM059H03 scFv
US-10-981-691-56

Query Match          67.6%;   Score 910;   DB 5;   Length 247;
Best Local Similarity 69.4%;   Pred. No. 5.5e-61;
Matches 172;   Conservative 24;   Mismatches 40;   Indels 14;   Gaps 3;

```

**Qy**      2 QVLEQGSGAEVKKPGASVKYSCAAGYRFSNFTVHWROAPGRFEWGMGWPYNPYNGKEF 61  
              :  
              :  
**Dh**      1 EVQLVSQGAELVKKPGASVKYSRASGYTTFSTGITVWRQAPGGLEGWGMSAYNKYNY 60

|    |  |     |  |             |     |
|----|--|-----|--|-------------|-----|
| Qy |  | 62  | SAKFODRVFTADTSANTAYMELSLRSADTAVVYCARVGEGWDDSPQNY---  | YMDVW       | 118 |
| Dd |  | 61  | VQELQGRVTMTDTSTSVTMELTSLSRDDTA VVYCARRG-----         | NNRYFGYFDWF | 111 |
| Qy |  | 119 | GKGTTVIVSGGGGGGGGGGGGSIE--LTPSGTSLSPGERATFSCRSHSIRSR | R           | 176 |
| Dd |  | 112 | GGCTLVTVSGGGGGGGGGGGGALETTLTQSPGTLSLSPGERATLSCRQSIS  | SSN         | 171 |
| Qy |  | 177 | VANYQHKGPAQLVTHGVSNRASIGSDRFSGSGSGTDFTLTITRVEPEDFALY | CQVYG       | 236 |
| Dd |  | 172 | LANYQQKRGAPRLLYGASSRAIGPDFRFSGSGSGTDFTLTISRLEAEDFAV  | YQCQYG      | 231 |
| Qy |  | 237 | ASSYTFGGQTKLERK                                      | 251         |     |
| Dd |  | 232 | SSPITFGQTRLEIK                                       | 246         |     |

## RESULT 8

```

US-10-422-628-14
; Sequence 14, Application US/10422628
; Publication No. US20040014174A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: MAYFIELD, Stephen P.
; APPLICANT: FRANKLIN, Scott E.
; TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN CHLOROPLASTS, AND COMPOSITIONS AND METHODS OF USE THEREOF
; TITLE OF INVENTION: FOR EXPRESSING SAME
; FILE REFERENCE: SCRIPT510-2
; CURRENT APPLICATION NUMBER: US/10/422,628
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/375,129
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/434,957
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Chloroplast codon optimized antibody specific for tetanus toxin
US-10-422-628-14

```

|                       |       |              |         |            |        |     |
|-----------------------|-------|--------------|---------|------------|--------|-----|
| Query Match           | 66.6% | Score        | 896.5   | DB 4       | Length | 263 |
| Best Local Similarity | 68.8% | Pred. No.    | 6.2e-60 |            |        |     |
| Matches               | 174   | Conservative | 27      | Mismatches | 37     |     |
|                       |       | Indels       | 15      | Gaps       | 4      |     |

QY 5 LEQSGAEVKKPGASVKVSQASGYRFSFTFVHWYRQAPGQRFENWGWINPYNGNKFEFSAK 64

db 2 LEQSGAEVKKPGSSVKVSCKRSGTFTNNYAIISWVRQAPGQGLEWMGGIIPFRNTAKYAAH 61

|    |  |     |
|----|--|-----|
| 65 | FQDRVTFADTSANTPAYMELRSLRSADTAVIYCARVE-----WMDUSFQDRIINDVW    | 113 |
| QY | :           :           :                                    |     |
| 66 | PCCGVTITADNPGSTGTAVMETSSIRGEDTATVVCAR-GDTIEGVNNGY-----YAMDVV | 113 |
| QY | :           :           :                                    |     |

DB           62 FQGRVILLADESICRATHEMCOCCNSD.MN.ICT.       GCTTIVIS  
QV          119 GKGTTVIVSGGGGGGGGGGGDIELTQSPGTLSLPCRATFSCRSHSIRSRVA 178

Db 114 GGGTTVTVSSGGGGGGGGGGSELVLTQSPGTLSLSPGERATLSCRASHSVSRAYLA 173

QY 179 WYQHKGQAPRLVIHGVSNRASGISDRFSGSGSGTDFLLTITRVEDFDALYVCQVYGAS 238

Db 174 WYQKPGQAPRLIIYGTSSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGG 233

Qy 239 SYTFGGQGTKLERK 251

Db 234 PW-FGQGTKVELK 245

RESULT 9  
US-09-880-748-12  
; Sequence 12, Application US/09880748  
; Publication No. US20030059937A1

```
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-12
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Query Match 65.6%; Score 884; DB 3; Length 251;
Best Local Similarity 68.4%; Pred. No. 5.2e-59;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHWVRAQPGQRFEMWGNINPYNGNKEF 61
Db 1 QVQLVQSGVEVKKPGASVKVSKASGYTFSNHGISWVRQAPGQGLEWGWISGHDDSTKY 60

Qy 62 SAKFQDRVTFTADTSTANTAYMELRSLSADTAVVYCARVGEWGWDDSPQDNY-YMDVMGK 120
Db 61 AQKQGRVTMTADTSTSTAYIELSLKSDDTAVVYCARP---FYDTLTRYVQYFDHWGQ 117

Qy 121 GTTVIVSSGGGGSGGGSGGGSDIE--LTQSPGTLSPGERATFSCRSHSIRSRVA 178
Db 118 GTMTVTVSSGGGGSGGGSGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

Qy 179 WYQHKPGQAPRLVTHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALVYCOVYGAS 238
Db 178 WYQKPGQAPRLMVGASRRATGVDPDRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYATS 237

Qy 239 SYTFGGQTGLERK 251
Db 238 PRTEGGQTRLEIK 250
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RESULT 10
US-09-880-748-26
; Sequence 26, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 251
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-26

Query Match 65.6%; Score 884; DB 3; Length 251;
Best Local Similarity 68.4%; Pred. No. 5.2e-59;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHWVRAQPGQRFEMWGNINPYNGNKEF 61
Db 1 QVQLVQSGVEVKKPGASVKVSKASGYTFSNHGISWVRQAPGQGLEWGWISGHDDSTKY 60

Qy 62 SAKFQDRVTFTADTSTANTAYMELRSLSADTAVVYCARVGEWGWDDSPQDNY-YMDVMGK 120
Db 61 AQKQGRVTMTADTSTSTAYIELSLKSDDTAVVYCARP---FYDTLTRYVQYFDHWGQ 117

Qy 121 GTTVIVSSGGGGSGGGSGGGSDIE--LTQSPGTLSPGERATFSCRSHSIRSRVA 178
Db 118 GTMTVTVSSGGGGSGGGSGGGSALETTLTQSPDTLSLSPGERATLSCRASQSVTRGWVA 177

Qy 179 WYQHKPGQAPRLVTHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALVYCOVYGAS 238
Db 178 WYQKPGQAPRLMVGASRRATGVDPDRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYATS 237

Qy 239 SYTFGGQTGLERK 251
Db 238 PRTEGGQTRLEIK 250
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RESULT 11
US-10-293-418-12
; Sequence 12, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 12
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-12

Query Match 65.6%; Score 884; DB 4; Length 251;
Best Local Similarity 68.4%; Pred. No. 5.2e-59;
Matches 173; Conservative 29; Mismatches 45; Indels 6; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHWVRAQPGQRFEMWGNINPYNGNKEF 61
Db 1 QVQLVQSGVEVKKPGASVKVSKASGYTFSNHGISWVRQAPGQGLEWGWISGHDDSTKY 60

Qy 62 SAKFQDRVTFTADTSTANTAYMELRSLSADTAVVYCARVGEWGWDDSPQDNY-YMDVMGK 120
Db 61 AQKQGRVTMTADTSTSTAYIELSLKSDDTAVVYCARP---FYDTLTRYVQYFDHWGQ 117
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-28

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[illegible]

Search completed: March 20, 2006, 07:49:20  
Job time : 70 secs

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RESULT 15
US-09-880-748-33
; Sequence 33, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-33

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|                           |                                       |   |                   |
|---------------------------|---------------------------------------|---|-------------------|
| Query Match               | 65.6%                                 | Score 883;  | DB 3; Length 251; |
| Best Local Similarity     | 67.2%;                                | Pred. No. 6.2e-59;  |                   |
| Matches 174; Conservative | 27; Mismatches 40; Indels 18; Gaps 4; |   |                   |
| Qy                        | 2                                     | QVQLQQSGAVKVPKPGASVKYSCQASGYRFSNFTVHWYRQAPGQRPFWMGWGINPYNGNKPEF | 61                |
| Dd                        | 1                                     | QVQLVDSGVVRKPGASVKYSCAKASYTFNSNHGISWRYRQAPGGGLEWVGWISGHDDSTKY   | 60                |
| Qy                        | 62                                    | SAXFDQRVTFTADTSANTAYMELRLSRSDATVYYCARVGEWGDDSP----              | QDNY--Y 114       |
| Dd                        | 61                                    | AQPKQGRVTMTADTSTATIELRLSKSDDTVAYICAR-----PFFVDILTYSVFQY         | 111               |
| Qy                        | 115                                   | MDVWKGKTIVIVSSGGGGGGGGGGGGSDIE--LTQSPGTLSLSPGERATFCSRSHSI       | 172               |

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:47:04 ; Search time 27 seconds  
(without alignments)  
768.578 Million cell updates/sec

Title: US-09-673-707-1

Perfect score: 1347

Sequence: 1 MQVLEQSGAEVKKPGASVK.....CQVYGASSYTFGGQTKLERK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 800.5 | 59.4        | 269    | 2  | US-08-646-265A-109 |
| 2          | 797   | 59.2        | 288    | 2  | US-09-423-439-38   |
| 3          | 797   | 59.2        | 673    | 2  | US-09-423-439-32   |
| 4          | 786   | 58.4        | 267    | 2  | US-09-485-737B-2   |
| 5          | 786   | 58.4        | 267    | 2  | US-10-071-485-2    |
| 6          | 786   | 58.4        | 541    | 2  | US-09-485-737B-85  |
| 7          | 786   | 58.4        | 541    | 2  | US-10-071-485-85   |
| 8          | 786   | 58.4        | 711    | 2  | US-09-485-737B-90  |
| 9          | 786   | 58.4        | 711    | 2  | US-10-071-485-90   |
| 10         | 770   | 57.2        | 240    | 1  | US-08-488-113B-148 |
| 11         | 770   | 57.2        | 240    | 1  | US-08-477-484B-148 |
| 12         | 770   | 57.2        | 240    | 1  | US-08-646-360-148  |
| 13         | 770   | 57.2        | 240    | 1  | US-08-839-765-148  |
| 14         | 770   | 57.2        | 240    | 2  | US-09-136-389-148  |
| 15         | 770   | 57.2        | 240    | 2  | US-09-610-838-148  |
| 16         | 770   | 57.2        | 240    | 2  | US-09-711-485-148  |
| 17         | 760   | 56.4        | 244    | 1  | US-08-553-497A-20  |
| 18         | 756.5 | 56.2        | 297    | 2  | US-09-486-814A-2   |
| 19         | 755   | 56.1        | 249    | 1  | US-08-797-689-18   |
| 20         | 755   | 56.1        | 249    | 1  | US-09-984-186-18   |
| 21         | 753.5 | 55.9        | 240    | 1  | US-08-800-198-8    |
| 22         | 753.5 | 55.9        | 240    | 2  | US-09-296-595-8    |
| 23         | 752.5 | 55.9        | 599    | 1  | US-08-463-163-3    |
| 24         | 749.5 | 55.6        | 256    | 2  | US-09-526-738A-2   |
| 25         | 749.5 | 55.6        | 258    | 2  | US-09-526-738A-4   |
| 26         | 747.5 | 55.5        | 239    | 2  | US-08-279-772A-8   |
| 27         | 747.5 | 55.5        | 239    | 2  | US-08-902-486-11   |

Query Match 59.4%; Score 800.5; DB 2; Length 269;

#### ALIGNMENTS

##### RESULT 1

US-08-646-265A-109

; Sequence 109, Application US/08646265A

; Patent No. 6214973

; GENERAL INFORMATION:

; APPLICANT: OHTOMO, Toshihiko

; APPLICANT: SATO, Koh

; APPLICANT: TSUCHIYA, Masayuki

; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS

; NUMBER OF SEQUENCES: 132

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,265A

; FILING DATE: 09-SEP-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/JP94/01763

; FILING DATE: 19-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 5-291078

; FILING DATE: 19-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: WEGNER, Harold C.

; REGISTRATION NUMBER: 25,258

; REFERENCE/DOCKET NUMBER: 53466/184

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 109:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 269 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-646-265A-109

Best Local Similarity 61.1%; Pred. No. 2e-61;  
Matches 154; Conservative 31; Mismatches 52; Indels 15; Gaps 3;  
Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGINPYGNKEF 61  
Db 23 QVQLVQSGAEVKKPGSSVKVSCKASGFINKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 82  
Qy 62 SAKFDQRTVFTADTSANTAYMELSLRSADTAVYYCARVGEWGWDSPQNYM--DVWG 119  
Db 83 DPKFQGRVTTTADSETNTAYMELSSLSRSEDATFYFCASA-----YYVNQDYWG 130  
Qy 120 KGTTVIVSSGGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHSIRSRVAV 179  
Db 131 QGTTTVIVSSGGGGGGGGGGGSDIQMTQSPSLASVGDRTTITCKASQNV-GTNVAV 189  
Qy 180 YQHPKGPQAPRLVIHGVNRSAGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGASS 239  
Db 190 YQKPGKAPKPLIYASVRYSGVPSRFSFGSGSGTDFTLTISLQPEDIATYYCQYNSYP 249  
Qy 240 YTFGQGTKLK 251  
Db 250 RAFQGGTKVEIK 261

## RESULT 2

US-09-423-439-38  
; Sequence 38, Application US/09423439  
; Patent No. 6339070  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, Stephen Charles  
; BLAKEY, David Charles  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Winthrop, L.L.P.  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/423,439  
; FILING DATE: 09-No. 6339070-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB98/01294  
; FILING DATE: 05-MAY-1998  
; APPLICATION NUMBER: GB 9709421.3  
; FILING DATE: 10-MAY-1997  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 288 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-423-439-38

Query Match 59.2%; Score 797; DB 2; Length 288;  
Best Local Similarity 58.1%; Pred. No. 4.4e-61;  
Matches 150; Conservative 43; Mismatches 47; Indels 18; Gaps 4;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGINPYGNKEF 61  
Db 23 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGINPYGNKEF 82  
Qy 62 SAKFDQRTVFTADTSANTAYMELSLRSADTAVYYCARVGEWGWDSPQNYM--DVWG 121

Db 83 NEFKPKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARERAYGYDDA-----MDYWGQG 136  
Qy 122 TTIVVSSGGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHI-----RSRR 176  
Db 137 TTVTVSSGGGGGGGGGGGSDIELSQSPSLAVSAGEKVTMSCKSSQSLNSTRKNY 196  
Qy 177 VAWYQHPKGPQAPRLVIHGVNRSAGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYG 236  
Db 197 LAWYQRPQGPQKLLIYMASTRTSGVDPDRFTGSGSGTDFTLTISVQAEDLAIYYCK--- 253  
Qy 237 ASSY---TFGQGTKLK 251  
Db 254 -QSYTLRTFGGTKLEIK 270

## RESULT 3

US-09-423-439-32  
; Sequence 32, Application US/09423439  
; Patent No. 6339070  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, Stephen Charles  
; BLAKEY, David Charles  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Winthrop, L.L.P.  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/423,439  
; FILING DATE: 09-No. 6339070-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB98/01294  
; FILING DATE: 05-MAY-1998  
; APPLICATION NUMBER: GB 9709421.3  
; FILING DATE: 10-MAY-1997  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 673 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-423-439-32

Query Match 59.2%; Score 797; DB 2; Length 673;  
Best Local Similarity 58.1%; Pred. No. 1.2e-60;  
Matches 150; Conservative 43; Mismatches 47; Indels 18; Gaps 4;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGINPYGNKEF 61  
Db 20 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFTVHVRQAPGQRFEMWGINPYGNKEF 79  
Qy 62 SAKFDQRTVFTADTSANTAYMELSLRSADTAVYYCARVGEWGWDSPQNYM--DVWG 121  
Db 80 NEFKPKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARERAYGYDDA-----MDYWGQG 133  
Qy 122 TTIVVSSGGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHI-----RSRR 176  
Db 134 TTVTVSSGGGGGGGGGGGSDIELSQSPSLAVSAGEKVTMSCKSSQSLNSTRKNY 193  
Qy 177 VAWYQHPKGPQAPRLVIHGVNRSAGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYG 236

Db 194 LAWYQORPGQSKLLIYWASTRTSGVPRDFTGSGSGTDTLTLSVQAEADLAIYCK--- 250  
Qy 237 ASSY---TFGQGTLEIK 251  
Db 251 -QSYTLRTFGGQTKLEIK 267

RESULT 4  
US-09-485-737B-2  
; Sequence 2, Application US/09485737B  
; Patent No. 6350860  
; GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Ange  
; APPLICANT: Sablon, Erwin  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
; FILE REFERENCE: INNS:015  
; CURRENT APPLICATION NUMBER: US/09/485,737B  
; CURRENT FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: EPO 98870139.7  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: EPO 97870122.5  
; PRIOR FILING DATE: 1997-08-18  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-485-737B-2

Query Match 58.4%; Score 786; DB 2; Length 267;  
Best Local Similarity 58.8%; Pred. No. 3.6e-60;  
Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWVROAPGQRPFWGWINPYNGNKEF 61  
Db 23 QVQLVQSGSELKPGASVKISCKASGYTFTDYGNNVWKQAPGQGLKWMGWINTYTGESTY 82  
Qy 62 SAKFDQRTVTADTTSANTAYMELRLSRADTAVYTCARVGEWGWDDSPQDNYMDVWGKG 121  
Db 83 VDDFKGRFVSLDTSVAAYLQISLKAEDTATYFCARRG-----FYAMDYWGQG 132  
Qy 122 TTIVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHRSRRVAVYQ 181  
Db 133 TTVTVSSGGGGGGGGGGSDIVLTQSPATMSASGERVTLTCSASSI--SYMPFWYH 190  
Qy 182 HKPGQAPRLVHGVSNRNASGISDRFSGSGSGTDTLTITRVEPDFAFYCQVYGASST 241  
Db 191 QRPQSPRLIYDTSNLASGVPARFSGSGSGTSYSLTISRMEPDFAFYCHQSSSYPT 250  
Qy 242 FQGQTKLERK 251  
Db 251 FQGQTKLEIK 260

RESULT 5  
US-10-071-485-2  
; Sequence 2, Application US/10071485  
; Patent No. 6830752  
; GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Ange  
; APPLICANT: Sablon, Erwin  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC  
; TITLE OF INVENTION: SHOCK, CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
; FILE REFERENCE: INNS:015  
; CURRENT APPLICATION NUMBER: US/10/071,485

; CURRENT FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: 09/485,737  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: EPO 98870139.7  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: EPO 97870122.5  
; PRIOR FILING DATE: 1997-08-18  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-071-485-2

Query Match 58.4%; Score 786; DB 2; Length 267;  
Best Local Similarity 58.8%; Pred. No. 3.6e-60;  
Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;

Qy 2 QVLEQSGAEVKKPGASVKVSQASGYRFSNFTVHWVROAPGQRPFWGWINPYNGNKEF 61  
Db 23 QVQLVQSGSELKPGASVKISCKASGYTFTDYGNNVWKQAPGQGLKWMGWINTYTGESTY 82  
Qy 62 SAKFDQRTVTADTTSANTAYMELRLSRADTAVYTCARVGEWGWDDSPQDNYMDVWGKG 121  
Db 83 VDDFKGRFVSLDTSVAAYLQISLKAEDTATYFCARRG-----FYAMDYWGQG 132  
Qy 122 TTIVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHRSRRVAVYQ 181  
Db 133 TTVTVSSGGGGGGGGGGSDIVLTQSPATMSASGERVTLTCSASSI--SYMPFWYH 190  
Qy 182 HKPGQAPRLVHGVSNRNASGISDRFSGSGSGTDTLTITRVEPDFAFYCQVYGASST 241  
Db 191 QRPQSPRLIYDTSNLASGVPARFSGSGSGTSYSLTISRMEPDFAFYCHQSSSYPT 250  
Qy 242 FQGQTKLERK 251  
Db 251 FQGQTKLEIK 260

RESULT 6  
US-09-485-737B-85  
; Sequence 85, Application US/09485737B  
; Patent No. 6350860  
; GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Ange  
; APPLICANT: Sablon, Erwin  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
; FILE REFERENCE: INNS:015  
; CURRENT APPLICATION NUMBER: US/09/485,737B  
; CURRENT FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: EPO 98870139.7  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: EPO 97870122.5  
; PRIOR FILING DATE: 1997-08-18  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 85  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC  
US-09-485-737B-85

Query Match 58.4%; Score 786; DB 2; Length 541;

Best Local Similarity 58.8%; Pred. No. 8.3e-60;  
Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;

Qy 2 QVQLQSGAEVKKPGASVKVSQCSAGYRFSNFTVHVRQAPGQRFPMWGMINPYNKKEF 61  
Db 1 QVQLVQSGSELKPGASVKISCKASGYTFTDYGMMWVKQAPGQGLKWMGWINTYTGESTY 60

Qy 62 SAKFDQRTVTADTSANTAYMELRLSRADTAIVYCARVGEWGDSDPDNYMDVWGKG 121  
Db 61 VDDFKGRFVSLDTSVSAAYLQISLKAEDTATYFCARRG-----FYAMDYWGQG 110

Qy 122 TTVIVSSGGSGGGGGGGSDIELTQSPGTLSPGERATPSCRSRSHSRIRRVAVYQ 181  
Db 111 TTVIVSSGGSGGGGGGGSDIVLTQSPATMSASPERVTLTCSASSI--SYMFWYH 168

Qy 182 HKPQAPRLVHGVSNRASGISDRFSGSGSDTFTLTITRVEPEDFALYYCQVYGASST 241  
Db 169 QRPQSPRLIYDTSNLAGVPAFSGSGSGTYSYLTISRMEPEDFATYFCHQSSSYPT 228

Qy 242 FGQGTKLERK 251  
Db 229 FGQGTKLEIK 238

RESULT 7  
US-10-071-485-85  
; Sequence 85, Application US/10071485  
; Patent No. 6830752  
; GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Ange  
; APPLICANT: Sablon, Erwin  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC  
; TITLE OF INVENTION: SHOCK,  
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
; FILE REFERENCE: INNS:015  
; CURRENT APPLICATION NUMBER: US/10/071,485  
; PRIOR FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: 09/485,737  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: EPO 98870139.7  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: EPO 97870122.5  
; PRIOR FILING DATE: 1997-08-18  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 85  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC

US-10-071-485-85  
Query Match 58.4%; Score 786; DB 2; Length 541;  
Best Local Similarity 58.8%; Pred. No. 8.3e-60;  
Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;

Qy 2 QVQLQSGAEVKKPGASVKVSQCSAGYRFSNFTVHVRQAPGQRFPMWGMINPYNKKEF 61  
Db 1 QVQLVQSGSELKPGASVKISCKASGYTFTDYGMMWVKQAPGQGLKWMGWINTYTGESTY 60

Qy 62 SAKFDQRTVTADTSANTAYMELRLSRADTAIVYCARVGEWGDSDPDNYMDVWGKG 121  
Db 61 VDDFKGRFVSLDTSVSAAYLQISLKAEDTATYFCARRG-----FYAMDYWGQG 110

Qy 122 TTVIVSSGGSGGGGGGGSDIELTQSPGTLSPGERATPSCRSRSHSRIRRVAVYQ 181  
Db 111 TTVIVSSGGSGGGGGGGSDIVLTQSPATMSASPERVTLTCSASSI--SYMFWYH 168

Qy 182 HKPQAPRLVHGVSNRASGISDRFSGSGSDTFTLTITRVEPEDFALYYCQVYGASST 241  
Db 169 QRPQSPRLIYDTSNLAGVPAFSGSGSGTYSYLTISRMEPEDFATYFCHQSSSYPT 228

Qy 242 FGQGTKLERK 251  
Db 229 FGQGTKLEIK 238

RESULT 7  
US-10-071-485-85  
; Sequence 85, Application US/10071485  
; Patent No. 6830752  
; GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Ange  
; APPLICANT: Sablon, Erwin  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC  
; TITLE OF INVENTION: SHOCK,  
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
; FILE REFERENCE: INNS:015  
; CURRENT APPLICATION NUMBER: US/10/071,485  
; PRIOR FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: 09/485,737  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: EPO 98870139.7  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: EPO 97870122.5  
; PRIOR FILING DATE: 1997-08-18  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 85  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC

US-10-071-485-85  
Query Match 58.4%; Score 786; DB 2; Length 541;  
Best Local Similarity 58.8%; Pred. No. 8.3e-60;  
Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;

Qy 2 QVQLQSGAEVKKPGASVKVSQCSAGYRFSNFTVHVRQAPGQRFPMWGMINPYNKKEF 61  
Db 1 QVQLVQSGSELKPGASVKISCKASGYTFTDYGMMWVKQAPGQGLKWMGWINTYTGESTY 60

Qy 62 SAKFDQRTVTADTSANTAYMELRLSRADTAIVYCARVGEWGDSDPDNYMDVWGKG 121  
Db 61 VDDFKGRFVSLDTSVSAAYLQISLKAEDTATYFCARRG-----FYAMDYWGQG 110

Qy 122 TTVIVSSGGSGGGGGGGSDIELTQSPGTLSPGERATPSCRSRSHSRIRRVAVYQ 181  
Db 111 TTVIVSSGGSGGGGGGGSDIVLTQSPATMSASPERVTLTCSASSI--SYMFWYH 168

Qy 182 HKPQAPRLVHGVSNRASGISDRFSGSGSDTFTLTITRVEPEDFALYYCQVYGASST 241  
Db 169 QRPQSPRLIYDTSNLAGVPAFSGSGSGTYSYLTISRMEPEDFATYFCHQSSSYPT 228

Qy 242 FGQGTKLERK 251  
Db 229 FGQGTKLEIK 238

RESULT 8  
US-09-485-737B-90  
; Sequence 90, Application US/09485737B  
; Patent No. 6350860  
; GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Ange  
; APPLICANT: Sablon, Erwin  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC  
; TITLE OF INVENTION: SHOCK,  
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
; FILE REFERENCE: INNS:015  
; CURRENT APPLICATION NUMBER: US/09/485,737B  
; CURRENT FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: EPO 98870139.7  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: EPO 97870122.5  
; PRIOR FILING DATE: 1997-08-18  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 90  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC

US-09-485-737B-90  
Query Match 58.4%; Score 786; DB 2; Length 711;  
Best Local Similarity 58.8%; Pred. No. 1.1e-59;  
Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;

Qy 2 QVQLQSGAEVKKPGASVKVSQCSAGYRFSNFTVHVRQAPGQRFPMWGMINPYNKKEF 61  
Db 473 QVQLVQSGSELKPGASVKISCKASGYTFTDYGMMWVKQAPGQGLKWMGWINTYTGESTY 532

Qy 62 SAKFDQRTVTADTSANTAYMELRLSRADTAIVYCARVGEWGDSDPDNYMDVWGKG 121  
Db 533 VDDFKGRFVSLDTSVSAAYLQISLKAEDTATYFCARRG-----FYAMDYWGQG 582

Qy 122 TTVIVSSGGSGGGGGGGSDIELTQSPGTLSPGERATPSCRSRSHSRIRRVAVYQ 181  
Db 583 TTVIVSSGGSGGGGGGGSDIVLTQSPATMSASPERVTLTCSASSI--SYMFWYH 640

Qy 182 HKPQAPRLVHGVSNRASGISDRFSGSGSDTFTLTITRVEPEDFALYYCQVYGASST 241  
Db 641 QRPQSPRLIYDTSNLAGVPAFSGSGSGTYSYLTISRMEPEDFATYFCHQSSSYPT 700

Qy 242 FGQGTKLERK 251  
Db 701 FGQGTKLEIK 710

RESULT 9  
US-10-071-485-90  
; Sequence 90, Application US/10071485  
; Patent No. 6830752  
; GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Ange  
; APPLICANT: Sablon, Erwin  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC  
; TITLE OF INVENTION: SHOCK,  
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
; FILE REFERENCE: INNS:015  
; CURRENT APPLICATION NUMBER: US/10/071,485  
; CURRENT FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: 09/485,737  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
PRIOR FILING DATE: 1998-08-14  
PRIOR APPLICATION NUMBER: EPO 98870139.7  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: EPO 97870122.5  
PRIOR FILING DATE: 1997-08-18  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 90  
LENGTH: 711  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-10-071-485-90

Query Match 58.4%; Score 786; DB 2; Length 711;  
Best Local Similarity 58.8%; Pred. No. 1.1e-59;  
Matches 147; Conservative 38; Mismatches 53; Indels 12; Gaps 2;  
QY 2 QVLEQSGAEVKKPGASVKVSQCOAGYRFSNFTVHWVROAPGQRFENWGMINPYNNGKEF 61  
DB 473 QVQLVQSGSELKPKGASVKISCKASGYTFDYGNNVYKQAPGQGLKRWGINTYTGESTY 532  
QY 62 SAKFQDRTVFTADTSANTAYMELRSADTAVYVCARVGEWGWDDSPQDNYYMDVWGKG 121  
DB 533 VDFKGRFVSLDTSVAAYLQISLKAEDTATVFCARRG-----FYAMDYWGQG 582  
QY 122 TTVIVSGGGGGGGGGGGGSDIELTQSPGTLSLSPGERATFSCRSRSHRSRRVAWYQ 181  
DB 583 TTVIVSGGGGGGGGGGGGSDIVLTQSPATMSASPGERVLTLCSSASSI--SYMPWYH 640  
QY 182 HKPQAPRLVIHGVSNRASGISDRFSGSGSGTDFTLTITRVEPDEPDAFYCOVYGASST 241  
DB 641 QRPQSPRLIYDTSNLASGVPARFSGSGSGTSYSLTISRMEPEDFATYFCHOSSYPFT 700  
QY 242 FGQGTKLERK 251  
DB 701 FGQGTKLEIK 710

RESULT 10  
US-08-488-113B-148  
Sequence 148, Application US/08488113B  
Patent No. 5744580  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 148:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-148  
Query Match 57.2%; Score 770; DB 1; Length 240;  
Best Local Similarity 56.4%; Pred. No. 7.6e-59;  
Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;  
QY 2 QVLEQSGAEVKKPGASVKVSQCOAGYRFSNFTVHWVROAPGQRFENWGMINPYNNGKEF 61  
DB 1 EIQLVQSGGLVPGGSRVRSRAAGYTFFTYGNWVYKQAPGKGLRWGINTYTGESTY 60  
QY 62 SAKFQDRTVFTADTSANTAYMELRSADTAVYVCARVGEWGWDDSPQDNYYMDVWGKG 121  
DB 61 ADSFKGRFTFLDSDKNTAYLQINSLRAEDTAVYFCTRRG-YDW-----YFDVWGQG 111  
QY 122 TTVIVSGGGGGGGGGGGGSDIELTQSPGTLSLSPGERATFSCRSRSHRSRRVAWYQ 181  
DB 112 TTVIVSGGGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQDINS-YLSWFG 170  
QY 182 HKPQAPRLVIHGVSNRASGISDRFSGSGSGTDFTLTITRVEPDEPDAFYCOVYGASST 241  
DB 171 QKPGKAPKTLIYRANRLESVPSRFGSGSGTDYTLTISLQYEDFGIYCCQYDESPWT 230  
QY 242 FGQGTKLERK 251  
DB 231 FGQGTKLEMK 240

RESULT 11  
US-08-477-484B-148  
Sequence 148, Application US/08477484B  
Patent No. 5756699  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-484B-148

Query Match 57.2%; Score 770; DB 1; Length 240;
Best Local Similarity 56.4%; Pred. No. 7.6e-59;
Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;

Qy 2 QVLEQSGAEVKFGASVKVSCQASGYRFSNFTVHVVRQAPGQRFEMWGINPYNGNKEF 61
Db 1 EIQLVQSGGLVKFGSVRISCAASGYTFTNYGMNVVRQAPGKGLWGMWINTHTGEPY 60

Qy 62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGEWGWDDSPQDNYMDVWKG 121
Db 61 ADSFKGRFTFLDSDSKNTAYLQINSLRAEDTAVYFCTRRG-YDW-----YFDVWGQG 111

Qy 122 TTVTVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHSIRSRVAVYQ 181
Db 112 TTVTVSSGGGGGGGGGGSDIQMTQSPSLASVGDRTVITCRASQDINS-YLSWFQ 170

Qy 182 HKPGQAPRLVIHGVSNRASGISDRFSGSGGTDTFTLITRVEPEDFALYYCQVYGASST 241
Db 171 QKPKAKPTLIYRANRLSEGVPSRFSFGSGGTDTFTLITSSQLQYEDFGIYYCQYDESPWT 230

Qy 242 FGQGTKLK 251
Db 231 FGGGTKLEMK 240

RESULT 12
US-08-646-360-148
; Sequence 148, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroli, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
;
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-360-148

Query Match 57.2%; Score 770; DB 1; Length 240;
Best Local Similarity 56.4%; Pred. No. 7.6e-59;
Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;

Qy 2 QVLEQSGAEVKFGASVKVSCQASGYRFSNFTVHVVRQAPGQRFEMWGINPYNGNKEF 61
Db 1 EIQLVQSGGLVKFGSVRISCAASGYTFTNYGMNVVRQAPGKGLWGMWINTHTGEPY 60

Qy 62 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGEWGWDDSPQDNYMDVWKG 121
Db 61 ADSFKGRFTFLDSDSKNTAYLQINSLRAEDTAVYFCTRRG-YDW-----YFDVWGQG 111

Qy 122 TTVTVSSGGGGGGGGGGSDIELTQSPGTLSPGERATFSCRSRSHSIRSRVAVYQ 181
Db 112 TTVTVSSGGGGGGGGGGSDIQMTQSPSLASVGDRTVITCRASQDINS-YLSWFQ 170

Qy 182 HKPGQAPRLVIHGVSNRASGISDRFSGSGGTDTFTLITRVEPEDFALYYCQVYGASST 241
Db 171 QKPKAKPTLIYRANRLSEGVPSRFSFGSGGTDTFTLITSSQLQYEDFGIYYCQYDESPWT 230

Qy 242 FGQGTKLK 251
Db 231 FGGGTKLEMK 240
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## RESULT 13

US-08-839-765-148  
; Sequence 148, Application US/08839765  
; Patent No. 6146631  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/839,765  
; FILING DATE: 15-APR-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 148:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 240 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-839-765-148

Query Match 57.2%; Score 770; DB 2; Length 240;

Best Local Similarity 56.4%; Pred. No. 7.6e-59;

Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;

Qy 2 QVLEQSGAEVKKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFEMWGHPYNGKKEF 61  
Db 1 EIQLVQSGGLVLPGGSVRSVSCAASGYTFYTNMNVVRQAPGKLEWGMWINTHTGEPT 60  
Qy 62 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVYICARVGEWGWDDSPQDNYMDVWGK 121  
Db 61 ADSFKGFTSLDDSKNTAVLQINSLRAETAVYFCTRRG-YDW-----YFDVWGQG 111  
Qy 122 TTVIVSSGGGGGGGGGGGGSDIELTQSPGRTLSLSPGERATFSCRSHSIRRRVAVYQ 181  
Db 112 TTVTVSSGGGGGGGGGGGGSDIQTQSPSSLSASVGDRTVITCRASQDINS-YLSWFQ 170

Qy 182 HKPGQAPRLVHGVSNRASGISDRFSGSGSGTDFLTITRVEPDEALYYCOVYGASSYT 241  
Db 171 QKPGKAPKTLIYRANRLSEGVPSRFSGSGSGTDTLTLISSLOYEDFGIYYCQYDSESPWT 230  
Qy 242 FGGGTKLERK 251  
Db 231 FGGGTKLEMK 240

## RESULT 14

US-09-136-389-148  
; Sequence 148, Application US/09136389  
; Patent No. 6146850  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/136,389  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/646,360  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70.P4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 148:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 240 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-136-389-148

Query Match 57.2%; Score 770; DB 2; Length 240;

Best Local Similarity 56.4%; Pred. No. 7.6e-59;

Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;

TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 148:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-610-838-148

Query Match 57.2%; Score 770; DB 2; Length 240;  
Best Local Similarity 56.4%; Pred. No. 7.6e-59;  
Matches 141; Conservative 43; Mismatches 56; Indels 10; Gaps 3;

QY 2 QVLEQSGAEVKKPGASVKVSQAQGRFNFTHVVRQAPGQRFVWGMWNPYNGKKEF 61  
Db 1 EIQLVQSGGLVKPGGSRVIRCAASGYTFNMGWVRQAPGKGLWGMWINTHTGEPT 60  
QY 62 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVYICARVGEWGDSPQDNYMDVWGK 121  
Db 61 ADSFKGRFTFSLDSSKNTAYLQINSLRAEDTAVYFCTRRG-YDW-----YFDVWGQG 111  
QY 122 TTVIVSSGGSGGGGGGGSDIELTQSPGTLSPGERATFSCRSSHSIRSRVAVYQ 181  
Db 112 TTVIVSSGGSGGGGGGGSDIQMTQSPSSLSASVGDRTITCRASQDINS-YLSW 170  
QY 182 HKPQAPRLVIHGVSNRASGISDRFSGSGGTDTLTITRVEPEDFALYYCQVYGAS 241  
Db 171 QKFGKAPKTLIYRANRLESVPSRFSFGSGSGTDYTLTISLQYEDFGIYYCQYDESP 230  
QY 242 FGGGTKLERK 251  
Db 231 FGGGTKLEMK 240

Search completed: March 20, 2006, 07:47:39  
Job time : 27 secs

QY 2 QVLEQSGAEVKKPGASVKVSQAQGRFNFTHVVRQAPGQRFVWGMWNPYNGKKEF 61  
Db 1 EIQLVQSGGLVKPGGSRVIRCAASGYTFNMGWVRQAPGKGLWGMWINTHTGEPT 60  
QY 62 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVYICARVGEWGDSPQDNYMDVWGK 121  
Db 61 ADSFKGRFTFSLDSSKNTAYLQINSLRAEDTAVYFCTRRG-YDW-----YFDVWGQG 111  
QY 122 TTVIVSSGGSGGGGGGGSDIELTQSPGTLSPGERATFSCRSSHSIRSRVAVYQ 181  
Db 112 TTVIVSSGGSGGGGGGGSDIQMTQSPSSLSASVGDRTITCRASQDINS-YLSW 170  
QY 182 HKPQAPRLVIHGVSNRASGISDRFSGSGGTDTLTITRVEPEDFALYYCQVYGAS 241  
Db 171 QKFGKAPKTLIYRANRLESVPSRFSFGSGSGTDYTLTISLQYEDFGIYYCQYDESP 230  
QY 242 FGGGTKLERK 251  
Db 231 FGGGTKLEMK 240

RESULT 15  
US-09-610-838-148  
Sequence 148, Application US/09610838  
Patent No. 6376217  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESS: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/610,838  
FILING DATE: 06-JUL-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE: 18-AUG-1998  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:36 ; Search time 75.5 Seconds  
(without alignments)

23.278 Million cell updates/sec

Title: US-09-673-707-10

Perfect score: 20

Sequence: 1 REDL 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

A\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 20    | 100.0       | 4      | 2  | Aar95220 Pseudomon |
| 2          | 20    | 100.0       | 4      | 2  | Aaw76395 Pseudomon |
| 3          | 20    | 100.0       | 4      | 2  | Aaw52263 C-termina |
| 4          | 20    | 100.0       | 4      | 2  | Abb76202 Peptide u |
| 5          | 20    | 100.0       | 4      | 2  | Aaw92910 Pseudomon |
| 6          | 20    | 100.0       | 4      | 2  | Aay49698 Pseudomon |
| 7          | 20    | 100.0       | 4      | 2  | Aay92924 Pseudomon |
| 8          | 20    | 100.0       | 4      | 4  | Aab49323 Endosomal |
| 9          | 20    | 100.0       | 4      | 5  | Aau96732 Human XAG |
| 10         | 20    | 100.0       | 4      | 5  | Aae28524 Endoplasm |
| 11         | 20    | 100.0       | 4      | 6  | Aae33356 Endoplasm |
| 12         | 20    | 100.0       | 4      | 6  | Abr61856 Pseudomon |
| 13         | 20    | 100.0       | 4      | 7  | Adc84561 Carboxyl  |
| 14         | 20    | 100.0       | 4      | 8  | Adg5841 Pseudomon  |
| 15         | 20    | 100.0       | 4      | 8  | Adn07007 Pseudomon |
| 16         | 20    | 100.0       | 4      | 8  | Adp64378 Carboxyl  |
| 17         | 20    | 100.0       | 4      | 8  | Adp79648 Pseudomon |
| 18         | 20    | 100.0       | 4      | 9  | Adz21546 Endoplasm |
| 19         | 20    | 100.0       | 4      | 9  | Aea50149 Pseudomon |
| 20         | 20    | 100.0       | 4      | 9  | Aeb27747 Anti-pros |
| 21         | 20    | 100.0       | 4      | 9  | Aeb31417 Endoplasm |
| 22         | 20    | 100.0       | 5      | 2  | Aar95064 Pseudomon |
| 23         | 20    | 100.0       | 5      | 2  | Aar95221 Pseudomon |
| 24         | 20    | 100.0       | 5      | 2  | Aaw76394 Pseudomon |

|    |    |       |    |   |           |           |
|----|----|-------|----|---|-----------|-----------|
| 25 | 20 | 100.0 | 5  | 2 | AAW52260  | C-termina |
| 26 | 20 | 100.0 | 5  | 2 | AAW92909  | Pseudomon |
| 27 | 20 | 100.0 | 5  | 2 | AAY49697  | Pseudomon |
| 28 | 20 | 100.0 | 5  | 2 | AAW92923  | Pseudomon |
| 29 | 20 | 100.0 | 5  | 5 | AAE28523  | Endoplasm |
| 30 | 20 | 100.0 | 5  | 6 | AAE33355  | Endoplasm |
| 31 | 20 | 100.0 | 5  | 8 | ADN07006  | Pseudomon |
| 32 | 20 | 100.0 | 5  | 9 | ADZ21545  | Endoplasm |
| 33 | 20 | 100.0 | 5  | 9 | AEb27746  | Anti-pros |
| 34 | 20 | 100.0 | 6  | 2 | AAW59000  | Human HLA |
| 35 | 20 | 100.0 | 6  | 2 | AAW58997  | Human HLA |
| 36 | 20 | 100.0 | 6  | 4 | AAAB35209 | Retrovira |
| 37 | 20 | 100.0 | 7  | 2 | AAAS0265  | Peptide c |
| 38 | 20 | 100.0 | 7  | 8 | ADf94279  | Human cel |
| 39 | 20 | 100.0 | 8  | 2 | AAAR43421 | La/SSb ep |
| 40 | 20 | 100.0 | 8  | 2 | AAW26557  | Soluble p |
| 41 | 20 | 100.0 | 8  | 4 | ABP15821  | HIV A24 s |
| 42 | 20 | 100.0 | 8  | 4 | ABP21200  | HIV A24 m |
| 43 | 20 | 100.0 | 8  | 4 | ABP24221  | HIV A24 m |
| 44 | 20 | 100.0 | 9  | 3 | AAAY66341 | HLA-A24-b |
| 45 | 20 | 100.0 | 9  | 4 | AAAB35211 | Retrovira |
| 46 | 20 | 100.0 | 9  | 9 | AEb87899  | Klebsiell |
| 47 | 20 | 100.0 | 9  | 9 | AEb87903  | G. stearo |
| 48 | 20 | 100.0 | 9  | 9 | AEb87895  | Pseudomon |
| 49 | 20 | 100.0 | 10 | 2 | AAAR41212 | Peptide f |
| 50 | 20 | 100.0 | 10 | 2 | AAAR83075 | HLA-B2702 |
| 51 | 20 | 100.0 | 10 | 2 | AAAR83094 | HLA-B2702 |
| 52 | 20 | 100.0 | 10 | 2 | AAAR95425 | HLA-B2702 |
| 53 | 20 | 100.0 | 10 | 2 | AAAR95423 | HLA-B2705 |
| 54 | 20 | 100.0 | 10 | 2 | AAW07513  | T-cell mo |
| 55 | 20 | 100.0 | 10 | 2 | AAW41477  | Fragment  |
| 56 | 20 | 100.0 | 10 | 2 | AAW47271  | Immunomod |
| 57 | 20 | 100.0 | 10 | 2 | AAW47269  | Immunomod |
| 58 | 20 | 100.0 | 10 | 2 | AAW33785  | Peptide B |
| 59 | 20 | 100.0 | 10 | 2 | AAW33787  | Peptide B |
| 60 | 20 | 100.0 | 10 | 4 | AAAY72488 | Immunosup |
| 61 | 20 | 100.0 | 11 | 6 | ABU60645  | Human met |
| 62 | 20 | 100.0 | 11 | 8 | ADH08133  | Human ADA |
| 63 | 20 | 100.0 | 12 | 3 | ABb14211  | Horse cyt |
| 64 | 20 | 100.0 | 12 | 6 | ADA77726  | Peptic pe |
| 65 | 20 | 100.0 | 13 | 2 | AAAR13625 | Peptide f |
| 66 | 20 | 100.0 | 14 | 2 | AAW26563  | Immunogen |
| 67 | 20 | 100.0 | 14 | 2 | AAW76392  | Pseudomon |
| 68 | 20 | 100.0 | 14 | 2 | AAAY06083 | Bovine ac |
| 69 | 20 | 100.0 | 14 | 2 | AAAY33212 | DAR1 deri |
| 70 | 20 | 100.0 | 14 | 4 | AAAB59407 | Human Cla |
| 71 | 20 | 100.0 | 14 | 6 | ADA77727  | Peptic pe |
| 72 | 20 | 100.0 | 14 | 6 | ADA77724  | Peptic pe |
| 73 | 20 | 100.0 | 14 | 6 | ADA77711  | Peptic pe |
| 74 | 20 | 100.0 | 15 | 3 | AAAR06573 | Bovine cy |
| 75 | 20 | 100.0 | 15 | 3 | AAAY79382 | Human ATP |
| 76 | 20 | 100.0 | 15 | 8 | ADM96212  | Wild type |
| 77 | 20 | 100.0 | 15 | 9 | ADV22374  | HIV-1 Pol |
| 78 | 20 | 100.0 | 16 | 2 | AAAR50266 | HLA B27 h |
| 79 | 20 | 100.0 | 16 | 2 | AAW26556  | Soluble p |
| 80 | 20 | 100.0 | 16 | 6 | ADA77725  | Peptic pe |
| 81 | 20 | 100.0 | 17 | 2 | AAAR71442 | Human HLA |
| 82 | 20 | 100.0 | 17 | 2 | AAAR71443 | Human [Ph |
| 83 | 20 | 100.0 | 18 | 2 | AAW42876  | Sequence  |
| 84 | 20 | 100.0 | 19 | 7 | AAU00634  | Human mem |
| 85 | 20 | 100.0 | 19 | 4 | ADB88777  | Membrane  |
| 86 | 20 | 100.0 | 19 | 8 | ABG75428  | Membrane  |
| 87 | 20 | 100.0 | 20 | 4 | AAAM19911 | Peptide # |
| 88 | 20 | 100.0 | 20 | 4 | ABB39884  | Peptide # |
| 89 | 20 | 100.0 | 20 | 4 | AAAM33495 | Peptide # |
| 90 | 20 | 100.0 | 20 | 4 | ABB24461  | Protein # |
| 91 | 20 | 100.0 | 20 | 4 | AAW73294  | Human bon |
| 92 | 20 | 100.0 | 20 | 4 | AAAM60623 | Human bra |
| 93 | 20 | 100.0 | 20 | 4 | ABG55009  | Human liv |
| 94 | 20 | 100.0 | 20 | 5 | ABG43145  | Human pep |
| 95 | 20 | 100.0 | 20 | 6 | ABP70216  | Amino aci |
| 96 | 20 | 100.0 | 20 | 9 | ADZ98085  | Human ami |
| 97 | 20 | 100.0 | 21 | 6 | ABR81775  | HPV cp45  |



PD 01-OCT-1998.  
 XX  
 PF 24-MAR-1998; 98WO-US005710.  
 XX  
 PR 26-MAR-1997; 97US-0042056P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Draper RK;  
 XX  
 DR WPI; 1998-532023/45.  
 XX  
 PT Delivering compounds to cells as new conjugate with detoxified exotoxin A  
 PT - able to cross membranes and deliver to the cytoplasm, e.g. nucleic  
 PT acids, antibodies, tumour suppressors etc.  
 XX  
 PS Disclosure; Page 8; 76pp; English.  
 XX  
 CC This peptide is located at the C-terminal end of exotoxin A (ETA, see  
 CC AAW76391) of Pseudomonas aeruginosa. The motif is important in the  
 CC intracellular transport and cytotoxicity of ETA. Loss of REDL inhibits  
 CC the ability of ETA to reach the cytoplasm. However, REDL can be  
 CC substituted by KDEL (see AAW76396) without loss of cytotoxicity. The  
 CC invention provides a means of delivering compounds to cells as conjugates  
 CC with modified ETA. The modified ETA is able to cross membranes and  
 CC deliver e.g. therapeutic agents to the cytoplasm, such as nucleic acids,  
 CC peptides, peptide nucleic acids, single chain antibodies and tumour  
 CC suppressors  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 REDL 4  
 Db ||||  
 1 REDL 4  
 RESULT 3  
 AAW52263  
 ID AAW52263 standard; peptide; 4 AA.  
 XX  
 AC AAW52263;  
 XX  
 DT 18-JUN-1998 (first entry)  
 XX  
 DE C-terminal fragment of pseudomonas exotoxin.  
 XX  
 KW Pseudomonas exotoxin; PE; cytotoxic.  
 XX  
 OS Pseudomonas sp.  
 XX  
 PN US5705163-A.  
 XX  
 PD 06-JAN-1998.  
 XX  
 PF 05-JUN-1995; 95US-00461233.  
 XX  
 PR 02-JAN-1990; 90US-00459635.  
 PR 12-MAY-1990; 90US-00522563.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Fitzgerald D, Pastan I, Chaudhary VK;  
 XX  
 DR WPI; 1998-086092/08.  
 XX  
 XX Methods for killing target cells - with recombinant Pseudomonas exotoxin  
 PT fusion proteins.  
 XX  
 PS Claim 8; Col 14; 12pp; English.

XX  
 CC This sequence represents a C-terminal fragment of a Pseudomonas exotoxin  
 CC (PE). This sequence can be used in the method of the invention for  
 CC killing a target cell, which comprises contacting the cell with a  
 CC recombinant Pseudomonas exotoxin (PE) having: (a) a recognition molecule  
 CC that binds to the target cell and is inserted in domain III after amino  
 CC acid 600 and before amino acid 613 of the PE, and (b) a carboxy-terminal  
 CC sequence of 4-16 amino acids that permits translocation of the PE into  
 CC the cytosol of the target cell. The insertion of a recognition molecule  
 CC allows selective killing of target cells without significant cytotoxicity  
 CC to other cells not recognised  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 REDL 4  
 Db ||||  
 1 REDL 4  
 RESULT 4  
 ABB76202  
 ID ABB76202 standard; peptide; 4 AA.  
 XX  
 AC ABB76202;  
 XX  
 DT 05-AUG-2002 (first entry)  
 XX  
 DE Peptide used to modify Pseudomonas exotoxin.  
 XX  
 KW Exotoxin; Pseudomonas; immunotoxin; mesothelin; scFv; mesothelioma;  
 KW ovarian cancer; stomach cancer; squamous cell cancer; antitumour;  
 KW therapy; diagnosis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9928471-A2.  
 XX  
 PD 10-JUN-1999.  
 XX  
 PF 25-NOV-1998; 98WO-US025270.  
 XX  
 PR 01-DEC-1997; 97US-0067175P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Pastan IH, Chowdhury PS;  
 XX  
 DR WPI; 1999-371123/31.  
 XX  
 PT New anti-mesothelin antibodies.  
 XX  
 PS Disclosure; Page 29; 63pp; English.  
 XX  
 CC The present sequence is a peptide that can be added to the C-terminal end  
 CC of a Pseudomonas exotoxin (PE) to produce a modified PE. Claimed  
 CC immunoconjugates comprise a therapeutic agent, such as PE or a cytotoxic  
 CC fragment of PE, and an anti-mesothelin antibody, such as scFv SS (see  
 CC ABB76197), and are obtained by recombinant methods. The recombinant  
 CC immunoconjugates are used in a claimed method for inhibiting the growth  
 CC of a malignant cell that expresses mesothelin on its cell surface,  
 CC especially in mesothelioma, ovarian cancer, stomach cancer or squamous  
 CC cell cancer  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
| | | |  
Db 1 REDL 4

RESULT 5  
AAW92910  
ID AAW92910 standard; protein; 4 AA.  
XX  
AC AAW92910;  
XX  
XX  
DT 17-MAY-1999 (first entry)  
XX  
DE Pseudomonas sp. exotoxin A PE ER retention peptide motif #2.  
XX  
XX Exotoxin A; chimeric immunogen; non-toxic; PE-like; vaccine; pathogen;  
KW antibody production; non-native epitope; immune response; antigen;  
KW cancer; parasite; cell binding domain; domain Ia; humoral; cell-mediated;  
KW secretory; IGA-mediated; mucosal surface; IGA antibody; retention domain;  
KW endoplasmic reticulum.  
XX  
OS Pseudomonas sp.  
XX  
PN WO9902712-A1.  
XX  
PD 21-JAN-1999.  
XX  
PF 10-JUL-1998; 98WO-US014336.  
XX  
XX 11-JUL-1997; 97US-0056924P.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (GETH ) GENENTECH INC.  
XX  
XX Fitzgerald DJ, Mreny RJ;  
XX WPI; 1999-120913/10.  
XX  
XX New Pseudomonas exotoxin chimeric immunogens - comprise a foreign epitope  
PT for producing an immune response to pathogens, e.g. virus, bacteria or  
PT protozoa or to cancer antigens.  
XX  
XX Disclosure; Page 33; 85pp; English.  
XX  
XX This invention describes a method in which a secretory IGA-mediated  
CC immune response is elicited in a subject. The method involves  
CC administering to at least 1 mucosal surface of the subject a non-toxic  
CC Pseudomonas exotoxin A-like (PE-like) chimeric immunogen comprising a  
CC cell recognition domain of that binds to a cell surface receptor on the  
CC mucosal surface, a translocation domain comprising an amino acid sequence  
CC of PE domain II to effect translocation to a cell cytosol, a foreign  
CC epitope domain comprising an amino acid sequence of that encodes a  
CC foreign epitope, and a sequence encoding an endoplasmic reticulum (ER)  
CC retention domain that comprises an ER retention sequence. Also described  
CC is a composition comprising secretory IGA antibodies that specifically  
CC recognise an epitope of HIV-1. The method can be used for eliciting an  
CC immune response to pathogens, e.g. virus, bacteria or parasitic protozoa  
CC or to a cancer antigen. The antibodies produced can also be isolated and  
CC used, e.g. for affinity chromatography. The PE immunogens can be made by  
CC wholly recombinant techniques which allows insertion of existing variants  
CC of an epitope, or new variants of rapidly evolving epitopes. The PE can  
CC be engineered to alter the function of its domains, thereby providing a  
CC variety of activities, e.g. by replacing the native cell binding domain  
CC of PE A (domain Ia) with a ligand for a particular cell type. By providing  
CC a cell recognition domain that binds to a mucosal surface a secretory  
CC immune response involving IGA can be elicited. This sequence represents a  
CC PE protein endoplasmic reticulum (ER) retention domain motif  
XX  
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
| | | |

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
| | | |  
Db 1 REDL 4

RESULT 6  
AAW49698  
ID AAY49698 standard; peptide; 4 AA.  
XX  
XX AAY49698;  
AC AAY49698;  
XX  
DT 18-JAN-2000 (first entry)  
XX  
DE Pseudomonas exotoxin peptide #2.  
XX  
XX Pseudomonas exotoxin; PE; mutagenised; IL-13; chimeric; interleukin;  
KW cytotoxin; fusion protein; cancer; glioma; neoplasia.  
XX  
OS Pseudomonas sp.  
XX  
PN WO9951643-A1.  
XX  
PD 14-OCT-1999.  
XX  
PF 31-MAR-1999; 99WO-US007188.  
XX  
PR 03-APR-1998; 98US-00054711.  
XX  
XX (PENN-) PENN STATE RES FOUND.  
PA  
XX Debinski W;  
XX WPI; 1999-633731/54.  
XX  
XX New mutagenized interleukin 13 molecules for delivery of cytotoxins to  
PT cells over expressing IL13 receptors.  
XX  
XX Disclosure; Page 17; 57pp; English.  
XX  
XX The present invention describes targeting ligands which are mutagenized  
CC IL13 (interleukin 13) molecules having one or more mutations in the  
CC domain that interacts with the hIL14 receptor subunit designated the 140  
CC kDa hIL4Beta subunit. A cytotoxic molecule covalently attached to a  
CC mutagenized hIL13 can be used for delivering an effector molecule to a  
CC cell bearing an IL13 receptor. Where the effector molecule is a  
CC cytotoxin, neoplastic cells (e.g. a glioma) can be killed or inhibited.  
CC The methods are used to target effector molecules to kidney cancers, to  
CC skin cancers (Kaposi's sarcoma) and to brain cancers (gliomas and  
CC medulloblastomas). When the mutagenized cell is attached to a detectable  
CC label the chimeric label can be used to detect the presence or absence of  
CC tumour cells, or localize and/or quantify a cell or cells expressing an  
CC IL13 receptor. The label localizes at the site of overexpression and  
CC indicates the presence, absence, quantity or location of such cells. If  
CC the effector molecule is an antibody the chimeric molecule may act to  
CC enhance and direct an immune response toward target cancer cells. The  
CC mutagenized IL13s may be conjugated to a drug such as vinblastine,  
CC doxorubicin, genistein, an antisense molecule, ribozymes or any other  
CC pharmacological agent to specifically target target cells over expressing  
CC IL13 receptors. The targeting ligands have increased specificity for  
CC cancer cells as compared to normal cells and are therefore very effective  
CC for specifically delivering effector molecules to various neoplasias. The  
CC present sequence is used in the exemplification of the present invention  
XX  
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
| | | |

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Db      1 REDL 4

RESULT 7
AAW92924
ID      AAW92924 standard; protein; 4 AA.
XX
AC      AAW92924;
XX
DT      17-MAY-1999 (first entry)
XX
DE      Pseudomonas sp. exotoxin A PE ER retention peptide motif #2.
XX
KW      Exotoxin A; chimeric immunogen; non-toxic; PE-like; vaccine; pathogen;
KW      antibody production; non-native epitope; immune response; antigen;
KW      cancer; parasite; cell binding domain; domain Ia; humoral; cell-mediated;
KW      secretory; ER; endoplasmic reticulum; retention sequence.
XX
OS      Pseudomonas sp.
XX
PN      WO9902713-A1.
XX
PD      21-JAN-1999.
XX
PF      10-JUL-1998; 98WO-US014341.
XX
PR      11-JUL-1997; 97US-0052375P.
XX
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI      Fitzgerald DJ;
XX
DR      WPI; 1999-120914/10.
XX
PT      New Pseudomonas exotoxin chimeric immunogens - comprise a non-native
PT      epitope for producing an immune response to pathogens, e.g. virus,
PT      bacteria, or protozoa or to cancer antigens.
XX
PS      Claim 13; Page 64; 92pp; English.
XX
CC      This invention describes a non-toxic Pseudomonas exotoxin A-like (PE-
CC      like) chimeric immunogen. This PE-like immunogen can be used in vaccines
CC      and for producing antibodies against the non-native epitope. It can be
CC      used for producing an immune response to a pathogen, e.g. a virus,
CC      bacteria or parasitic protozoa or a cancer antigen. The antibodies can
CC      also be isolated and used for e.g. affinity chromatography. The PE
CC      immunogen can be made by wholly recombinant techniques which allows
CC      insertion of existing variants of an epitope, or new variants of rapidly
CC      evolving epitopes. The PE can be engineered to alter the function of its
CC      domains, thereby providing a variety of activities, e.g. by replacing the
CC      native cell binding domain of PE A (domain Ia) with a ligand for a
CC      particular cell receptor, the chimera can be targeted to bind to the
CC      particular cell type. The immunogens can elicit humoral, cell-mediated
CC      and secretory immune responses against the non-native epitope. This
CC      sequence represents a PE protein endoplasmic reticulum (ER) retention
CC      domain motif
XX
SQ      Sequence 4 AA;

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
DB      1 REDL 4

RESULT 8
AAB49323
ID      AAB49323 standard; protein; 4 AA.
XX
AC      AAB49323;
XX

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XX      01-MAR-2001 (first entry)
DT
XX      Endosomal escape motif.
DE
XX      Permeation enhancer; nucleic-acid based drug; caprylic acid;
KW      intracellular delivery; capric acid.
XX
OS      Unidentified.
XX
PN      WO200067798-A2.
XX
PD      16-NOV-2000.
XX
PF      05-MAY-2000; 2000WO-GB001726.
XX
PR      05-MAY-1999; 99US-0132603P.
XX
PA      (ELAN-) ELAN CORP PLC.
PA      (DENI/) DENISON C M.
XX
PI      Seveso M, O'mahony DJ, Page DT;
XX      WPI; 2001-049723/06.
XX
PT      Method for enhancing the intracellular delivery of a nucleic acid-based
PT      drug comprises administering in combination with an enhancer.
XX
PS      Disclosure; Page 8; 42pp; English.
XX
CC      The present invention provides novel methods of enhancing the
CC      intracellular delivery of nucleic-acid based drugs. These involve the use
CC      of formulations containing not only the nucleic acid of interest, but
CC      also a permeation enhancer such as caprylic acid or capric acid. This is
CC      particularly useful for the delivery of drugs into the cells of the
CC      gastrointestinal tract, especially the small intestine
XX
SQ      Sequence 4 AA;

Query Match      100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
DB      1 REDL 4

RESULT 9
AAU96732
ID      AAU96732 standard; peptide; 4 AA.
XX
AC      AAU96732;
XX
DT      30-JUL-2002 (first entry)
XX
DE      Human XAGE-1 p9 and XAGE-1 p16 associated C-terminal peptide #2.
XX
KW      XAGE-1; p9; p16; major histocompatibility complex; T lymphocyte; cancer;
KW      prostate cancer; lung cancer; small cell carcinoma;
KW      non-small cell carcinoma; squamous cell carcinoma; adenocarcinoma;
KW      ovarian cancer; breast cancer; glioblastoma; pancreatic cancer;
KW      T cell lymphoma; melanoma; histocytic lymphoma; Ewing's sarcoma;
KW      rhabdomyosarcoma; osteosarcoma.
XX
OS      Unidentified.
XX
PN      WO200218584-A2.
XX
PD      07-MAR-2002.
XX
PF      31-AUG-2001; 2001WO-US027258.
XX

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PR 01-SEP-2000; 2000US-0229684P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Pastan IH, Liu XF, Bera TK, Lee B, Eglund KA;
XX
XX WPI; 2002-382965/41.
XX
XX Polypeptide from xage-1 p9 or pl6 protein, which is expressed by a gene
XX expressed in multiple cancers useful for activating T lymphocytes against
XX cells expressing the protein.
XX
XX Disclosure; Page 44; 79pp; English.
XX
XX The invention describes an isolated polypeptide (I) comprising xage-1 p9
XX or pl6 protein (p9p/pl6p) which, when processed and presented in context
XX of major histocompatibility complex molecules, activates T lymphocytes
XX against cells which express p9p/pl6p. (I), a vector encoding the protein
XX (II) or a composition containing (I) is useful for the manufacture of a
XX medicament for treatment of cancer e.g. of the prostate, lung (especially
XX lung cancer from small cell carcinoma, non-small cell carcinoma, squamous
XX cell carcinoma, and adenocarcinoma), ovarian, breast, glioblastoma,
XX pancreatic, T cell lymphoma, melanoma, and histocytic lymphoma; or
XX Ewing's sarcoma, rhabdomyosarcoma and osteosarcoma. The method involves
XX administering (II) in a recombinant virus, or immunising the subject with
XX an expression vector that expresses polypeptide comprising an epitope of
XX p9p and which is an autologous recombinant cell. The method is useful for
XX inhibiting the growth of a cancer cell expressing p9p on its exterior
XX surface. (II) is useful for determining if a subject has an p9p
XX expressing cancer by taking a cell sample from the subject from a site
XX other than the testes, and determining if a cell in the sample contains a
XX nucleic acid transcript encoding p9p, or detecting p9p produced by
XX transfection of the transcript, where the method preferably comprises
XX contacting RNA from the cell with a nucleic acid probe that specifically
XX hybridises to the transcript under hybridisation conditions and detecting
XX hybridisation, or comprises disrupting the cell preferably a lymph node
XX and contacting a portion of the cell contents with a chimeric molecule
XX comprising a targeting moiety and a detectable label, where the targeting
XX moiety specifically binds to p9p and detecting the label bound to p9p.
XX This sequence represents a peptide that can be added to the C-terminal of
XX the human membrane associated XAGE-1 pl6 protein or intracellular XAGE-1
XX p9 protein in order to study protein expression
XX
XX Sequence 4 AA;
XX
XX Query Match 100.0%; Score 20; DB 5; Length 4;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 REDL 4
XX |||||
XX Db 1 REDL 4
XX
XX RESULT 10
XX AAE28524
XX ID AAE28524 standard; peptide; 4 AA.
XX AC AAE28524;
XX
XX DT 27-DEC-2002 (first entry)
XX
XX DE Endoplasmic reticulum (ER) retention peptide #2.
XX
XX Pseudomonas exotoxin A; PE; type IV pilin loop; immune response;
XX infection; gene therapy; antimicrobial; endoplasmic reticulum; ER;
XX immunostimulant.
XX
XX OS Unidentified.
XX
XX PN WO200260935-A2.
XX
XX DB 08-AUG-2002.
XX

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XX 20-DEC-2001; 2001WO-US049143.
XX
XX 21-DEC-2000; 2000US-0257877P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Fitzgerald D;
XX
XX WPI; 2002-698546/75.
XX
XX New chimeric proteins comprising a non-toxic Pseudomonas exotoxin A
XX sequence and a Type IV pilin loop sequence, useful for preventing and
XX treating infections of microorganisms, e.g. Pseudomonas aeruginosa,
XX Neisseria meningitidis.
XX
XX Disclosure; Page 66; 89pp; English.
XX
XX The invention relates to chimeric proteins comprising a non-toxic
XX Pseudomonas exotoxin A (PE) and a Type IV pilin loop. The chimeric
XX proteins are useful for eliciting an immune response in a host. They are
XX also useful for preventing and treating infections of microorganisms,
XX e.g. Pseudomonas aeruginosa, Neisseria meningitidis, Neisseria
XX gonorrhoeae, Vibrio cholera, Pasteurella multocida or Candida. The
XX chimeric proteins and compositions are useful for diagnostic tests such
XX as immunoassays, to detect the presence of microorganisms bearing a Type
XX IV pilin loop sequence, or to determine whether a host has antisera
XX against a Type IV pilin loop due to an infection. They can also be used
XX to purify antibodies against the Type IV pilin loop sequence. The
XX invention is also used in gene therapy. The present sequence is
XX endoplasmic reticulum (ER) retention peptide used in the invention
XX
XX Sequence 4 AA;
XX
XX Query Match 100.0%; Score 20; DB 5; Length 4;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 REDL 4
XX |||||
XX Db 1 REDL 4
XX
XX RESULT 11
XX AAE33356
XX ID AAE33356 standard; peptide; 4 AA.
XX AC AAE33356;
XX
XX DT 02-APR-2003 (first entry)
XX
XX DE Endoplasmic retention peptide #2.
XX
XX MUC-1; 3D; variable light domain; VL; variable heavy domain; VH; diabody;
XX cancer; antibody; therapy.
XX
XX OS Unidentified.
XX
XX PN WO200279429-A2.
XX
XX PD 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009735.
XX
XX 30-MAR-2001; 2001US-0280721P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Denardo SJ, Winthrop MD, Denardo GL;
XX
XX WPI; 2003-046804/04.
XX
XX Novel antibody that specifically binds to cancer antigen MUC-1 useful for
XX

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PT detecting a cell bearing MUC-1 antigen, comprises variable light or  
XX variable heavy domains of antibodies 12E, 3D, A5 or C4.  
XX  
XX Disclosure; Page 23; 75pp; English.  
XX  
CC The invention relates to a novel antibody that specifically binds to the  
CC cancer antigen MUC-1. The antibody comprises a domain having a sequence  
CC of a polypeptide selected from 12E variable light (VL) or variable heavy  
CC (VH) domain, 3D VL or VH domain, A5 VL or VH domain and C4 VL or VH  
CC domain. Antibodies of the invention are useful for detecting a cell  
CC bearing a MUC-1 antigen. The invention is useful for producing a variety  
CC of human or humanised antibodies or diabodies. The invention is also  
CC useful for treating cancer. The present sequence is endoplasmic retention  
XX peptide, used in the invention  
XX  
SQ Sequence 4 AA;  
  
Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 REDL 4  
Db 1 REDL 4  
  
RESULT 12  
ABR61856  
ID ABR61856 standard; peptide; 4 AA.  
XX  
XX ABR61856;  
AC  
XX  
XX 12-SEP-2003 (first entry)  
DT  
XX  
XX Pseudomonas exotoxin carboxy terminal fragment.  
DE  
XX  
XX Interleukin; IL-13; antiallergic; antiasthmatic; respiratory; PE;  
XX antiinflammatory; tuberculostatic; antimicrobial; antibacterial;  
XX antiparasitic; virucide; fungicide; exotoxin.  
XX  
XX Pseudomonas sp.  
OS  
XX  
XX WO2003047632-A1.  
FN  
XX  
XX 12-JUN-2003.  
PD  
XX  
XX 28-FEB-2002; 2002WO-IB000616.  
PF  
XX  
XX 04-DEC-2001; 2001US-0337179P.  
PR  
XX  
XX (UNMI ) UNIV MICHIGAN.  
PA  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX  
XX Puri RK, Hogaboam CM, Jakubzick C, Kunkel SL;  
PI  
XX  
XX WPI; 2003-523269/49.  
DR  
XX  
XX  
XX  
XX Use of chimeric molecule comprising a toxic moiety and a targeting moiety  
PT binding to interleukin-13 receptor or a nucleic acid sequence encoding  
PT the molecule in the treatment of e.g. allergy and asthma.  
XX  
XX Disclosure; Page 34; 105pp; English.  
XX  
XX  
XX The invention provides a chimeric molecule comprising a toxic moiety and  
CC a targeting moiety or a nucleic acid sequence encoding the chimeric  
CC molecule, for use in the manufacture of a medicament. The targeting  
CC moiety binds specifically to a cell surface receptor for interleukin-13  
CC (IL-13). The molecule can be used for application to a respiratory tract  
CC of a mammal to alleviate symptoms of a TH-2-type cytokine mediated  
CC disorders e.g. allergy, asthma, excess mucus production, airway  
CC inflammation, airway hyper responsiveness, tuberculosis, formation of  
CC granulomas during tuberculosis; and respiratory tract symptoms of viral,  
CC bacterial, fungal and parasitic infections (e.g. leishmania, filariasis

CC and schistosomiasis). Sequences ABR61855-56 represent pseudomonas  
CC exotoxin carboxy terminal fragments  
XX  
XX SQ Sequence 4 AA;  
  
Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 REDL 4  
Db 1 REDL 4  
  
RESULT 13  
ADC84561  
ID ADC84561 standard; peptide; 4 AA.  
XX  
XX ADC84561;  
AC  
XX  
XX 01-JAN-2004 (first entry)  
DT  
XX  
XX Carboxyl terminus peptide sequence of the invention #2.  
DE  
XX  
XX anti-CD22 antibody; RFB4; Cytostatic; Gene therapy; CD22-Antagonist;  
XX cancer.  
XX  
XX Unidentified.  
OS  
XX  
XX WO2003027135-A2.  
FN  
XX  
XX 03-APR-2003.  
PD  
XX  
XX 25-SEP-2002; 2002WO-US030316.  
PF  
XX  
XX 26-SEP-2001; 2001US-0325360P.  
PR  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX  
XX Pastan IH, Salvatore G, Beers R, Kreitman RJ;  
PI  
XX  
XX WPI; 2003-402972/38.  
DR  
XX  
XX New anti-CD22 antibody, useful for the manufacture of a medicament for  
PT detecting or inhibiting growth of CD22+ cancer cell, comprising variable  
PT heavy and light chains of RFB4 antibody.  
XX  
XX Disclosure; SEQ ID NO 6; 59pp; English.  
XX  
XX The present invention relates to a new anti-CD22 antibody has variable  
CC light (VL) and variable heavy (VH) chains of the antibody RFB4. The anti-  
CC CD22 antibody is useful for the manufacture of a medicament for detecting  
CC or inhibiting growth of CD22+ cancer cell. The present sequence  
CC represents a carboxyl terminus sequence of the invention.  
XX  
XX SQ Sequence 4 AA;  
  
Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 REDL 4  
Db 1 REDL 4  
  
RESULT 14  
ADG25841  
ID ADG25841 standard; peptide; 4 AA.  
XX  
XX ADG25841;  
AC  
XX  
XX 11-MAR-2004 (first entry)  
DT

Mon Mar 20 08:51:25 2006

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XX DE Pseudomonas exotoxin (PE) related peptide SEQ ID NO:31.  
XX KW antibody; CD30; anti-CD30 antibody; cytostatic; gene therapy; cancer.  
XX OS Synthetic.  
XX OS Pseudomonas sp.  
XX PN WO2003104432-A2.  
XX PD 18-DEC-2003.  
XX PF 09-JUN-2003; 2003WO-US018373.  
XX PR 07-JUN-2002; 2002US-0387293P.  
XX PR 16-SEP-2002; 2002US-0411032P.  
XX PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PA Pastan IH, Nagata S, Onda M, Numata Y, Santora K, Beers R;  
XX PI Kreitman R, Sinha A;  
XX PS WPI; 2004-062352/06.  
XX PT New antibody that binds specifically to a stalk of CD30 of a cell, or to  
XX PT an epitope destroyed upon cleavage of soluble CD30 (sCD30) from intact  
XX PT CD30, useful for inhibiting the growth of a CD30+ cancer cell.  
XX PS Disclosure; SEQ ID NO 31; 102pp; English.  
XX CC The present invention describes an isolated antibody that binds  
XX CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed  
XX CC upon cleavage of soluble CD30 (sCD30) from intact CD30. Also described:  
XX CC (1) a composition comprising the antibody conjugated or fused to a  
XX CC therapeutic part; (2) a nucleic acid encoding an antibody that binds  
XX CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed  
XX CC upon cleavage of sCD30 from intact CD30; (3) an expression vector  
XX CC comprising the nucleic acid operably linked to a promoter; (4) inhibiting  
XX CC growth of a CD30+ cancer cell; (5) detecting the presence of a CD30+ cell  
XX CC in a biological sample; (6) a host cell expressing the isolated nucleic  
XX CC acid encoding the antibody having variable heavy and variable light  
XX CC chains; and (7) a kit for detecting the presence of a CD30+ cancer cell  
XX CC in a biological sample comprising a container and an anti-CD30 antibody.  
XX CC An anti-CD30 antibody has cytostatic activity, and can be used in gene  
XX CC therapy. The anti-CD30 antibody that binds specifically to a stalk of  
XX CC CD30 of a cell, or to an epitope destroyed upon cleavage of sCD30 from  
XX CC intact CD30 is useful for the manufacture of a medicament for inhibiting  
XX CC the growth of a CD30+ cancer cell. The present sequence is used in the  
XX CC exemplification of the present invention.  
XX SQ Sequence 4 AA;  
Query Match 100.0%; Score 20; DB 8; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 REDL 4  
Db ||||  
1 REDL 4  
RESULT 15  
ADN07007  
ID ADN07007 standard; peptide; 4 AA.  
AC ADN07007;  
XX 01-JUL-2004 (first entry)  
DE Pseudomonas aeruginosa translocation signalling peptide #2.  
XX Bispecific single chain; bs-scFv; cancer;  
KW epidermal growth factor receptor; EGFR; therapy;

KW translocation signalling peptide.  
XX Pseudomonas aeruginosa.  
XX PN US2004071696-A1.  
XX PD 15-APR-2004.  
XX PF 04-APR-2003; 2003US-00406830.  
XX PR 05-APR-2002; 2002US-0370276P.  
XX XX (REGC ) UNIV CALIFORNIA.  
XX PA (FOXC-) FOX CHASE CANCER CENT.  
XX PI Adams GP, Horak EM, Weiner LM, Marks JD;  
XX DR WPI; 2004-328525/30.  
XX XX Novel bispecific antibody comprising first and second antibody joined to  
XX PT each other and having binding specificity to different epitopes of  
XX PT Epidermal Growth Factor Receptor protein, useful for treating cancer.  
XX PS Disclosure; SEQ ID NO 24; 57pp; English.  
XX CC The present invention provides bispecific single chain (bs-scFv) antibody  
XX CC molecules which may be used to treat various forms of cancer associated  
XX CC with the overexpression of the epidermal growth factor receptor (EGFR)  
XX CC family. The invention is useful for specifically delivering an effector  
XX CC molecule to a cell bearing a receptor from EGFR protein family chosen  
XX CC from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the  
XX CC treatment of cancer. The present sequence is Pseudomonas aeruginosa  
XX CC translocation signalling peptide. The peptide is used in the invention.  
XX SQ Sequence 4 AA;  
Query Match 100.0%; Score 20; DB 8; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 REDL 4  
Db ||||  
1 REDL 4  
RESULT 16  
ADP64378  
ID ADP64378 standard; peptide; 4 AA.  
XX AC ADP64378;  
XX XX 09-SEP-2004 (first entry)  
XX DE Carboxyl terminus peptide SEQ ID NO:6.  
XX KW human; breast cancer and salivary gland expression protein; BASE;  
XX KW cytostatic; immunostimulant; gene therapy;  
XX KW radioimmunotherapeutic targeted therapy; breast cancer.  
XX OS Synthetic.  
XX PN WO2004053098-A2.  
XX PD 24-JUN-2004.  
XX PF 10-DEC-2003; 2003WO-US039476.  
XX PR 10-DEC-2002; 2002US-0432531P.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Pastan IH, England KA, Vincent JJ, Lee B, Strausberg R;  
XX XX





CC variety of antibodies that specifically target the MUC-1 antigen and  
 CC cells bearing/displaying the antigen. The antibodies are useful targeting  
 CC moieties for specifically directing imaging agents and various  
 CC therapeutic moieties to a cancer. A claimed method of inhibiting the  
 CC growth or proliferation of a cell bearing a MUC-1 antigen comprises  
 CC contacting the cell with a chimeric molecule comprising an anti-MUC-1  
 CC antibody attached to a cytotoxin, a radionuclide, a liposome comprising  
 CC an anti-cancer drug, a prodrug or an anti-cancer drug. The present  
 CC sequence is that of an endoplasmic reticulum retention peptide that can  
 CC be added to the Pseudomonas exotoxin A (PE) moiety of chimeric molecules  
 CC of the invention. Note: this sequence is referred to as SEQ ID NO:12 on  
 CC page 24 of the specification, but differs from the sequence given as SEQ  
 CC ID NO:12 on page 16 ADZ21534.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
 ||||  
 Db 1 REDL 4

RESULT 19  
 AEA50149  
 ID AEA50149 standard; peptide; 4 AA.

AC AEA50149;

DT 11-AUG-2005 (first entry)

XX Pseudomonas endotoxin cytosolic translocation sequence #2.

XX Cytostatic; Antibody therapy; complementarity determining region; CDR;  
 KW CD22; Pseudomonas exotoxin; PB; antibody; cancer.

XX Homo sapiens.  
 OS Synthetic.

PN WO2005052006-A2.

XX 09-JUN-2005.

XX 24-NOV-2004; 2004WO-US039617.

XX 25-NOV-2003; 2003US-0525371P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Paestan IH, Ho M, Bang S;

XX WPI; 2005-405363/41.

XX New antibody that specifically binds CD22, useful for the manufacture of  
 PT a medicament to inhibit the growth of a CD22+ cancer cell, thus useful  
 PT for treating cancer.

XX Disclosure; SEQ ID NO 6; 106pp; English.

XX This sequence represents a fragment of Pseudomonas endotoxin (PE) which  
 CC maintains the ability of the construct to translocate into the cytosol.  
 CC The PE was used in conjunction with the antibody of the invention which  
 CC specifically binds CD22. The antibody of the invention may be used in the  
 CC generation of a chimeric molecule, which may also comprise a therapeutic  
 CC moiety. The therapeutic moiety is preferably a Pseudomonas exotoxin (PE)  
 CC or its cytotoxic fragment or mutant, where the PE has a Gly, Ala, Val,  
 CC Leu or Ile in place of Arg at position 490 of the 613 amino acids wild  
 CC type PE sequence. The antibody and chimeric molecule are useful for the  
 CC manufacture of a medicament to inhibit the growth of a CD22+ cancer cell,  
 CC and thus are useful for treating cancer.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
 ||||  
 Db 1 REDL 4

RESULT 20  
 AEB27747  
 ID AEB27747 standard; peptide; 4 AA.

XX AEB27747;

XX 22-SEP-2005 (first entry)

XX Anti-prostate cancer-antibody related translocation peptide SEQ ID NO 19.  
 DE cytostatic; antibody therapy; pharmaceutical; cancer; metastasis;  
 KW solid tumor; prostate tumor; neoplasm.

XX Synthetic.

XX WO2005062977-A2.

XX 14-JUL-2005.

XX 21-DEC-2004; 2004WO-US043574.

XX 23-DEC-2003; 2003US-0532433P.

XX (REGC ) UNIV CALIFORNIA.

XX Liu B, Marks JD;

XX WPI; 2005-522452/53.

XX Novel antibody that specifically binds and is internalized into prostate  
 PT cancer cell, useful for inhibiting growth or proliferation of prostate  
 PT cancer cell and for detecting prostate cancer cell.

XX Disclosure; SEQ ID NO 19; 77pp; English.

XX The invention describes an antibody (I) that specifically binds and is  
 CC internalized into a prostate cancer cell, comprising an antibody that  
 CC specifically binds an epitope that is specifically bound by an antibody  
 CC chosen from A33 (SEQ ID No. 22), M10A12 (SEQ ID No. 23), M9P4 (SEQ ID No.  
 CC 24), OA12 (SEQ ID No. 25), M1G12 (SEQ ID No. 26), M1F12 (SEQ ID No.  
 CC 27), and C10 (SEQ ID No. 28). Also described are: a chimeric molecule  
 CC (II), comprising an effector attached to (I); a pharmaceutical  
 CC formulation (III) comprising an excipient and (I) or (II); detecting (M1)  
 CC a prostate cancer cell, comprising contacting the prostate cancer cell  
 CC with (II) attached to an epitope tag, contacting (II) with a chelate  
 CC comprising a detectable group, where the chelate binds to the epitope tag  
 CC therefore associating the detectable group with the chelate and detecting  
 CC the detectable group; a nucleic acid (IV) comprising a nucleic acid that  
 CC encodes (I); an expression vector (V) comprising (IV); a cell comprising  
 CC (V); and a kit (VI) comprising a container containing (I), (I) and a  
 CC chimeric molecule (II) are useful for inhibiting the growth or  
 CC proliferation of a prostate cancer cell, which involves contacting the  
 CC cell with (I), or with (II) attached to a cytotoxin or radionuclide. The  
 CC cell is a metastatic cell or solid tumor cell. (II) is useful for  
 CC detecting a prostate cancer cell, which involves contacting the prostate  
 CC cancer cell with (II) attached to a detectable label and detecting the  
 CC presence or absence of the detectable label. This is the amino acid  
 CC sequence of a cell membrane translocation peptide used in the creation of  
 CC single chain anti-prostate cancer-antibodies.

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
 ||||  
 Db 1 REDL 4

RESULT 21  
 AEB31417  
 ID AEB31417 standard; peptide; 4 AA.

XX AC AEB31417;

XX DT 22-SEP-2005 (first entry)

XX DE Endoplasmic reticulum localization signal #16.

XX KW screening; antibody; caspase; apoptosis; cell proliferation; cancer;  
 KW transfection; autoimmune disease; inflammation; infectious disease;  
 KW cytostatic; immunosuppressive; anti-inflammatory; antimicrobial;  
 KW endoplasmic reticulum; ER; protein localization; antibody engineering.

XX OS Unidentified.

XX PN W02005063817-A2.

XX PD 14-JUL-2005.

XX PF 21-DEC-2004; 2004WO-US042937.

XX PR 22-DEC-2003; 2003US-0531714P.

XX PR 31-AUG-2004; 2004US-0605902P.

XX PA (AMGE-) AMGEN INC.

XX PI Yan W, Shen W, Zhou H, Zhou C, Cosman DJ, Carter P, Martin FH;  
 XX WPI; 2005-497894/50.

XX PT Enriching for nucleic acids encoding functional antibodies, useful for  
 PT treating cancer, autoimmune, inflammatory and infectious diseases, by  
 PT transfecting cells with polynucleotides encoding multimeric antibodies  
 and a vector.

XX PS Disclosure; Page 16; 93pp; English.

XX CC This invention describes a novel method of screening for nucleic acids  
 CC encoding multimeric antibodies having a biological function e.g. caspase  
 CC activity, apoptosis, and/or inhibition of proliferation of cancer cells.  
 CC The invention also describes 1) a method for identifying mammalian  
 CC transfectants expressing scFv-Fcs on their cell surfaces; 2) a method for  
 CC enriching for variant proteins that bind to a molecule with different  
 CC affinity than the original and 3) a group of mammalian cells displaying a  
 CC group of at least 100 different recombinant human antibodies on their  
 CC cell surfaces, where a library of nucleic acids encoding the group of  
 CC antibodies has been introduced into the cells via transfection using a  
 CC vector that does not comprise sequences derived from vaccinia virus or a  
 CC group of mammalian cells transfected with nucleic acids encoding at least  
 CC 100 different scFv-Fcs, where the transfected cells express at least 100  
 CC different scFv-Fcs on their cell surfaces. The products of the invention  
 CC can be used for treating cancer, autoimmune, inflammatory and infectious  
 CC diseases. This sequence represents an endoplasmic reticulum localization  
 CC sequence which can direct a protein to be retained within a cell.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4

Db 1 REDL 4  
 ||||

RESULT 22

AAR95064  
 ID AAR95064 standard; peptide; 5 AA.

XX AC AAR95064;

XX DT 18-AUG-1996 (first entry)

XX DE Pseudomonas exotoxin endoplasmic reticulum retention signal.

XX KW Nucleic acid transfer system; Gene transfer; gene therapy;

XX KW cell targeting; multidomain protein; vector; cancer;

XX KW endoplasmic reticulum; Pseudomonas; exotoxin.

XX OS Synthetic.

XX PN W09613599-A1.

XX PD 09-MAY-1996.

XX PF 31-OCT-1995; 95WO-EP004270.

XX PR 01-NOV-1994; 94EP-00810627.

XX PA (WELS/) WELS W.

XX PI Wels W, Fominaya J;

XX DR WPI; 1996-239505/24.

XX PT Nucleic acid transfer system for gene therapy, e.g. against cancer -  
 PT includes toxin translocation domain to target nucleic acid to specific  
 PT cell.

XX PS Disclosure; Page 11; 106pp; English.

XX CC Endoplasmic reticulum retention signals include a mammalian signal  
 CC (AAR95063), a bacterial signal (AAT05064) from Pseudomonas exotoxin, and  
 CC a yeast signal (AAR95065). The signal may form part of a multidomain  
 CC protein (see also AAR95063-56) that is used with an effector nucleic acid  
 CC for the transfer of nucleic acids to targeted cells as a means of gene  
 CC therapy. The endoplasmic reticulum retention signal functions to affect  
 CC intracellular routing of the internalized protein/nucleic acid complex

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4

Db 1 REDL 4

RESULT 23

AAR95221

ID AAR95221 standard; protein; 5 AA.

XX AC AAR95221;

XX DT 16-DEC-1996 (first entry)

XX DE Pseudomonas exotoxin C-terminal peptide.

XX KW Antibody; fusion protein; single chain; inhibition; tumour; diagnosis;  
 KW detection; imaging; immunotoxin; targeting; assay; immunoassay;  
 KW Lewis(Y) carbohydrate antigen.



XX This sequence represents a C-terminal fragment of a *Pseudomonas* exotoxin  
 CC (PE). This sequence can be used in the method of the invention for  
 CC killing a target cell, which comprises contacting the cell with a  
 CC recombinant *Pseudomonas* exotoxin (PE) having: (a) a recognition molecule  
 CC that binds to the target cell and is inserted in domain III after amino  
 CC acid 600 and before amino acid 613 of the PE, and (b) a carboxy-terminal  
 CC sequence of 4-16 amino acids that permits translocation of the PE into  
 CC the cytosol of the target cell. The insertion of a recognition molecule  
 CC allows selective killing of target cells without significant cytotoxicity  
 CC to other cells not recognised

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
 ||||  
 Db 1 REDL 4

#### RESULT 26

AAW92909  
 ID AAW92909 standard; protein; 5 AA.

AC AAW92909;

DT 17-MAY-1999 (first entry)

XX *Pseudomonas* sp. exotoxin A PE ER retention peptide motif #1.

XX Exotoxin A; chimeric immunogen; non-toxic; PE-like; vaccine; pathogen;  
 KW antibody production; non-native epitope; immune response; antigen;  
 KW cancer; parasite; cell binding domain; domain Ia; humoral; cell-mediated;  
 KW secretory; IGA-mediated; mucosal surface; IGA antibody; retention domain;  
 KW endoplasmic reticulum.

XX *Pseudomonas* sp.

XX WO9902712-A1.

XX 21-JAN-1999.

XX 10-JUL-1998; 98WO-US014336.

XX 11-JUL-1997; 97US-0056924P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (GETH ) GENENTECH INC.

XX Fitzgerald DJ, Mzensy RJ;

XX WPI; 1999-120913/10.

XX New *Pseudomonas* exotoxin chimeric immunogens - comprise a foreign epitope  
 PT for producing an immune response to pathogens, e.g. virus, bacteria or  
 PT protozoa or to cancer antigens.

XX Disclosure; Page 33; 85pp; English.

XX This invention describes a method in which a secretory IGA-mediated  
 CC immune response is elicited in a subject. The method involves  
 CC administering to at least 1 mucosal surface of the subject a non-toxic  
 CC *Pseudomonas* exotoxin A-like (PE-like) chimeric immunogen comprising a  
 CC cell recognition domain of that binds to a cell surface receptor on the  
 CC mucosal surface, a translocation domain comprising an amino acid sequence  
 CC of PE domain II to effect translocation to a cell cytosol, a foreign  
 CC epitope domain comprising an amino acid sequence of that encodes a  
 CC foreign epitope, and a sequence encoding an endoplasmic reticulum (ER)  
 CC retention domain that comprises an ER retention sequence. Also described  
 CC is a composition comprising secretory IGA antibodies that specifically

CC recognise an epitope of HIV-1. The method can be used for eliciting an  
 CC immune response to pathogens, e.g. virus, bacteria or parasitic protozoa  
 CC or to a cancer antigen. The antibodies produced can also be isolated and  
 CC used, e.g. for affinity chromatography. The PE immunogens can be made by  
 CC wholly recombinant techniques which allows insertion of existing variants  
 CC of an epitope, or new variants of rapidly evolving epitopes. The PE can  
 CC be engineered to alter the function of its domains, thereby providing a  
 CC variety of activities, e.g. by replacing the native cell binding domain  
 CC of PE A (domain Ia) with a ligand for a particular cell receptor, the  
 CC chimera can be targeted to bind to the particular cell type. By providing  
 CC a cell recognition domain that binds to a mucosal surface a secretory  
 CC immune response involving IGA can be elicited. This sequence represents a  
 CC PE protein endoplasmic reticulum (ER) retention domain motif

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
 ||||  
 Db 1 REDL 4

#### RESULT 27

AAV49697

ID AAV49697 standard; peptide; 5 AA.

AC AAV49697;

XX 18-JAN-2000 (first entry)

XX *Pseudomonas* exotoxin peptide #1.

XX *Pseudomonas* exotoxin; PE; mutagenised; IL-13; chimeric; interleukin;  
 KW cytotoxin; fusion protein; cancer; glioma; neoplasia.

XX *Pseudomonas* sp.

XX WO9951643-A1.

XX 14-OCT-1999.

XX 31-MAR-1999; 99WO-US007188.

XX 03-APR-1998; 98US-00054711.

XX (PENN-) PENN STATE RES FOUND.

XX Debinski W;

XX WPI; 1999-633731/54.

XX New mutagenized interleukin 13 molecules for delivery of cytotoxins to  
 PT cells over expressing IL13 receptors.

XX Disclosure; Page 17; 57pp; English.

XX The present invention describes targeting ligands which are mutagenized  
 CC IL13 (interleukin 13) molecules having one or more mutations in the  
 CC domain that interacts with the IL13 receptor subunit designated the 140  
 CC kDa IL13Rbeta subunit. A cytotoxic molecule covalently attached to a  
 CC mutagenized IL13 can be used for delivering an effector molecule to a  
 CC cell bearing an IL13 receptor. Where the effector molecule is a  
 CC cytotoxin, neoplastic cells (e.g. a glioma) can be killed or inhibited.  
 CC The methods are used to target effector molecules to kidney cancers, to  
 CC skin cancers (Kaposi's sarcoma) and to brain cancers (gliomas and  
 CC medulloblastomas). When the mutagenized cell is attached to a detectable  
 CC label the chimeric label can be used to detect the presence or absence of  
 CC tumour cells, or localize and/or quantify a cell or cells expressing an  
 CC IL13 receptor. The label localizes at the site of overexpression and  
 CC indicates the presence, absence, quantity or location of such cells. If

CC the effector molecule is an antibody the chimeric molecule may act to  
CC enhance and direct an immune response toward target cancer cells. The  
CC mutagenized IL13s may be conjugated to a drug such as vinblastine,  
CC doxorubicin, genistein, an antisense molecule, ribozymes or any other  
CC pharmacological agent to specifically target target cells over expressing  
CC IL13 receptors. The targeting ligands have increased specificity for  
CC cancer cells as compared to normal cells and are therefore very effective  
CC for specifically delivering effector molecules to various neoplasias. The  
CC present sequence is used in the exemplification of the present invention  
XX  
SQ Sequence 5 AA;

Query Match 100.0%; Score 20; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 REDL 4  
|||||  
Db 1 REDL 4

RESULT 28  
AAW92923  
ID AAW92923 standard; protein; 5 AA.

AC AAW92923;  
XX  
DT 17-MAY-1999 (first entry)

XX Pseudomonas sp. exotoxin A PE ER retention peptide motif #1.

XX Exotoxin A; chimeric immunogen; non-toxic; PE-like; vaccine; pathogen;  
KW antibody production; non-native epitope; immune response; antigen;  
KW cancer; parasite; cell binding domain; domain Ia; humoral; cell-mediated;  
secretory; ER; endoplasmic reticulum; retention sequence.

XX Pseudomonas sp.  
XX WO9902713-A1.

XX 21-JAN-1999.

XX 10-JUL-1998; 98WO-US014341.

XX 11-JUL-1997; 97US-0052375P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Fitzgerald DU;

XX WPI; 1999-120914/10.

XX New Pseudomonas exotoxin chimeric immunogens - comprise a non-native  
PT epitope for producing an immune response to pathogens, e.g. virus,  
PT bacteria, or protozoa or to cancer antigens.

XX Claim 13; Page 64; 92pp; English.

XX This invention describes a non-toxic Pseudomonas exotoxin A-like (PE-  
CC like) chimeric immunogen. This PE-like immunogen can be used in vaccines  
CC and for producing antibodies against the non-native epitope. It can be  
CC used for producing an immune response to a pathogen, e.g. a virus,  
CC bacteria or parasitic protozoa or a cancer antigen. The antibodies can  
CC also be isolated and used for e.g. affinity chromatography. The PE  
CC immunogens can be made by wholly recombinant techniques which allows  
CC insertion of existing variants of an epitope, or new variants of rapidly  
CC evolving epitopes. The PE can be engineered to alter the function of its  
CC domains, thereby providing a variety of activities, e.g. by replacing the  
CC native cell binding domain of PE A (domain Ia) with a ligand for a  
CC particular cell receptor, the chimera can be targeted to bind to the  
CC and secretory immune responses against the non-native epitope. This  
CC sequence represents a PE protein endoplasmic reticulum (ER) retention

CC domain motif  
XX Sequence 5 AA;

Query Match 100.0%; Score 20; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 REDL 4  
|||||  
Db 1 REDL 4

RESULT 29  
AAE28523  
ID AAE28523 standard; peptide; 5 AA.

XX AAE28523;

XX 27-DEC-2002 (first entry)

XX Endoplasmic reticulum (ER) retention peptide #1.

XX Pseudomonas exotoxin A; PE; type IV pilin loop; immune response;  
KW infection; gene therapy; antimicrobial; endoplasmic reticulum; ER;  
KW immunostimulant.

XX Unidentified.

XX WO200260935-A2.

XX 08-AUG-2002.

XX 20-DEC-2001; 2001WO-US049143.

XX 21-DEC-2000; 2000US-0257877P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Fitzgerald D;

XX WPI; 2002-698546/75.

XX New chimeric proteins comprising a non-toxic Pseudomonas exotoxin A  
PT sequence and a Type IV pilin loop sequence, useful for preventing and  
PT treating infections of microorganisms, e.g. Pseudomonas aeruginosa,  
PT Neisseria meningitidis.

XX Disclosure; Page 66; 89pp; English.

XX The invention relates to chimeric proteins comprising a non-toxic  
CC Pseudomonas exotoxin A (PE) and a Type IV pilin loop. The chimeric  
CC proteins are useful for eliciting an immune response in a host. They are  
CC also useful for preventing and treating infections of microorganisms,  
CC e.g. Pseudomonas aeruginosa, Neisseria meningitidis, Neisseria  
CC gonorrhoeae, Vibrio cholera, Pasteurella multocida or Candida. The  
CC chimeric proteins and compositions are useful for diagnostic tests such  
CC as immunoassays, to detect the presence of microorganisms bearing a Type  
CC IV pilin loop sequence, or to determine whether a host has antisera  
CC against a Type IV pilin loop due to an infection. They can also be used  
CC to purify antibodies against the Type IV pilin loop sequence. The  
CC invention is also used in gene therapy. The present sequence is  
CC endoplasmic reticulum (ER) retention peptide used in the invention

XX Sequence 5 AA;

Query Match 100.0%; Score 20; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 REDL 4  
|||||  
Db 1 REDL 4

RESULT 30  
 AAEE33355  
 ID AAE33355 standard; peptide; 5 AA.  
 XX  
 AC AAE33355;  
 DT  
 DT 02-APR-2003 (first entry)  
 XX  
 DE Endoplasmic retention peptide #1.  
 XX  
 KW MUC-1; 3D; variable light domain; VL; variable heavy domain; VH; diabody;  
 KW cancer; antibody; therapy.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200279429-A2.  
 PN  
 XX  
 PD 10-OCT-2002.  
 XX  
 XX 28-MAR-2002; 2002WO-US009735.  
 PF  
 XX  
 PR 30-MAR-2001; 2001US-0280721P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 XX Denardo SJ, Winthrop MD, Denardo GL;  
 PI  
 XX WPI; 2003-046804/04.  
 DR  
 XX  
 XX Novel antibody that specifically binds to cancer antigen MUC-1 useful for  
 PT detecting a cell bearing MUC-1 antigen, comprises variable light or  
 PT variable heavy domains of antibodies 12E, 3D, A5 or C4.  
 XX  
 PS Disclosure; Page 23; 75pp; English.  
 XX  
 CC The invention relates to a novel antibody that specifically binds to the  
 CC cancer antigen MUC-1. The antibody comprises a domain having a sequence  
 CC of a polypeptide selected from 12E variable light (VL) or variable heavy  
 CC (VH) domain, 3D VL or VH domain, A5 VL or VH domain and C4 VL or VH  
 CC domain. Antibodies of the invention are useful for detecting a cell  
 CC bearing a MUC-1 antigen. The invention is useful for producing a variety  
 CC of human or humanised antibodies or diabodies. The invention is also  
 CC useful for treating cancer. The present sequence is endoplasmic retention  
 CC peptide, used in the invention  
 XX  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 20; DB 6; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 REDL 4  
 Db 1 REDL 4  
 RESULT 31  
 ADN07006  
 ID ADN07006 standard; peptide; 5 AA.  
 XX  
 AC ADN07006;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Pseudomonas aeruginosa translocation signalling peptide #1.  
 XX  
 KW Bispecific single chain; bs-scFv; cancer;  
 KW epidermal growth factor receptor; EGFR; therapy;  
 KW translocation signalling peptide.  
 XX  
 OS Pseudomonas aeruginosa.

XX US2004071696-A1.  
 PN  
 XX 15-APR-2004.  
 PD  
 XX 04-APR-2003; 2003US-00406830.  
 PF  
 XX 05-APR-2002; 2002US-0370276P.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA (FOXC-) FOX CHASE CANCER CENT.  
 PA  
 XX Adams GP, Horak EM, Weiner LM, Marks JD;  
 PI  
 XX WPI; 2004-328525/30.  
 DR  
 XX  
 XX Novel bispecific antibody comprising first and second antibody joined to  
 PT each other and having binding specificity to different epitopes of  
 PT Epidermal Growth Factor Receptor protein, useful for treating cancer.  
 XX  
 PS Disclosure; SEQ ID NO 23; 57pp; English.  
 XX  
 CC The present invention provides bispecific single chain (bs-scFv) antibody  
 CC molecules which may be used to treat various forms of cancer associated  
 CC with the overexpression of the epidermal growth factor receptor (EGFR)  
 CC family. The invention is useful for specifically delivering an effector  
 CC molecule to a cell bearing a receptor from EGFR protein family chosen  
 CC from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the  
 CC treatment of cancer. The present sequence is Pseudomonas aeruginosa  
 CC translocation signalling peptide. The peptide is used in the invention.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 20; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 REDL 4  
 Db 1 REDL 4  
 RESULT 32  
 ADZ21545  
 ID ADZ21545 standard; peptide; 5 AA.  
 XX  
 AC ADZ21545;  
 XX  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Endoplasmic reticulum retention peptide.  
 DE  
 XX Single chain antibody; MUC-1; tumor-associated antigen; antibody therapy;  
 KW cytostatic.  
 KW  
 OS Synthetic.  
 OS  
 XX WO2005032454-A2.  
 PN  
 XX 14-APR-2005.  
 PD  
 XX 07-MAY-2004; 2004WO-US014159.  
 PF  
 XX 09-MAY-2003; 2003US-00435614.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Denardo SJ, Winthrop MD, Denardo GL, Xiong C;  
 PI  
 XX WPI; 2005-285319/29.  
 DR  
 XX New antibodies that specifically bind to cancer antigen MUC-1, useful for  
 PT tumor targeting, for inhibiting the growth or proliferation of cancer

PT cells or as diagnostic agents to identify tumors and monitor levels of  
 PT circulating antigen.  
 XX  
 XX Disclosure; SEQ ID NO 11; 79pp; English.  
 XX  
 XX The invention provides novel antibodies that specifically bind to the MUC  
 CC -1 cancer antigen. Preferred single chain antibodies were obtained from a  
 CC phage display library and were designated as 12E, 3D, A5, C4, B5, E1 and  
 CC B9 AD221537-AD221543. The heavy chain variable regions (VH) and light  
 CC chain variable regions (VL) of these antibodies are also provided  
 CC AD221523-AD221536. The VH and VL domains govern the specificity and  
 CC binding affinity of the antibodies and permit the construction of a  
 CC variety of antibodies that specifically target the MUC-1 antigen and  
 CC cells bearing/displaying the antigen. The antibodies are useful targeting  
 CC moieties for specifically directing imaging agents and various  
 CC therapeutic moieties to a cancer. A claimed method of inhibiting the  
 CC growth or proliferation of a cell bearing a MUC-1 antigen comprises  
 CC contacting the cell with a chimeric molecule comprising an anti-MUC-1  
 CC antibody attached to a cytotoxin, a radionuclide, a liposome comprising  
 CC an anti-cancer drug, a prodrug or an anti-cancer drug. The present  
 CC sequence is that of an endoplasmic reticulum retention peptide that can  
 CC be added to the Pseudomonas exotoxin A (PE) moiety of chimeric molecules  
 CC of the invention. Note: this sequence is referred to as SEQ ID NO:11 on  
 CC page 24 of the specification, but differs from the sequence given as SEQ  
 CC ID NO:11 on page 16 AD221533.

XX Sequence 5 AA;

Query Match 100.0%; Score 20; DB 9; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 1 REDL 4

RESULT 33

AE27746  
 ID AEB27746 standard; peptide; 5 AA.

XX AC AEB27746;

XX DT 22-SEP-2005 (first entry)

XX DE Anti-prostate cancer-antibody related translocation peptide SEQ ID NO 18.

XX DE cytosstatic; antibody therapy; pharmaceutical; cancer; metastasis;  
 XX KW solid tumor; prostate tumor; neoplasm.

XX OS Synthetic.

XX PN WO2005062977-A2.

XX PD 14-JUL-2005.

XX PF 21-DEC-2004; 2004WO-US043574.

XX PR 23-DEC-2003; 2003US-0532433P.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Liu B, Marks JD;

XX DR WPI; 2005-522452/53.

XX PT Novel antibody that specifically binds and is internalized into prostate  
 PT cancer cell, useful for inhibiting growth or proliferation of prostate  
 PT cancer cell and for detecting prostate cancer cell.

XX PS Disclosure; SEQ ID NO 18; 77pp; English.

XX XX The invention describes an antibody (I) that specifically binds and is

CC internalized into a prostate cancer cell, comprising an antibody that  
 CC specifically binds an epitope that is specifically bound by an antibody  
 CC chosen from A33 (SEQ ID No. 22), M10A12 (SEQ ID No. 23), M9E4 (SEQ ID No.  
 CC 24), OA12 (SEQ ID No. 25), M11G12 (SEQ ID No. 26), M11F12 (SEQ ID No.  
 CC 27), and C10 (SEQ ID No. 28). Also described are: a chimeric molecule  
 CC (II), comprising an effector attached to (I); a pharmaceutical  
 CC formulation (III) comprising an excipient and (I) or (II); detecting (M1)  
 CC a prostate cancer cell, comprising contacting the prostate cancer cell  
 CC with (II) attached to an epitope tag, contacting (II) with a chelate  
 CC comprising a detectable group, where the chelate binds to the epitope tag  
 CC therefore associating the detectable group with the chelate and detecting  
 CC the detectable group; a nucleic acid (IV) comprising a nucleic acid that  
 CC encodes (I); an expression vector (V) comprising (IV); a cell comprising  
 CC (V); and a kit (VI) comprising a container containing (I), (I) and a  
 CC chimeric molecule (II) are useful for inhibiting the growth or  
 CC proliferation of a prostate cancer cell, which involves contacting the  
 CC cell with (I), or with (II) attached to a cytotoxin or radionuclide. The  
 CC cell is a metastatic cell or solid tumor cell. (II) is useful for  
 CC detecting a prostate cancer cell, which involves contacting the prostate  
 CC cancer cell with (II) attached to a detectable label and detecting the  
 CC presence or absence of the detectable label. This is the amino acid  
 CC sequence of a cell membrane translocation peptide used in the creation of  
 CC single chain anti-prostate cancer-antibodies.

XX Sequence 5 AA;

Query Match 100.0%; Score 20; DB 9; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 1 REDL 4

RESULT 34

AAW59000  
 ID AAW59000 standard; peptide; 6 AA.

XX AC AAW59000;

XX DT 30-JUL-1998 (first entry)

XX DE Human HLA-B27 peptide B27PB derived fragment #4.

XX DE Human leucocyte antigen; HLA; alpha-1 domain; alpha-2 domain; HLA-B27;  
 KW keratin VI; diagnosis; treatment; HLA-dependent autoimmune disease;  
 KW Class I-associated autoimmune disease; iritis; uveitis; psoriasis;  
 KW Class II-associated autoimmune disease; rheumatic disease; arthritis;  
 KW ankylosing spondylitis; antigen; regulator.

XX OS Homo sapiens.

XX PN WO9812221-A1.

XX PD 26-MAR-1998.

XX PF 18-SEP-1997; 97WO-EP005124.

XX PR 18-SEP-1996; 96DE-01038108.

XX PA (WILD/) WILDNER G.

XX PI Wildner G;

XX DR WPI; 1998-217206/19.

XX XX Treatment and diagnosis of HLA-dependent autoimmune disease - using  
 PT peptide(s) derived from HLA-B27 or human keratin VI, e.g. for iritis,  
 PT uveitis, rheumatic disease etc.

XX PS Disclosure; Page 14; 57pp; German.



CC AAW58992-W59001 are peptides isolated from the alpha-1 or alpha-2 domain  
 CC of HLA-B27 or human keratin IV and are used in methods for diagnosis  
 CC and/or treatment of HLA (human leucocyte antigen)-dependent autoimmune  
 CC diseases. Such peptides have implications in the treatment of cases of  
 CC Class I and II-associated autoimmune diseases, especially non-HLA-B27  
 CC diseases (iritis, uveitis, psoriasis and rheumatic diseases such as  
 CC arthritis, psoriatic arthritis or juvenile rheumatoid arthritis) and HLA-  
 CC B27 diseases e.g. ankylosing spondylitis (AS). These fragments can be  
 CC administered intravenously, subcutaneously or intramuscularly, or to the  
 CC mucosa (orally, or as nasal or pulmonary spray). This method results in  
 CC antigens that are more specific than complete protein antigens, so  
 CC provide a more exact classification of disease, and thus a more specific  
 CC treatment. In the case of keratin-derived peptides, they also have better  
 CC solubility. Compared with complete proteins, peptides are easier to  
 CC prepare, do not require recovery from natural tissue or recombinant  
 CC methods of production, have better storage stability when dry, are less  
 CC likely to cause allergy and have a regulatory effect on the immune system  
 XX  
 SQ Sequence 6 AA;

Query Match 100.0%; Score 20; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 3 REDL 6  
 ||||  
 ||||

RESULT 35  
 AAW58997  
 ID AAW58997 standard; peptide; 6 AA.  
 AC AAW58997;  
 XX

DT 30-JUL-1998 (first entry)

XX Human HLA-B27 peptide B27PB derived fragment #1.

XX Human leucocyte antigen; HLA; alpha-1 domain; alpha-2 domain; HLA-B27;  
 KW keratin VI; diagnosis; treatment; HLA-dependent autoimmune disease;  
 KW Class I-associated autoimmune disease; iritis; uveitis; psoriasis;  
 KW Class II-associated autoimmune disease; rheumatic disease; arthritis;  
 KW ankylosing spondylitis; antigen; regulator.

XX Homo sapiens.

XX WO9812221-A1.

XX 26-MAR-1998.

XX 18-SEP-1997; 97WO-EP005124.

XX 18-SEP-1996; 96DE-01038108.

XX (WILD/) WILDNER G.

XX Wildner G;

XX WPI; 1998-217206/19.

XX Treatment and diagnosis of HLA-dependent autoimmune disease - using  
 PT peptide(s) derived from HLA-B27 or human keratin VI, e.g. for iritis,  
 PT uveitis, rheumatic disease etc.

XX Disclosure; Page 13; 57pp; German.

XX AAW58992-W59001 are peptides isolated from the alpha-1 or alpha-2 domain  
 CC of HLA-B27 or human keratin IV and are used in methods for diagnosis  
 CC and/or treatment of HLA (human leucocyte antigen)-dependent autoimmune  
 CC diseases. Such peptides have implications in the treatment of cases of  
 CC Class I and II-associated autoimmune diseases, especially non-HLA-B27  
 CC diseases (iritis, uveitis, psoriasis and rheumatic diseases such as

CC arthritis, psoriatic arthritis or juvenile rheumatoid arthritis) and HLA-  
 CC B27 diseases e.g. ankylosing spondylitis (AS). These fragments can be  
 CC administered intravenously, subcutaneously or intramuscularly, or to the  
 CC mucosa (orally, or as nasal or pulmonary spray). This method results in  
 CC antigens that are more specific than complete protein antigens, so  
 CC provide a more exact classification of disease, and thus a more specific  
 CC treatment. In the case of keratin-derived peptides, they also have better  
 CC solubility. Compared with complete proteins, peptides are easier to  
 CC prepare, do not require recovery from natural tissue or recombinant  
 CC methods of production, have better storage stability when dry, are less  
 CC likely to cause allergy and have a regulatory effect on the immune system  
 XX  
 SQ Sequence 6 AA;

Query Match 100.0%; Score 20; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 3 REDL 6  
 ||||  
 ||||

RESULT 36  
 AAB35209  
 ID AAB35209 standard; peptide; 6 AA.  
 XX  
 AC AAB35209;  
 XX

DT 24-APR-2001 (first entry)

XX Retroviral recombination assay peptide fragment #7.

XX Retroviral recombination assay; gene therapy vector; viral vector; gag;  
 KW pol; replication; HIV.

XX Unidentified.

XX WO200104360-A2.

XX 18-JAN-2001.

XX 06-JUL-2000; 2000WO-US018597.

XX 09-JUL-1999; 99US-0143015P.

XX 10-NOV-1999; 99US-0164626P.

XX (UABR-) UAB RES FOUND.

XX (TRAN-) TRANZYME INC.

XX Kappes JC, Wu X, Wakefield J;

XX WPI; 2001-091927/10.

XX N-PSDB; AAF24368.

XX Retroviral recombination assays, systems and cells, useful for evaluating  
 PT the risk of producing a replication-competent retrovirus from a  
 PT retroviral-based vector.

XX Example 9; Fig 23; 88pp; English.

XX The present invention describes a method for detecting a retroviral  
 CC genetic recombinant having gag and pol functions, involving a cell  
 CC suspected of having a recombinant and propagating the recombinant in the  
 CC presence of any necessary helper functions. This is useful as it enables  
 CC the detection of vectors which are able to replicate in the host cell,  
 CC and allows the production of vectors suitable for gene therapy. The  
 CC present sequence is a peptide fragment used to demonstrate the method of  
 CC the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 20; DB 4; Length 6;

```
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 REDL 4
Db 3 REDL 6

RESULT 37
AAR50265
ID AAR50265 standard; peptide; 7 AA.
XX
AC AAR50265;
XX
DT 25-MAR-2003 (revised)
DT 13-OCT-1994 (first entry)
XX
DE Peptide corresponding to a shared sequence of an HLA molecule.
XX
XX Peptide; HLA; human leucocyte antigen; diagnosis; treatment;
KW autoimmune disease; uveitis; spondylitis; psoriasis;
KW inflammatory bowel disease; enteric bacteria; Klebsiella pneumoniae.
XX
XX Klebsiella pneumoniae.
OS
XX
XX WO9405303-A1.
XX
XX 17-MAR-1994.
XX
XX 31-AUG-1993; 93WO-US008214.
XX
XX 31-AUG-1992; 92US-00944143.
XX
XX (OKLA ) UNIV OKLAHOMA STATE.
XX
XX Scofield RH, Harley JB;
PI
XX
XX WPI; 1994-100843/12.
DR
XX
XX Peptide corresponding to shared sequences of HLA molecules and enteric
PT bacteria - used for the diagnosis and treatment of auto-immune disorders,
PT partic. spondylarthropathies.
XX
XX Disclosure; Page 41; 58pp; English.
PS
XX
XX The peptide is a fragment of the HLA B27 hypervariable region described
CC in AAR50266. The peptide can be used for the diagnosis and treatment of
CC autoimmune disorders, e.g. spondylarthropathies including uveitis and
CC spondylitis associated with inflammatory bowel disease or psoriasis.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 20; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 4 REDL 7

RESULT 38
ADF94279
ID ADF94279 standard; peptide; 7 AA.
XX
AC ADF94279;
XX
DT 26-FEB-2004 (first entry)
DT
DE Human cell protein fragment #4.
XX
XX
KW affinity-labelled RNA; drug discovery; HCV infection; biotin labelled;
```

```
human.
KW
XX Homo sapiens.
XX
XX US2003194712-A1.
XX
XX 16-OCT-2003.
XX
XX 12-APR-2002; 2002US-00122675.
XX
XX 12-APR-2002; 2002US-00122675.
XX
XX (RIGE-) RIGEL PHARM INC.
XX
XX Lu H, Li W, Anderson D;
XX
XX WPI; 2004-010212/01.
XX
XX Screening for polypeptides that bind to an RNA, useful for treating
PT hepatitis C virus infection, comprises incubating an affinity-labelled RNA
PT with a cellular extract, isolating the RNA and identifying polypeptides
PT bound to the RNA.
XX
XX Example 2; Page 11; 14pp; English.
XX
XX The invention relates to a method of screening for polypeptides that bind
CC to an RNA comprising incubating an affinity-labelled RNA with a
CC cytoplasmic extract, where the RNA is linked to an affinity-labelled
CC oligonucleotide, isolating the affinity-labelled RNA, and identifying
CC polypeptides bound to the affinity-labelled RNA. The method is useful in
CC identifying polypeptide factors interacting with RNA. The polypeptide may
CC be used for drug discovery and in preventing or treating diseases, e.g.
CC HCV infection. The present sequence represents the amino acid sequence of
CC a cell protein fragment extracted by a biotinylated hepatitis C virus
CC IRES.
XX
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 20; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 2 REDL 5

RESULT 39
AAR43421
ID AAR43421 standard; peptide; 8 AA.
XX
XX AAR43421;
AC
XX
XX 25-MAR-2003 (revised)
DT 12-MAY-1994 (first entry)
XX
XX La/SSB epitope 246.
XX
XX Linear; epitope; 60 kD; Ro/SSA; La/SSB; autoantigen; E/F; G; 70 kD;
KW nuclear ribonucleoprotein; nRNP; Sm B/B'; polypeptide; antigen; D;
KW systemic lupus erythematosus; SLE; autoantibody; U4/U6; U5; B; B';
KW RNA polymerase III; U1; U2; Sjogrens syndrome; SS; human; vaccine; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9321223-A1.
XX
XX 28-OCT-1993.
XX
XX 13-APR-1993; 93WO-US003484.
XX
XX 13-APR-1992; 92US-00867819.
XX
```

PA (OKLA ) UNIV OKLAHOMA STATE.

XX Harley JB;

XX WPI; 1993-351658/44.

XX New linear epitope(s) for human auto-antibodies - from the Ro/SSA, La/SSB  
PT and Sm B/B' antigens and ribonucleoprotein, used for diagnosing and  
PT treating auto-immune disorders e.g. systemic lupus erythematosus.

PS Claim 1; Page 30; 43pp; English.

XX The sequences given in AAR43391-562 are linear epitopes which are derived  
CC from the 60 kD Ro/SSA peptide, the La/SSB autoantigen, the 70 kD nuclear  
CC ribonucleoprotein (rNRP) and the Sm B/B' polypeptide. These antigens are  
CC common in systemic lupus erythematosus (SLE) and closely related  
CC disorders. The Ro/SSA family of proteins has been shown to have several  
CC molecular forms which are defined by the molecular weight of the antigen  
CC identified. The major form has a molecular weight of 60 kD and two  
CC additional forms have molecular weights of 52 and 54 kD. La/SSB is also a  
CC member of this group of autoantibodies and binds small RNAs with a  
CC polyuridine terminus. La/SSB is bound by a third of the anti-Ro/SSA  
CC precipitin positive sera. La/SSB has been shown to be a 46-50 kD  
CC monomeric phosphoprotein which associates with RNA polymerase III  
CC transcripts. Anti-Sm antibodies precipitate snRNPs containing the U1, U2,  
CC U4/U6 and U5 RNA. Anti-Sm antibodies may be directed against one or a  
CC combination of the polypeptides: B (26 kD), B' (27 kD), D (13 kD), E/F  
CC (11 kD doublet) and G (less than 10 kD). These epitopes may be used for  
CC preventing, treating or screening autoimmune disorders, especially SLE or  
CC Sjogrens syndrome (SS). They bind to a human autoantibody and may  
CC therefore be used as vaccines. (Updated on 25-MAR-2003 to correct PN  
CC field.)

XX Sequence 8 AA;

Query Match 100.0%; Score 20; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 1 REDL 4

RESULT 40

AAW26557

ID AAW26557 standard; peptide; 8 AA.

AC AAW26557;

XX 16-JAN-1998 (first entry)

DE Soluble peptide inhibitor of retroviral protease.

XX Retrovirus; gag-pol; protease; transframe region; inhibitor;  
KW human immunodeficiency virus type 1; HIV-1; infection; therapy;  
KW antiviral agent; virucide; screening; antibody; vaccine.

XX Synthetic.

XX WO9712907-A1.

XX 10-APR-1997.

XX 24-SEP-1996; 96WO-US015304.

XX 05-OCT-1995; 95US-00539432.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Medabalmi JL;

XX WPI; 1997-226161/20.

XX

PT New peptide from trans-frame region of retroviral protein - useful for  
PT inhibiting activity and maturation of retroviral, esp. HIV, protease,  
PT e.g. for treatment of infection and for screening for antiviral agents.

PS Claim 3; Page 37; 53pp; English.

XX 17 Claimed peptides comprise the peptides given in AAW26557-61 as well as  
CC the dipeptides Asp-Asp, Asp-Glu and Asp-Gln and the tripeptides Glu-Asp-  
CC Leu, Arg-Glu-Asp, Asp-Glu-Leu, Glu-Glu-Leu, Asp-Asp-Leu, Glu-Asn-Leu, Glu-  
CC Lys-Phe, Glu-Asp-Phe and Asp-Asp-Phe. They are derived from, or related  
CC to, a claimed peptide (see AAW26556) from the transframe region (TFR) of  
CC HIV-1 Gag-Pol polyprotein. Also claimed are: antibodies (Ab) reactive  
CC with the TFR peptide; and (3) anti-idiotypic antibodies (AAb) reactive  
CC retroviral, especially HIV-1, protease activity and inhibitors of  
CC maturation) so can be used: (1) to treat cells infected with retrovirus;  
CC (2) to screen for other compounds having similar antiviral activity; (3)  
CC to stabilise retroviral compositions, especially vaccines, against  
CC proteolysis; (4) to screen compounds for more general inhibition of  
CC aspartyl proteases; and (5) to inhibit other aspartyl proteases. Since  
CC the peptides competitively inhibit protease and block its maturation,  
CC they should not lead to rapid selection of viral variants that are  
CC resistant

XX Sequence 8 AA;

Query Match 100.0%; Score 20; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 3 REDL 6

RESULT 41

ABP15821

ID ABP15821 standard; peptide; 8 AA.

AC ABP15821;

XX 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX HIV A24 super motif pol peptide #1.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US027766.

XX 05-OCT-1999; 99US-00412863.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Cellis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.

XX Claim 32; Page 193; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 20; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 3 REDL 6

RESULT 43  
ABP24221  
ID ABP24221 standard; peptide; 8 AA.  
XX  
AC ABP24221;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A24 motif pol peptide #29.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
FN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
PS Claim 32; Page 365; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 20; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 3 REDL 6

RESULT 42  
ABP21200  
ID ABP21200 standard; peptide; 8 AA.  
XX  
AC ABP21200;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A03 motif pol peptide #195.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
FN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
PS Claim 32; Page 304; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CII and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 8 AA;

Query Match 100.0%; Score 20; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 3 REDL 6

RESULT 44

AAAY66341  
ID AAY66341 standard; peptide; 9 AA.

XX AAY66341;

DT 12-SEP-2003 (revised)

DT 22-FEB-2000 (first entry)

DE HLA-A24-binding HIV-1 Pol peptide #143.

XX HIV-1; MHC; major histocompatibility complex; Class I; HLA;  
KW human leukocyte antigen; allele; binding; conserved; genome; peptide;  
KW targeting; toxic; drug; antibody; antigen; antiviral;  
KW molecular conjugate therapeutic; diagnosis; treatment; pathogen;  
KW localisation; quantification; detection; infection; drug resistance;  
KW immune response.

XX Human immunodeficiency virus 1.

XX WO9949893-A1.

XX 07-OCT-1999.

PF 31-MAR-1999; 99WO-US007111.

PR 31-MAR-1998; 98US-00052530.

XX (UYBO-) UNIV BOSTON.

PI Delisi C, Berzofsky J, Gulukota K, Vaccaro D, Weng Z, Zhang C;

DR WPI; 2000-038361/03.

XX Novel methods for designing molecular conjugate therapeutics which are used for diagnosis, imaging and treatment against pathogens.

PS Example 3; Page 45; 62pp; English.

XX AAY66199-Y66413 are peptides derived from conserved portions of the HIV-1 genome which bind to different HLA alleles of MHC (major histocompatibility complex) Class I molecules. The peptides are used to construct targetting antigens comprising one or more peptides bound to

CC the corresponding MHC Class I molecule, which can be used to raise  
CC antibodies. The antibody may then be used as a targetting vehicle to  
CC deliver a potentially toxic drug to its target site of action, rather  
CC than administering it systemically, which may result in adverse side  
CC effects. The invention relates to improved methods for the design of  
CC molecular conjugate therapeutics for the diagnosis and treatment of  
CC infections caused by pathogens with a high mutation rate (such as HIV-1).  
CC This method involves identifying conserved peptide-encoding regions among  
CC the genomes of multiple variants of a pathogen, identifying the Class I  
CC MHC molecules which occur with greatest frequency in a population of  
CC interest (e.g., human sub-populations), and determining which of the  
CC peptides bind to the Class I MHC molecules. The MHC-binding peptides and  
CC the corresponding Class I MHC molecules are selected and used to  
CC construct targetting antigens, which are in turn used to produce  
CC targetting antibodies. The methods may be used in localisation,  
CC quantification and in situ detection of specific peptide-MHC Class I  
CC complexes and also to detect and treat viral infection. The methods of  
CC the invention mitigate against the development of viral resistance to  
CC drugs and to the immune response, as well as providing a solution for  
CC targetting toxic compounds to destroy viruses sequestered in sites not  
CC accessible to T cells. In addition, the methods eliminate the virus,  
CC whereas current therapies only arrest viral replication. (Updated on 12-  
CC SEP-2003 to standardise OS field)

XX Sequence 9 AA;

Query Match 100.0%; Score 20; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 3 REDL 6

RESULT 45

AAAB35211  
ID AAB35211 standard; peptide; 9 AA.

XX AAB35211;

XX 24-APR-2001 (first entry)

XX Retroviral recombination assay peptide fragment #9.

XX Retroviral recombination assay; gene therapy vector; viral vector; gag;  
KW pol; replication; HIV.

XX Unidentified.

XX WO200104360-A2.

XX 18-JAN-2001.

XX 06-JUL-2000; 2000WO-US018597.

XX 09-JUL-1999; 99US-0143015P.

XX 10-NOV-1999; 99US-0164626P.

PA (UABR-) UAB RES FOUND.

PA (TRAN-) TRANZYME INC.

XX Kappes JC, Wu X, Wakefield J;

XX WPI; 2001-091927/10.

DR N-PSDB; AAF24370.

XX Retroviral recombination assays, systems and cells, useful for evaluating  
PT the risk of producing a replication-competent retrovirus from a  
PT retroviral-based vector.

XX Example 10; Fig 24; 88pp; English.

CC The present invention describes a method for detecting a retroviral  
CC genetic recombinant having gag and pol functions, involving a cell  
CC suspected of having a recombinant and propagating the recombinant in the  
CC presence of any necessary helper functions. This is useful as it enables  
CC the detection of vectors which are able to replicate in the host cell,  
CC and allows the production of vectors suitable for gene therapy. The  
CC present sequence is a peptide fragment used to demonstrate the method of  
CC the invention  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 20; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 6 REDL 9

RESULT 46  
AEB87899  
ID AEB87899 standard; peptide; 9 AA.

XX AC AEB87899;

XX DT 20-OCT-2005 (first entry)

XX DE Klebsiella aerogenes pullulanase PUL1 conserved fragment II.

XX KW carbohydrolase; LSA; hydrolysis; starch; polysaccharide; decontamination;  
XX KW tooth disease; sugar; antibacterial; pullulanase; PUL1.

XX OS Klebsiella aerogenes.

XX PN WO2005073369-A1.

XX PD 11-AUG-2005.

XX PF 27-JAN-2005; 2005WO-KR000235.

XX PR 30-JAN-2004; 2004KR-00006186.

XX PA (LIFE-) LIFENZA CO LTD.

XX PI Kang H, Lee J;

XX DR WPI; 2005-555696/56.

XX PT New proteins that hydrolyze amylopectin, starch, glycogen or amylose,  
XX PT useful for removing dextran or polysaccharide contaminants during sugar  
XX PT production, or for eliminating plaques or as mouthwash.

XX PS Example 4; Page 18; 42pp; English.

XX CC This invention describes a novel carbohydrolase AEB87861 which is capable  
XX CC of hydrolyzing amylopectin, starch, glycogen or amylose, or its  
XX CC derivative or fragment. The invention also describes 1) a gene, or its  
XX CC derivative or fragment, comprising AEB87862 which encodes AEB87861 or its  
XX CC derivative or fragment; 2) a transformed prokaryotic or eukaryotic cell  
XX CC expressing AEB87862 or its derivative or fragment e.g. Escherichia coli  
XX CC B121 (DES) pYES deposited with the accession number of KCTC10573HP; 3) a  
XX CC starch, glycogen or amylose; 4) an enzyme produced by the method of 3)  
XX CC are useful for removing dextran or polysaccharide contaminants during  
XX CC sugar production. The novel enzyme inhibits the formation of dental  
XX CC plaque and eliminates previously formed plaque and this anticaries  
XX CC activity is useful for anti-plaque compositions or mouthwashes. This  
XX CC sequence represents a conserved region of Klebsiella aerogenes  
XX CC pullulanase PUL1.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 20; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 3 REDL 6

RESULT 47

AEB87903

ID AEB87903 standard; peptide; 9 AA.

XX AC AEB87903;

XX DT 20-OCT-2005 (first entry)

XX DE G. stearothermophilus pullulanase PUL2 conserved fragment II.

XX KW carbohydrolase; LSA; hydrolysis; starch; polysaccharide; decontamination;  
XX KW tooth disease; sugar; antibacterial; pullulanase; PUL2.

XX OS Geobacillus stearothermophilus.

XX PN WO2005073369-A1.

XX PD 11-AUG-2005.

XX PF 27-JAN-2005; 2005WO-KR000235.

XX PR 30-JAN-2004; 2004KR-00006186.

XX PA (LIFE-) LIFENZA CO LTD.

XX PI Kang H, Lee J;

XX DR WPI; 2005-555696/56.

XX PT New proteins that hydrolyze amylopectin, starch, glycogen or amylose,  
XX PT useful for removing dextran or polysaccharide contaminants during sugar  
XX PT production, or for eliminating plaques or as mouthwash.

XX PS Example 4; Page 18; 42pp; English.

XX CC This invention describes a novel carbohydrolase AEB87861 which is capable  
XX CC of hydrolyzing amylopectin, starch, glycogen or amylose, or its  
XX CC derivative or fragment. The invention also describes 1) a gene, or its  
XX CC derivative or fragment, comprising AEB87862 which encodes AEB87861 or its  
XX CC derivative or fragment; 2) a transformed prokaryotic or eukaryotic cell  
XX CC expressing AEB87862 or its derivative or fragment e.g. Escherichia coli  
XX CC B121 (DES) pYES deposited with the accession number of KCTC10573HP; 3) a  
XX CC method of producing an enzyme having activity of hydrolyzing amylopectin,  
XX CC starch, glycogen or amylose; 4) an enzyme produced by the method of 3)  
XX CC are useful for removing dextran or polysaccharide contaminants during  
XX CC sugar production. The novel enzyme inhibits the formation of dental  
XX CC plaque and eliminates previously formed plaque and this anticaries  
XX CC activity is useful for anti-plaque compositions or mouthwashes. This  
XX CC sequence represents a conserved region of Geobacillus stearothermophilus  
XX CC pullulanase PUL2.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 20; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 3 REDL 6

## RESULT 48

AE887895  
ID AEB87895 standard; peptide; 9 AA.

XX  
AC AEB87895;

XX  
DT 20-OCT-2005 (first entry)

XX  
DE Pseudomonas amyloclavata isoamylase IAM conserved fragment II.

XX  
KW carboxylase; LSA; hydrolysis; starch; polysaccharide; decontamination;  
XX  
KW tooth disease; sugar; antibacterial; isoamylase; IAM.

XX  
OS Pseudomonas amyloclavata.

XX  
PN WO2005073369-A1.

XX  
PD 11-AUG-2005.

XX  
PF 27-JAN-2005; 2005WO-KR000235.

XX  
PR 30-JAN-2004; 2004KR-00006186.

XX  
PA (LIFE-) LIFENZA CO LTD.

XX  
PI Kang H, Lee J;

XX  
DR WPI; 2005-555696/56.

XX  
PT New proteins that hydrolyze amylopectin, starch, glycogen or amylose,  
XX  
PT useful for removing dextran or polysaccharide contaminants during sugar  
XX  
PT production, or for eliminating plaques or as mouthwash.

XX  
PS Example 4; Page 18; 42pp; English.

XX  
CC This invention describes a novel carboxylase AEB87861 which is capable  
XX  
CC of hydrolyzing amylopectin, starch, glycogen or amylose, or its  
XX  
CC derivative or fragment. The invention also describes 1) a gene, or its  
XX  
CC derivative or fragment, comprising AEB87862 which encodes AEB87861 or its  
XX  
CC derivative or fragment; 2) a transformed prokaryotic or eukaryotic cell  
XX  
CC expressing AEB87862 or its derivative or fragment e.g. Escherichia coli  
XX  
CC B121 (DES) plasmid deposited with the accession number of KCTC10573HP; 3) a  
XX  
CC method of producing an enzyme having activity of hydrolyzing amylopectin,  
XX  
CC starch, glycogen or amylose; 4) an enzyme produced by the method of 3)  
XX  
CC and 5) a composition comprising the enzyme. The composition and methods  
XX  
CC are useful for removing dextran or polysaccharide contaminants during  
XX  
CC sugar production. The novel enzyme inhibits the formation of dental  
XX  
CC plaque and eliminates previously formed plaque and this anticaries  
XX  
CC activity is useful for anti-plaque compositions or mouthwashes. This  
XX  
CC sequence represents a conserved region of Pseudomonas amyloclavata  
XX  
CC isoamylase IAM.

XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 20; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db |||||

3 REDL 6

## RESULT 49

AE41212  
ID AAR41212 standard; peptide; 10 AA.

XX  
AC AAR41212;

XX  
DT 25-MAR-2003 (revised)

XX  
DT 15-MAR-1994 (first entry)

XX  
DE Peptide fragment of Class I HLA peptide.

XX

KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
KW parasitic disease; cytotoxic T lymphocyte; modulation.

XX  
OS Synthetic.

XX  
PN WO9317699-A1.

XX  
PD 16-SEP-1993.

XX  
PF 25-FEB-1993; 93WO-US001758.

XX  
PR 02-MAR-1992; 92US-00844716.

XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.

XX  
PI Clayberger CA, Krensky AM;

XX  
DR WPI; 1993-303134/38.

XX  
PT New peptide(s) based on Class I HLA antigen domains - used for modulating  
XX  
PT cytotoxic T-lymphocyte activity towards targets.

XX  
PS Claim 11; Page 54; 61pp; English.

XX  
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity,  
XX  
CC either by inhibition or stimulation. It can be used for inhibiting CTL  
XX  
CC toxicity in transplantations, for inducing CTL activity in parasitic  
XX  
CC diseases and neoplasia and in studies on viral infection. The peptide can  
XX  
CC also be used for identifying CTLs which bind to it and removing subsets  
XX  
CC of CTLs from a T-cell composition. This peptide sequence is more commonly  
XX  
CC found within larger peptide compounds of not more than 30 amino acids in  
XX  
CC length. (Updated on 25-MAR-2003 to correct PN field.)

XX  
SQ Sequence 10 AA;

Query Match 100.0%; Score 20; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db |||||

1 REDL 4

## RESULT 50

AE83075  
ID AAR83075 standard; peptide; 10 AA.

XX  
AC AAR83075;

XX  
DT 16-MAY-1996 (first entry)

XX  
DE HLA-B2702 CTL modulating peptide (B2702.75-84).

XX  
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
XX  
KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
XX  
KW Class I MHC; HLA-B2702.

XX  
OS Synthetic.

XX  
PN WO9526979-A1.

XX  
PD 12-OCT-1995.

XX  
PF 05-APR-1995; 95WO-US004349.

XX  
PR 05-APR-1994; 94US-00222851.

XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.

XX  
PI Clayberger C, Krensky AM, Parham P;

Mon Mar 20 08:51:25 2006

DR WPI; 1995-358582/46.  
XX  
PT Extension of acceptance period of transplants from MHC unmatched donor  
PT hosts - using Class I B75-84 MHC antigen of the recipient host.  
XX  
PS Example 14; Page 34; 80pp; English.  
XX  
CC AAR81061-R83085, AAR81090-R83096 and AAR92907-R92913 represent fragments  
CC of class I major histocompatibility complex (MHC) antigens. This sequence  
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC  
CC HLA-B2702. These sequences can be used to extend the period of acceptance  
CC by a recipient of a transplant from an MHC unmatched donor. The peptides  
CC are administered to a patient in conjunction with a subtherapeutic amount  
CC of an immunosuppressant. This is administered to the patient for a  
CC limited period of time (compared to the lifetime administration for  
CC current treatments). The peptides particularly modulate (or inhibit) the  
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient  
XX  
SQ Sequence 10 AA;  
Query Match 100.0%; Score 20; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 REDL 4  
Db 1 REDL 4

Search completed: March 20, 2006, 07:52:26  
Job time : 80.5 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:51:44 ; Search time 18.5 Seconds  
(without alignments)  
17.876 Million cell updates/sec

Title: US-09-673-707-10

Perfect score: 20

Sequence: 1 REDL 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 20    | 100.0       | 4      | 1  | US-08-405-615-15  |
| 2          | 20    | 100.0       | 4      | 1  | US-08-331-398A-52 |
| 3          | 20    | 100.0       | 4      | 1  | US-08-461-234-15  |
| 4          | 20    | 100.0       | 4      | 1  | US-08-463-480-15  |
| 5          | 20    | 100.0       | 4      | 1  | US-08-821-840-3   |
| 6          | 20    | 100.0       | 4      | 1  | US-08-665-202-27  |
| 7          | 20    | 100.0       | 4      | 1  | US-08-809-668-13  |
| 8          | 20    | 100.0       | 4      | 1  | US-08-331-397B-52 |
| 9          | 20    | 100.0       | 4      | 1  | US-08-759-804A-52 |
| 10         | 20    | 100.0       | 4      | 1  | US-08-722-258-60  |
| 11         | 20    | 100.0       | 4      | 2  | US-09-397-951-13  |
| 12         | 20    | 100.0       | 4      | 2  | US-08-776-271-5   |
| 13         | 20    | 100.0       | 4      | 2  | US-09-047-148-11  |
| 14         | 20    | 100.0       | 4      | 2  | US-09-215-035-5   |
| 15         | 20    | 100.0       | 4      | 2  | US-09-479-479-34  |
| 16         | 20    | 100.0       | 4      | 2  | US-09-297-851-34  |
| 17         | 20    | 100.0       | 4      | 2  | US-09-315-574-27  |
| 18         | 20    | 100.0       | 4      | 2  | US-08-913-370-3   |
| 19         | 20    | 100.0       | 4      | 2  | US-09-581-345-9   |
| 20         | 20    | 100.0       | 4      | 4  | PCT-US93-12078-4  |
| 21         | 20    | 100.0       | 5      | 1  | US-08-405-615-14  |
| 22         | 20    | 100.0       | 5      | 1  | US-08-331-398A-53 |
| 23         | 20    | 100.0       | 5      | 1  | US-08-082-849B-33 |
| 24         | 20    | 100.0       | 5      | 1  | US-08-406-192-20  |
| 25         | 20    | 100.0       | 5      | 1  | US-08-461-234-14  |
| 26         | 20    | 100.0       | 5      | 1  | US-08-545-151-20  |
| 27         | 20    | 100.0       | 5      | 1  | US-08-463-480-14  |
| 28         | 20    | 100.0       | 5      | 1  | US-08-405-615-15  |
| 29         | 20    | 100.0       | 5      | 1  | US-08-331-398A-52 |
| 30         | 20    | 100.0       | 5      | 1  | US-08-461-234-15  |
| 31         | 20    | 100.0       | 5      | 1  | US-08-463-480-15  |
| 32         | 20    | 100.0       | 5      | 1  | US-08-821-840-3   |
| 33         | 20    | 100.0       | 5      | 1  | US-08-665-202-27  |
| 34         | 20    | 100.0       | 5      | 1  | US-08-809-668-13  |
| 35         | 20    | 100.0       | 5      | 1  | US-08-331-397B-52 |
| 36         | 20    | 100.0       | 5      | 1  | US-08-759-804A-52 |
| 37         | 20    | 100.0       | 5      | 1  | US-08-722-258-60  |
| 38         | 20    | 100.0       | 5      | 2  | US-09-397-951-13  |
| 39         | 20    | 100.0       | 5      | 2  | US-08-776-271-5   |
| 40         | 20    | 100.0       | 5      | 2  | US-09-047-148-11  |
| 41         | 20    | 100.0       | 5      | 2  | US-09-215-035-5   |
| 42         | 20    | 100.0       | 5      | 2  | US-09-479-479-34  |
| 43         | 20    | 100.0       | 5      | 2  | US-09-297-851-34  |
| 44         | 20    | 100.0       | 5      | 2  | US-09-315-574-27  |
| 45         | 20    | 100.0       | 5      | 2  | US-08-913-370-3   |
| 46         | 20    | 100.0       | 5      | 2  | US-09-581-345-9   |
| 47         | 20    | 100.0       | 5      | 4  | PCT-US93-12078-4  |
| 48         | 20    | 100.0       | 5      | 1  | US-08-405-615-14  |
| 49         | 20    | 100.0       | 5      | 1  | US-08-331-398A-53 |
| 50         | 20    | 100.0       | 5      | 1  | US-08-082-849B-33 |
| 51         | 20    | 100.0       | 5      | 1  | US-08-406-192-20  |
| 52         | 20    | 100.0       | 5      | 1  | US-08-461-234-14  |
| 53         | 20    | 100.0       | 5      | 1  | US-08-545-151-20  |
| 54         | 20    | 100.0       | 5      | 1  | US-08-463-480-14  |
| 55         | 20    | 100.0       | 5      | 1  | US-08-405-615-15  |
| 56         | 20    | 100.0       | 5      | 1  | US-08-331-398A-52 |
| 57         | 20    | 100.0       | 5      | 1  | US-08-461-234-15  |
| 58         | 20    | 100.0       | 5      | 1  | US-08-463-480-15  |
| 59         | 20    | 100.0       | 5      | 1  | US-08-821-840-3   |
| 60         | 20    | 100.0       | 5      | 1  | US-08-665-202-27  |
| 61         | 20    | 100.0       | 5      | 1  | US-08-809-668-13  |
| 62         | 20    | 100.0       | 5      | 1  | US-08-331-397B-52 |
| 63         | 20    | 100.0       | 5      | 1  | US-08-759-804A-52 |
| 64         | 20    | 100.0       | 5      | 1  | US-08-722-258-60  |
| 65         | 20    | 100.0       | 5      | 2  | US-09-397-951-13  |
| 66         | 20    | 100.0       | 5      | 2  | US-08-776-271-5   |
| 67         | 20    | 100.0       | 5      | 2  | US-09-047-148-11  |
| 68         | 20    | 100.0       | 5      | 2  | US-09-215-035-5   |
| 69         | 20    | 100.0       | 5      | 2  | US-09-479-479-34  |
| 70         | 20    | 100.0       | 5      | 2  | US-09-297-851-34  |
| 71         | 20    | 100.0       | 5      | 2  | US-09-315-574-27  |
| 72         | 20    | 100.0       | 5      | 2  | US-08-913-370-3   |
| 73         | 20    | 100.0       | 5      | 2  | US-09-581-345-9   |
| 74         | 20    | 100.0       | 5      | 4  | PCT-US93-12078-4  |
| 75         | 20    | 100.0       | 5      | 1  | US-08-405-615-14  |
| 76         | 20    | 100.0       | 5      | 1  | US-08-331-398A-53 |
| 77         | 20    | 100.0       | 5      | 1  | US-08-082-849B-33 |
| 78         | 20    | 100.0       | 5      | 1  | US-08-406-192-20  |
| 79         | 20    | 100.0       | 5      | 1  | US-08-461-234-14  |
| 80         | 20    | 100.0       | 5      | 1  | US-08-545-151-20  |
| 81         | 20    | 100.0       | 5      | 1  | US-08-463-480-14  |
| 82         | 20    | 100.0       | 5      | 1  | US-08-405-615-15  |
| 83         | 20    | 100.0       | 5      | 1  | US-08-331-398A-52 |
| 84         | 20    | 100.0       | 5      | 1  | US-08-461-234-15  |
| 85         | 20    | 100.0       | 5      | 1  | US-08-463-480-15  |
| 86         | 20    | 100.0       | 5      | 1  | US-08-821-840-3   |
| 87         | 20    | 100.0       | 5      | 1  | US-08-665-202-27  |
| 88         | 20    | 100.0       | 5      | 1  | US-08-809-668-13  |
| 89         | 20    | 100.0       | 5      | 1  | US-08-331-397B-52 |
| 90         | 20    | 100.0       | 5      | 1  | US-08-759-804A-52 |
| 91         | 20    | 100.0       | 5      | 1  | US-08-722-258-60  |
| 92         | 20    | 100.0       | 5      | 2  | US-09-397-951-13  |
| 93         | 20    | 100.0       | 5      | 2  | US-08-776-271-5   |
| 94         | 20    | 100.0       | 5      | 2  | US-09-047-148-11  |
| 95         | 20    | 100.0       | 5      | 2  | US-09-215-035-5   |
| 96         | 20    | 100.0       | 5      | 2  | US-09-479-479-34  |
| 97         | 20    | 100.0       | 5      | 2  | US-09-297-851-34  |
| 98         | 20    | 100.0       | 5      | 2  | US-09-315-574-27  |
| 99         | 20    | 100.0       | 5      | 2  | US-08-913-370-3   |
| 100        | 20    | 100.0       | 5      | 2  | US-09-581-345-9   |



; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-126110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-331-398A-52

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 3  
US-08-461-234-15  
; Sequence 15, Application US/08461234  
; Patent No. 5821238  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira H.  
; APPLICANT: Fitzgerald, David J.  
; TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with  
; TITLE OF INVENTION: Increased Activity  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,234  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,709  
; FILING DATE: 18-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/405,615  
; FILING DATE: 15-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 15280-36-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; US-08-461-234-15

Query Match 100.0%; Score 20; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 REDL 4  
Db 1 REDL 4  
RESULT 4  
US-08-463-480-15  
; Sequence 15, Application US/08463480  
; Patent No. 5854044  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira H.  
; APPLICANT: Fitzgerald, David J.  
; TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with  
; TITLE OF INVENTION: Increased Activity  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/463,480  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,709  
; FILING DATE: 18-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/405,615  
; FILING DATE: 15-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 15280-36-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; US-08-463-480-15

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 5  
US-08-821-840-3  
; Sequence 3, Application US/08821840  
; Patent No. 5919456  
; GENERAL INFORMATION:  
; APPLICANT: Puri, Raj K.  
; APPLICANT: Debinski, Waldemar

Mon Mar 20 08:51:25 2006

APPLICANT: Pastan, Ira  
APPLICANT: Obiri, Nicholas  
TITLE OF INVENTION: IL-13 Receptor Specific Chimeric  
TITLE OF INVENTION: Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/821,840  
FILING DATE: 21-MAR-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/404,685  
FILING DATE: 15-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-217100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-821-840-3

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 6  
US-08-665-202-27  
Sequence 27, Application US/08665202  
Patent No. 5977322  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
TITLE OF INVENTION: Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061410  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-665-202-27

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 7  
US-08-809-668-13  
Sequence 13, Application US/08809668  
Patent No. 5980895  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Kuan, Chien-Tsun  
TITLE OF INVENTION: Immunotoxin Containing a  
TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a  
TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 5980895 Require Proteolytic  
TITLE OF INVENTION: Activation  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/809,668  
FILING DATE: 21-AUG-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,388  
FILING DATE: 13-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US96/16327  
FILING DATE: 11-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-253100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-809-668-13

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 8  
US-08-331-397B-52  
; Sequence 52, Application US/08331397B  
; Patent No. 5981726  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Benhar, Itai  
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-  
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/331.397B  
; FILING DATE: 28-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-126120US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-331-397B-52

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 1 REDL 4  
||||

RESULT 9  
US-08-759-804A-52  
; Sequence 52, Application US/08759804A  
; Patent No. 5990296  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Willingham, Mark  
; APPLICANT: Fitzgerald, David J.  
; APPLICANT: Brinkmann, Ulrich  
; APPLICANT: Pai, Lee  
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,  
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/759,804A  
; FILING DATE: 03-DEC-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/331,398  
; FILING DATE: 28-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen L.  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-126140US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-759-804A-52

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 10  
US-08-722-258-60  
; Sequence 60, Application US/08722258  
; Patent No. 6011002  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira

Mon Mar 20 08:51:25 2006

```

; APPLICANT: Kreitman, Robert J.
; APPLICANT: Puri, Raj K.
; TITLE OF INVENTION: Circularly Permuted Ligands and
; TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,258
; FILING DATE: 08-JAN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/04468
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/225,224
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-193100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-722-258-60

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 11
US-09-397-951-13
; Sequence 13, Application US/09397951
; Patent No. 6074644
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Kuan, Chien-Tsun
; TITLE OF INVENTION: Immunotoxin Containing a
; TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a
; TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 6074644 Require Proteolytic
; TITLE OF INVENTION: Activation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; APPLICANT: Pastan, Ira
; APPLICANT: Chang, Kai
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,271
; FILING DATE: 01-DEC-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/00224
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,166
; FILING DATE: 05-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; US-09-397-951-13

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 12
US-08-776-271-5
; Sequence 5, Application US/08776271
; Patent No. 6083502
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Chang, Kai
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,271
; FILING DATE: 01-DEC-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/00224
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,166
; FILING DATE: 05-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; US-09-397-951-13

```

; REGISTRATION NUMBER: 41,739  
; REFERENCE/DOCKET NUMBER: 015280-259100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-776-271-5

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 13  
US-09-047-148-11  
; Sequence 11, Application US/09047148  
; Patent No. 6086300  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Rockford  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USING  
; TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/047,148  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/042,056  
; FILING DATE: 26-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: UTSF:072  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-9577  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-09-047-148-11

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

Db 1 REDL 4  
RESULT 14  
US-09-215-035-5  
; Sequence 5, Application US/09215035  
; Patent No. 6153430  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Chang, Kai  
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen  
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers  
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/215,035  
; FILING DATE: No. 6153430 yet assigned  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/776,271  
; FILING DATE: 01-DEC-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/00224  
; FILING DATE: 03-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/010,166  
; FILING DATE: 05-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Faris, Susan K.  
; REGISTRATION NUMBER: 41,739  
; REFERENCE/DOCKET NUMBER: 015280-259110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-215-035-5

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 15  
US-09-479-479-34  
; Sequence 34, Application US/09479479  
; Patent No. 6423513  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; APPLICANT:

```

;
; TITLE OF INVENTION: Protease-Activatable Pseudomonas
; TITLE OF INVENTION: Exotoxin A-Like Proteins
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/297,851
; FILING DATE: 30-JUL-1999
; APPLICATION NUMBER: US 60/030,376
; FILING DATE: 06-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/20207
; FILING DATE: 05-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015280-29810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-479-479-34

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 16
US-09-297-851-34
; Sequence 34, Application US/09297851
; Patent No. 6426075
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Protease-Activatable Pseudomonas
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996

```

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/297,851
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,376
; FILING DATE: 06-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/20207
; FILING DATE: 05-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015280-29810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-297-851-34

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 17
US-09-315-574-27
; Sequence 27, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996

```



ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061411  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-315-574-27

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 18  
US-08-913-370-3  
Sequence 3, Application US/08913370  
Patent No. 6518061  
GENERAL INFORMATION:  
APPLICANT: Puri, Raj K.  
APPLICANT: Debinski, Waldemar  
APPLICANT: Pastan, Ira  
APPLICANT: Obiri, Nicholas  
TITLE OF INVENTION: IL-13 Receptor Specific Chimeric  
TITLE OF INVENTION: Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/913,370  
FILING DATE: 17-FEB-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/404,685  
FILING DATE: 15-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US96/03486  
FILING DATE: 15-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-217110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-913-370-3

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 19  
US-09-581-345-9  
Sequence 9, Application US/09581345  
Patent No. 6809184  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira H.  
APPLICANT: Chowdhury, Partha S.  
APPLICANT: The Government of the United States  
APPLICANT: as represented by The Secretary of the  
APPLICANT: Department of Health and Human Services  
TITLE OF INVENTION: Antibodies, Including Fv Molecules, and  
TITLE OF INVENTION: Immunocjugates Having High Binding Affinity for  
TITLE OF INVENTION: Mesothelin and Methods for Their Use  
FILE REFERENCE: 015280-339100US  
CURRENT APPLICATION NUMBER: US/09/581,345  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: US 60/067,175  
PRIOR FILING DATE: 1997-12-01  
PRIOR APPLICATION NUMBER: WO PCT/US98/25270  
PRIOR FILING DATE: 1998-11-25  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:carboxyl  
OTHER INFORMATION: terminus  
US-09-581-345-9

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 20  
PCT-US93-12078-4  
Sequence 4, Application PC/TUS9312078  
GENERAL INFORMATION:  
APPLICANT: BOARD OF REGENTS, THE UNIVERSITY OF TEXAS  
APPLICANT: NAME:  
APPLICANT: SYSTEM  
APPLICANT: STREET: 201 West 7th Street  
APPLICANT: CITY: Austin  
APPLICANT: STATE: Texas  
APPLICANT: COUNTRY: United States of America  
APPLICANT: POSTAL CODE: 78701  
APPLICANT: TELEPHONE NO: (512)499-4462  
APPLICANT: TELEFAX: (512)499-4523  
TITLE OF INVENTION: POTENT AND SPECIFIC  
TITLE OF INVENTION: CHEMICALLY-CONJUGATED  
TITLE OF INVENTION: IMMUNOTOXINS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DURKEE  
STREET: P.O. BOX 4433  
CITY: HOUSTON

STATE: TEXAS  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK/ASKII  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/12078  
FILING DATE: UNKNOWN  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/992,900  
FILING DATE: 16.12.92  
ATTORNEY/AGENT INFORMATION:  
NAME: HODGINS, DANIEL S.  
REGISTRATION NUMBER: 31,026  
REFERENCE/DOCKET NUMBER: UTF046PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-320-7200  
TELEFAX: 713-789-2676  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acid residues  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-12078-4

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 1 REDL 4

RESULT 21  
US-08-405-615-14  
Sequence 14, Application US/08405615  
Patent No. 5602095  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: FitzGerald, David J.  
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with  
TITLE OF INVENTION: Increased Activity  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ellen L. Weber  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/405,615  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/901,709  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-36  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-405-615-14

Query Match 100.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 1 REDL 4

RESULT 22  
US-08-331-398A-53  
Sequence 53, Application US/08331398A  
Patent No. 5608039  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Willingham, Mark  
APPLICANT: FitzGerald, David  
APPLICANT: Brinkmann, Ulrich  
APPLICANT: Pai, Lee  
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
TITLE OF INVENTION: and Their Uses (as amended)  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,398A  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-331-398A-53

Query Match 100.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|  
|  
|  
|  
Db 1 REDL 4

## RESULT 23

US-08-082-849B-33  
; Sequence 33, Application US/08082849B  
; Patent No. 5677274  
; GENERAL INFORMATION:  
; APPLICANT: Lepplia, Stephen H.  
; APPLICANT: Klimpel, Kurt R.  
; APPLICANT: Arora, Naveen  
; APPLICANT: Singh, Yogendra  
; APPLICANT: Nichols, Peter J.  
; TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and  
; TITLE OF INVENTION: Related Methods  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082.849B  
; FILING DATE: 25-JUN-1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/021,601  
; FILING DATE: 12-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A.  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 15280-161-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-082-849B-33

Query Match 100.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|  
|  
|  
|  
Db 1 REDL 4

## RESULT 24

US-08-406-192-20  
; Sequence 20, Application US/08406192  
; Patent No. 5739287  
; GENERAL INFORMATION:  
; APPLICANT: Wilbur, D. Scott  
; APPLICANT: Prathare, Pradip M  
; TITLE OF INVENTION: Biotinylated Cobalamins  
; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness  
; STREET: 1420 Fifth Avenue, Suite 2800  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: U.S.A.  
; ZIP: WA 98101-2333  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/406.192  
; FILING DATE: 16-MAR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/224,831  
; FILING DATE: 08-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Renzoni, George E  
; REGISTRATION NUMBER: 37,919  
; REFERENCE/DOCKET NUMBER: RECL18947  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 682 8100  
; TELEFAX: (206) 224 0779  
; TELEX: 4938023  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-406-192-20

Query Match 100.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|  
|  
|  
|  
Db 1 REDL 4

## RESULT 25

US-08-461-234-14  
; Sequence 14, Application US/08461234  
; Patent No. 5821238  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira H.  
; APPLICANT: Fitzgerald, David J.  
; TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with  
; TITLE OF INVENTION: Increased Activity  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,234  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,709

```

; FILING DATE: 18-JUN-1992
; PRIOR APPLICATION DATA: US 08/405,615
; APPLICATION NUMBER: 15-MAR-1995
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-36-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-461-234-14

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 26
US-08-545-151-20
; Sequence 20, Application US/08545151
; Patent No. 5840712
; GENERAL INFORMATION:
; APPLICANT: Morgan Jr, A. Charles
; APPLICANT: Wilbur, D. Scott
; APPLICANT: Prathare, Pradip M
; TITLE OF INVENTION: Water Soluble Vitamin B12 Receptor
; TITLE OF INVENTION: Modulating Agents and Methods Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson & KindnessPLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: WA 98101-2333
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,151
; FILING DATE: 19-OCT-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04404
; FILING DATE: 07-APR-1995
; APPLICATION NUMBER: US 08/406,192
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: US 08/406,194
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: US 08/406,191
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: US 08/224,831
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Renzoni, George E
; REGISTRATION NUMBER: 37,919
; REFERENCE/DOCKET NUMBER: RECL18878
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 682 8100
; TELEFAX: (206) 224 0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-545-151-20

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 27
US-08-463-480-14
; Sequence 14, Application US/08463480
; Patent No. 5854044
; GENERAL INFORMATION:
; APPLICANT: Pastan, Iza H.
; APPLICANT: Fitzgerald, David J.
; TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
; TITLE OF INVENTION: Increased Activity
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,480
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,709
; FILING DATE: 18-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/405,615
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-36-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-463-480-14

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 REDL 4  
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|  
Db 1 REDL 4

## RESULT 28

US-08-821-840-2  
; Sequence 26, Application US/08821840  
; Patent No. 5919456  
; GENERAL INFORMATION:  
; APPLICANT: Puri, Raj K.  
; APPLICANT: Debinski, Waldemar  
; APPLICANT: Pastan, Ira  
; APPLICANT: Obiri, Nicholas  
; TITLE OF INVENTION: IL-13 Receptor Specific Chimeric  
; TITLE OF INVENTION: Proteins and Uses Thereof  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/821,840  
; FILING DATE: 21-MAR-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/404,685  
; FILING DATE: 15-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-217100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-821-840-2

Query Match 100.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
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|  
Db 1 REDL 4

## RESULT 29

US-08-665-202-26  
; Sequence 26, Application US/08665202  
; Patent No. 5977322  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D.  
; APPLICANT: Schier, Robert  
; TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,202  
; FILING DATE: 13-JUN-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,238  
; FILING DATE: 14-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,250  
; FILING DATE: 15-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 02307E-061410  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-665-202-26

Query Match 100.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
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|  
|  
Db 1 REDL 4

## RESULT 30

US-08-809-668-8  
; Sequence 8, Application US/08809668  
; Patent No. 5980895  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Kuan, Chien-Tsun  
; TITLE OF INVENTION: Immunotoxin Containing a  
; TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a  
; TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 5980895 Require Proteolytic  
; TITLE OF INVENTION: Activation  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,668  
; FILING DATE: 21-AUG-1997

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-331-397B-53

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 32
US-08-759-804A-53
; Sequence 53, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/759,804A
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-759-804A-53

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 31
US-08-331-397B-53
; Sequence 53, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 53:

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||||  
Db 1 REDL 4

## RESULT 33

US-08-722-258-59  
; Sequence 59, Application US/08722258  
; Patent No. 6011002  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Kreitman, Robert J.  
; APPLICANT: Puri, Raj K.  
; TITLE OF INVENTION: Circularly Permuted Ligands and  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/722,258  
; FILING DATE: 08-JAN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US95/04468  
; FILING DATE: 06-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/225,224  
; FILING DATE: 08-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; FILING DATE: 08-APR-1994  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-193100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-722-258-59

Query Match 100.0%; Score 20; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||||  
Db 1 REDL 4

## RESULT 34

US-08-722-258-65  
; Sequence 65, Application US/08722258  
; Patent No. 6011002  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Kreitman, Robert J.  
; APPLICANT: Puri, Raj K.

; TITLE OF INVENTION: Circularly Permuted Ligands and  
; TITLE OF INVENTION: Circularly Permuted Chimeric Molecules  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/722,258  
; FILING DATE: 08-JAN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US95/04468  
; FILING DATE: 06-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/225,224  
; FILING DATE: 08-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-193100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-722-258-65

Query Match 100.0%; Score 20; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||||  
Db 1 REDL 4

## RESULT 35

US-09-397-951-8  
; Sequence 8, Application US/09397951  
; Patent No. 6074644  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Kuan, Chien-Tsun

; TITLE OF INVENTION: Immunotoxin Containing a  
; TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a  
; TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 6074644 Require Proteolysis  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/397,951
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,668
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16327
; FILING DATE: 11-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-253100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-397-951-8

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 1 REDL 4

RESULT 36
US-09-776-271-4
; Sequence 4, Application US/08776271
; Patent No. 6083502
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,271
; FILING DATE: 01-DEC-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/00224
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,166
; FILING DATE: 05-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Farie, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-259100US

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-776-271-4

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 1 REDL 4

RESULT 37
US-09-047-148-10
; Sequence 10, Application US/09047148
; Patent No. 6086900
; GENERAL INFORMATION:
; APPLICANT: Draper, Rockford
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USING
; TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
; TITLE OF INVENTION: CELL MEMBRANES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/047,148
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,056
; FILING DATE: 26-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSP-072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-047-148-10

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 1 REDL 4
```



## RESULT 38

US-09-215-035-4  
; Sequence 4, Application US/09215035  
; Patent No. 6153430  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Chang, Kai  
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen  
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers  
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/215,035  
; FILING DATE: No. 6153430 yet assigned  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/776,271  
; FILING DATE: 01-DEC-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/00224  
; FILING DATE: 03-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/010,166  
; FILING DATE: 05-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Faris, Susan K.  
; REGISTRATION NUMBER: 41,739  
; REFERENCE/DOCKET NUMBER: 015280-259110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-215-035-4

Query Match 100.0%; Score 20; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 1 REDL 4

## RESULT 39

US-09-479-479-33  
; Sequence 33, Application US/09479479  
; Patent No. 6423513  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: Protease-Activatable Pseudomonas  
; TITLE OF INVENTION: Exotoxin A-Like Proteins

NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/479,479  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/297,851  
; FILING DATE: 30-JUL-1999  
; APPLICATION NUMBER: US 60/030,376  
; FILING DATE: 06-NOV-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/20207  
; FILING DATE: 05-NOV-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015280-29810US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-479-479-33

Query Match 100.0%; Score 20; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 1 REDL 4

## RESULT 40

US-09-297-851-33  
; Sequence 33, Application US/09297851  
; Patent No. 6426075  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: Protease-Activatable Pseudomonas  
; TITLE OF INVENTION: Exotoxin A-Like Proteins  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/297,851
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,376
; FILING DATE: 06-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/20207
; FILING DATE: 05-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015280-29810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-297-851-33

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 41
US-08-840-713-46
; Sequence 46, Application US/08840713
; Patent No. 6498233
; GENERAL INFORMATION:
; APPLICANT: WELS, Winfried, Dr.
; APPLICANT: FOYMINA, Jesus
; TITLE OF INVENTION: NUCLEIC ACID TRANSFER SYSTEM
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 15th St., N.W., Suite 330 - G St. Lobby
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,713
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kittle, Monica Chin
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: 1614-7014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638 - 5000
; TELEFAX: (202) 638 - 4810
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-840-713-46

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 42
US-09-315-574-26
; Sequence 26, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-315-574-26

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 43

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US-08-913-370-2  
; Sequence 2, Application US/08913370  
; Patent No. 6518061  
; GENERAL INFORMATION:  
; APPLICANT: Puri, Raj K.  
; APPLICANT: Debinski, Waldemar  
; APPLICANT: Pastan, Ira  
; APPLICANT: Obiri, Nicholas  
; TITLE OF INVENTION: IL-13 Receptor Specific Chimeric  
; TITLE OF INVENTION: Proteins and Uses Thereof  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913,370  
; FILING DATE: 17-FEB-1998  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/404,685  
; FILING DATE: 15-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US96/03486  
; FILING DATE: 15-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-217110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-913-370-2

Query Match 100.0%; Score 20; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 44  
US-10-122-675-6  
; Sequence 6, Application US/10122675  
; Patent No. 6927031  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; APPLICANT: Li, Weiqun  
; APPLICANT: Lu, Henry  
; APPLICANT: Rigel Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Methods for Identifying Polypeptide Factors Interacting  
; TITLE OF INVENTION: With RNA  
; FILE REFERENCE: 021044-002000US  
; CURRENT APPLICATION NUMBER: US/10/122,675  
; CURRENT FILING DATE: 2002-10-31  
; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:40S ribosomal  
; OTHER INFORMATION: protein S18 peptide  
US-10-122-675-6

Query Match 100.0%; Score 20; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 2 REDL 5

RESULT 45  
PCT-US93-08214-15  
; Sequence 15, Application PC/TUS9308214  
; GENERAL INFORMATION:  
; APPLICANT: Oklahoma Medical Research Foundation  
; TITLE OF INVENTION: Peptide Diagnostics and Therapeutics for Spondyloarthropat  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kilpatrick & Cody  
; STREET: 1100 Peachtree Street, Suite 2800  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: United States  
; ZIP: 30309-4530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08214  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMRF138  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 815-6508  
; TELEFAX: (404) 815-6555  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: Klebsiella pneumoniae  
PCT-US93-08214-15

Query Match 100.0%; Score 20; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 4 REDL 7

RESULT 46

Mon Mar 20 08:51:25 2006

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US-08-539-432-1
; Sequence 1, Application US/08539432
; Patent No. 5872210
; GENERAL INFORMATION:
; APPLICANT: MEDABALIMI, JOHN L.
; TITLE OF INVENTION: TRANSFRAME INHIBITORY
; TITLE OF INVENTION: ELEMENT OF VIRAL
; TITLE OF INVENTION: PROTEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,432
; FILING DATE: 05-OCT-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 759-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-08-539-432-1

Query Match 100.0%; Score 20; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 3 REDL 6

RESULT 47
US-08-475-955-33
; Sequence 33, Application US/08475955
; Patent No. 6641813
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; TITLE OF INVENTION: AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,955
; FILING DATE: June 7, 1995

US-09-673-707-10.ra1

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1..8
US-08-475-955-33

Query Match 100.0%; Score 20; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 48
US-07-867-819D-33
; Sequence 33, Application US/07867819D
; Patent No. 6897287
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
; FILE REFERENCE: OMRF 114 CIP (2)
; CURRENT APPLICATION NUMBER: US/07/867,819D
; CURRENT FILING DATE: 1992-04-13
; PRIOR APPLICATION NUMBER: 07/472,947
; PRIOR FILING DATE: 1990-01-31
; PRIOR APPLICATION NUMBER: 07/648,205
; PRIOR FILING DATE: 1991-01-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(8)
; OTHER INFORMATION: Binding site
US-07-867-819D-33

Query Match 100.0%; Score 20; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

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RESULT 49  
US-08-222-851-14  
; Sequence 14, Application US/08222851  
; Patent No. 5723128  
; GENERAL INFORMATION:  
; APPLICANT: CLAYBERGER, CAROL A.  
; APPLICANT: KRENSKY, ALAN M.  
; APPLICANT: PARHAM, PETER  
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")  
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222,851  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MILLMAN, ROBERT A.  
; REGISTRATION NUMBER: 36,217  
; REFERENCE/DOCKET NUMBER: 28600-20200.22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 494-0792  
; TELEX: 90-4030 MRSNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-222-851-14

Query Match 100.0%; Score 20; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 50  
US-08-222-851-30  
; Sequence 30, Application US/08222851  
; Patent No. 5723128  
; GENERAL INFORMATION:  
; APPLICANT: CLAYBERGER, CAROL A.  
; APPLICANT: KRENSKY, ALAN M.  
; APPLICANT: PARHAM, PETER  
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")  
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222,851  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MILLMAN, ROBERT A.  
; REGISTRATION NUMBER: 36,217  
; REFERENCE/DOCKET NUMBER: 28600-20200.22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 494-0792  
; TELEX: 90-4030 MRSNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-222-851-30

Query Match 100.0%; Score 20; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

Search completed: March 20, 2006, 07:52:32  
Job time : 19.5 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: March 20, 2006, 07:52:57 ; Search time 62.5 Seconds  
(without alignments)  
26.741 Million cell updates/sec

Title: US-09-673-707-10  
Perfect score: 20  
Sequence: 1 REDL 4  
Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5  
Searched: 1867569 seqs, 417829326 residues  
Total number of hits satisfying chosen parameters: 1867569  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description          |
|------------|-------|-------------|--------|-------|----------------------|
| 1          | 20    | 100.0       | 4      | 3     | US-09-480-236-7      |
| 2          | 20    | 100.0       | 4      | 3     | US-09-462-713-12     |
| 3          | 20    | 100.0       | 4      | 4     | US-10-112-788-16     |
| 4          | 20    | 100.0       | 4      | 4     | US-10-297-337-16     |
| 5          | 20    | 100.0       | 4      | 4     | US-10-406-830-24     |
| 6          | 20    | 100.0       | 4      | 4     | US-10-432-412-22     |
| 7          | 20    | 100.0       | 4      | 4     | US-10-432-412-23     |
| 8          | 20    | 100.0       | 4      | 4     | US-10-363-233-7      |
| 9          | 20    | 100.0       | 4      | 5     | US-10-659-036-12     |
| 10         | 20    | 100.0       | 4      | 5     | US-10-490-535-6      |
| 11         | 20    | 100.0       | 4      | 5     | US-10-973-718-9      |
| 12         | 20    | 100.0       | 4      | 6     | US-11-021-438-19     |
| 13         | 20    | 100.0       | 5      | 3     | US-09-480-236-6      |
| 14         | 20    | 100.0       | 5      | 3     | US-09-462-713-11     |
| 15         | 20    | 100.0       | 5      | 4     | US-10-112-788-15     |
| 16         | 20    | 100.0       | 5      | 4     | US-10-297-337-15     |
| 17         | 20    | 100.0       | 5      | 4     | US-10-406-830-23     |
| 18         | 20    | 100.0       | 5      | 4     | US-10-432-412-21     |
| 19         | 20    | 100.0       | 5      | 5     | US-10-659-036-11     |
| 20         | 20    | 100.0       | 5      | 5     | US-10-490-535-7      |
| 21         | 20    | 100.0       | 5      | 6     | US-11-021-438-18     |
| 22         | 20    | 100.0       | 7      | 4     | US-10-132-675-6      |
| 23         | 20    | 100.0       | 8      | 4     | US-10-137-867-296    |
| 24         | 20    | 100.0       | 8      | 4     | US-10-376-121A-33    |
| 25         | 20    | 100.0       | 9      | 4     | US-10-133-210-114    |
| 26         | 20    | 100.0       | 10     | 5     | US-10-780-321-40     |
| 27         | 20    | 100.0       | 11     | 3     | US-09-955-504-29     |
| 28         | 20    | 100.0       | 11     | 4     | US-10-125-452-29     |
| 29         | 20    | 100.0       | 19     | 4     | US-10-136-845-4      |
| 30         | 20    | 100.0       | 19     | 4     | US-10-136-845-62     |
| 31         | 20    | 100.0       | 19     | 4     | US-10-116-275-92     |
| 32         | 20    | 100.0       | 19     | 4     | US-10-764-235-4      |
| 33         | 20    | 100.0       | 19     | 5     | US-10-955-656-4      |
| 34         | 20    | 100.0       | 19     | 5     | US-10-955-656-62     |
| 35         | 20    | 100.0       | 20     | 3     | US-09-864-761-39759  |
| 36         | 20    | 100.0       | 20     | 4     | US-10-136-187-5      |
| 37         | 20    | 100.0       | 20     | 4     | US-10-136-187-9      |
| 38         | 20    | 100.0       | 20     | 5     | US-10-850-873-5      |
| 39         | 20    | 100.0       | 20     | 5     | US-10-850-873-9      |
| 40         | 20    | 100.0       | 20     | 5     | US-10-690-276-239    |
| 41         | 20    | 100.0       | 21     | 4     | US-10-302-547-89     |
| 42         | 20    | 100.0       | 21     | 4     | US-10-302-547-90     |
| 43         | 20    | 100.0       | 23     | 4     | US-10-029-386-32550  |
| 44         | 20    | 100.0       | 23     | 6     | US-11-155-043-23     |
| 45         | 20    | 100.0       | 28     | 3     | US-09-864-761-37447  |
| 46         | 20    | 100.0       | 28     | 3     | US-09-864-761-42724  |
| 47         | 20    | 100.0       | 28     | 5     | US-10-808-187-236    |
| 48         | 20    | 100.0       | 28     | 5     | US-10-807-807-236    |
| 49         | 20    | 100.0       | 31     | 3     | US-09-932-367A-33    |
| 50         | 20    | 100.0       | 33     | 4     | US-10-425-115-269508 |
| 51         | 20    | 100.0       | 35     | 4     | US-10-012-542-324    |
| 52         | 20    | 100.0       | 35     | 4     | US-10-115-123-324    |
| 53         | 20    | 100.0       | 35     | 4     | US-10-424-599-159103 |
| 54         | 20    | 100.0       | 35     | 4     | US-10-800-834-324    |
| 55         | 20    | 100.0       | 36     | 4     | US-10-424-599-242042 |
| 56         | 20    | 100.0       | 36     | 5     | US-10-896-169-3      |
| 57         | 20    | 100.0       | 37     | 6     | US-11-077-752-15     |
| 58         | 20    | 100.0       | 38     | 4     | US-10-437-963-195320 |
| 59         | 20    | 100.0       | 38     | 4     | US-10-425-115-287477 |
| 60         | 20    | 100.0       | 38     | 6     | US-11-077-752-14     |
| 61         | 20    | 100.0       | 39     | 3     | US-09-864-761-43161  |
| 62         | 20    | 100.0       | 40     | 4     | US-10-424-599-256593 |
| 63         | 20    | 100.0       | 41     | 4     | US-10-425-115-273706 |
| 64         | 20    | 100.0       | 42     | 4     | US-10-425-115-205956 |
| 65         | 20    | 100.0       | 42     | 4     | US-10-425-115-230741 |
| 66         | 20    | 100.0       | 43     | 4     | US-10-424-599-269749 |
| 67         | 20    | 100.0       | 43     | 4     | US-10-425-115-332906 |
| 68         | 20    | 100.0       | 43     | 5     | US-10-450-763-30799  |
| 69         | 20    | 100.0       | 44     | 3     | US-09-873-637-28     |
| 70         | 20    | 100.0       | 44     | 4     | US-10-264-049-4105   |
| 71         | 20    | 100.0       | 44     | 4     | US-10-424-599-231706 |
| 72         | 20    | 100.0       | 44     | 4     | US-10-437-963-174698 |
| 73         | 20    | 100.0       | 45     | 3     | US-09-864-761-42644  |
| 74         | 20    | 100.0       | 45     | 4     | US-10-767-701-54557  |
| 75         | 20    | 100.0       | 46     | 4     | US-10-425-115-319937 |
| 76         | 20    | 100.0       | 47     | 3     | US-09-864-761-45129  |
| 77         | 20    | 100.0       | 47     | 4     | US-10-424-599-214990 |
| 78         | 20    | 100.0       | 47     | 4     | US-10-424-599-249770 |
| 79         | 20    | 100.0       | 47     | 4     | US-10-437-963-198312 |
| 80         | 20    | 100.0       | 47     | 4     | US-10-425-115-201052 |
| 81         | 20    | 100.0       | 47     | 4     | US-10-425-115-293536 |
| 82         | 20    | 100.0       | 48     | 4     | US-10-424-599-177161 |
| 83         | 20    | 100.0       | 49     | 3     | US-09-864-761-47908  |
| 84         | 20    | 100.0       | 49     | 4     | US-10-029-386-31181  |
| 85         | 20    | 100.0       | 49     | 4     | US-10-029-386-33086  |
| 86         | 20    | 100.0       | 49     | 4     | US-10-424-599-187483 |
| 87         | 20    | 100.0       | 49     | 4     | US-10-425-115-363870 |
| 88         | 20    | 100.0       | 50     | 3     | US-09-864-761-43361  |
| 89         | 20    | 100.0       | 50     | 5     | US-10-776-013-485    |
| 90         | 20    | 100.0       | 51     | 3     | US-09-864-761-39015  |
| 91         | 20    | 100.0       | 51     | 4     | US-10-425-115-190326 |
| 92         | 20    | 100.0       | 51     | 4     | US-10-425-115-232249 |
| 93         | 20    | 100.0       | 52     | 4     | US-10-424-599-257365 |
| 94         | 20    | 100.0       | 52     | 4     | US-10-437-963-115604 |
| 95         | 20    | 100.0       | 52     | 4     | US-10-437-963-184184 |
| 96         | 20    | 100.0       | 52     | 4     | US-10-425-115-205954 |
| 97         | 20    | 100.0       | 52     | 4     | US-10-425-115-278676 |
| 98         | 20    | 100.0       | 53     | 3     | US-09-864-761-44873  |
| 99         | 20    | 100.0       | 53     | 4     | US-10-097-065-378    |
| 100        | 20    | 100.0       | 53     | 4     | US-10-372-876-378    |





US-10-112-788-16

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
|||  
Db 1 REDL 4

## RESULT 4

US-10-297-337-16  
; Sequence 16, Application US/10297337  
; Publication No. US20040018203A1  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira H.  
; APPLICANT: Tautsumi, Yasuo  
; APPLICANT: Onda, Masanori  
; APPLICANT: Nagata, Satoshi  
; APPLICANT: Lee, Byungkook  
; APPLICANT: Kreitman, Robert J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: PEGylation of Linkers Improves Antitumor Activity and  
; TITLE OF INVENTION: Reduces Toxicity of Immunoconjugates  
; FILE REFERENCE: 015280-423200US  
; CURRENT APPLICATION NUMBER: US/10/297,337  
; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/211,331  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: US 60/213,804  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: WO PCT/US01/18503  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:C-terminal  
; OTHER INFORMATION: variation to maintain ability of construct to  
; OTHER INFORMATION: translocate to cytosol  
US-10-297-337-16

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
|||  
Db 1 REDL 4

## RESULT 5

US-10-406-830-24  
; Sequence 24, Application US/10406830  
; Publication No. US20040071696A1  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, GREGORY P.  
; APPLICANT: HORAK, EVA M.  
; APPLICANT: WEINER, LOUIS M.  
; APPLICANT: JAMES, MARKS D.  
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 407T-000410US  
; CURRENT APPLICATION NUMBER: US/10/406,830  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/370,276  
; PRIOR FILING DATE: 2002-04-05

; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24

; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Translocation signaling sequence.

US-10-406-830-24

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
|||  
Db 1 REDL 4

## RESULT 6

US-10-432-412-22  
; Sequence 22, Application US/10432412  
; Publication No. US20040071731A1  
; GENERAL INFORMATION:  
; APPLICANT: FitzGerald, David J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas  
; TITLE OF INVENTION: Exotoxin A and Type IV Pilin Sequences  
; FILE REFERENCE: 015280-429100US  
; CURRENT APPLICATION NUMBER: US/10/432,412  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/257,877  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:endoplasmic  
; OTHER INFORMATION: reticulum (ER) retention domain  
US-10-432-412-22

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
|||  
Db 1 REDL 4

## RESULT 7

US-10-432-412-23  
; Sequence 23, Application US/10432412  
; Publication No. US20040071731A1  
; GENERAL INFORMATION:  
; APPLICANT: FitzGerald, David J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas  
; TITLE OF INVENTION: Exotoxin A and Type IV Pilin Sequences  
; FILE REFERENCE: 015280-429100US  
; CURRENT APPLICATION NUMBER: US/10/432,412  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/257,877  
; PRIOR FILING DATE: 2000-12-21

|  |  |   |  |
|--|--|---|--|
| ; PRIOR APPLICATION NUMBER: WO PCT/US01/49143                                |  | ; APPLICANT: Department of Health and Human Services                          |  |
| ; PRIOR FILING DATE: 2001-12-20  |  | ; APPLICANT: Genentech, Inc.  |  |
| ; NUMBER OF SEQ ID NOS: 36   |  | ; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens for     |  |
| ; SOFTWARE: PatentIn Ver. 2.1  |  | ; TITLE OF INVENTION: Eliciting a Secretory Iga-Mediated Immune Response      |  |
| ; SEQ ID NO 23   |  | ; FILE REFERENCE: 015280-361200US   |  |
| ; LENGTH: 4  |  | ; CURRENT APPLICATION NUMBER: US/10/659,036                                   |  |
| ; TYPE: PRT  |  | ; CURRENT FILING DATE: 2003-09-09   |  |
| ; ORGANISM: Artificial Sequence  |  | ; PRIOR APPLICATION NUMBER: US 60/056,924                                     |  |
| ; FEATURE:   |  | ; PRIOR FILING DATE: 1997-07-11   |  |
| ; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic         |  | ; PRIOR APPLICATION NUMBER: WO PCT/US98/14336                                 |  |
| ; OTHER INFORMATION: reticulum (ER) retention domain                         |  | ; PRIOR FILING DATE: 1998-07-10   |  |
| US-10-432-412-23   |  | ; PRIOR APPLICATION NUMBER: US 09/462,713                                     |  |
| Query Match  |  | ; PRIOR FILING DATE: 2000-05-12   |  |
| Best Local Similarity 100.0%; Score 20; DB 4; Length 4;                      |  | ; NUMBER OF SEQ ID NOS: 13  |  |
| Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                   |  | ; SOFTWARE: PatentIn Ver. 2.1   |  |
| QY 1 REDL 4  |  | ; SEQ ID NO 12  |  |
| Db 1 REDL 4  |  | ; LENGTH: 4   |  |
| RESULT 8   |  | ; TYPE: PRT   |  |
| US-10-363-233-7  |  | ; ORGANISM: Artificial Sequence   |  |
| ; Sequence 7, Application US/10363233  |  | ; FEATURE:  |  |
| ; Publication No. US2004008772A1   |  | ; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic          |  |
| ; GENERAL INFORMATION:   |  | ; OTHER INFORMATION: reticulum (ER) retention sequence                        |  |
| ; APPLICANT: Pastan, Ira H.  |  | US-10-659-036-12  |  |
| ; APPLICANT: Liu, Xiu Fen  |  | Query Match   |  |
| ; APPLICANT: Bera, Tapan K.  |  | Best Local Similarity 100.0%; Score 20; DB 5; Length 4;                       |  |
| ; APPLICANT: Lee, Byungkook  |  | Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                    |  |
| ; APPLICANT: Eglund, Kristi A.   |  | QY 1 REDL 4   |  |
| ; APPLICANT: The Government of the United States of America                  |  | Db 1 REDL 4   |  |
| ; APPLICANT: as represented by The Secretary of the                          |  | RESULT 10   |  |
| ; TITLE OF INVENTION: XAGE-1, a Gene Expressed in Multiple Cancers, and Uses |  | US-10-490-535-6   |  |
| ; TITLE OF INVENTION: Thereof  |  | ; Sequence 6, Application US/10490535   |  |
| ; FILE REFERENCE: 015280-420100US  |  | ; Publication No. US20050118182A1   |  |
| ; CURRENT APPLICATION NUMBER: US/10/363,233                                  |  | ; GENERAL INFORMATION:  |  |
| ; CURRENT FILING DATE: 2003-03-04  |  | ; APPLICANT: Pastan, Ira H.   |  |
| ; PRIOR APPLICATION NUMBER: US 60/229,684                                    |  | ; APPLICANT: Salvatore, Giuliana  |  |
| ; PRIOR FILING DATE: 2000-09-01  |  | ; APPLICANT: Beers, Richard   |  |
| ; PRIOR APPLICATION NUMBER: WO PCT/US01/27258                                |  | ; APPLICANT: Kreitman, Robert J.  |  |
| ; PRIOR FILING DATE: 2001-08-31  |  | ; APPLICANT: The Government of the United States of America                   |  |
| ; NUMBER OF SEQ ID NOS: 11   |  | ; APPLICANT: as represented by The Secretary of the                           |  |
| ; SOFTWARE: PatentIn Ver. 2.1  |  | ; APPLICANT: Department of Health and Human Services                          |  |
| ; SEQ ID NO 7  |  | ; TITLE OF INVENTION: Mutated Anti-CD22 Antibodies With Increased Affinity to |  |
| ; LENGTH: 4  |  | ; TITLE OF INVENTION: CD22-Expressing Leukemia Cells                          |  |
| ; TYPE: PRT  |  | ; FILE REFERENCE: 015280-438100US   |  |
| ; ORGANISM: Artificial Sequence  |  | ; CURRENT APPLICATION NUMBER: US/10/490,535                                   |  |
| ; FEATURE:   |  | ; CURRENT FILING DATE: 2004-03-24   |  |
| ; OTHER INFORMATION: Description of Artificial Sequence: Pseudomonas         |  | ; PRIOR APPLICATION NUMBER: US 60/325,360                                     |  |
| ; OTHER INFORMATION: exotoxin carboxy terminus addition                      |  | ; PRIOR FILING DATE: 2001-09-26   |  |
| US-10-363-233-7  |  | ; PRIOR APPLICATION NUMBER: WO PCT/US02/30316                                 |  |
| Query Match  |  | ; PRIOR FILING DATE: 2002-09-25   |  |
| Best Local Similarity 100.0%; Score 20; DB 4; Length 4;                      |  | ; NUMBER OF SEQ ID NOS: 38  |  |
| Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                   |  | ; SOFTWARE: PatentIn Ver. 2.1   |  |
| QY 1 REDL 4  |  | ; SEQ ID NO 6   |  |
| Db 1 REDL 4  |  | ; LENGTH: 4   |  |
| RESULT 9   |  | ; TYPE: PRT   |  |
| US-10-659-036-12   |  | ; ORGANISM: Artificial Sequence   |  |
| ; Sequence 12, Application US/10659036                                       |  | ; FEATURE:  |  |
| ; Publication No. US20050079171A1  |  | ; OTHER INFORMATION: Description of Artificial Sequence: carboxyl             |  |
| ; GENERAL INFORMATION:   |  | ; OTHER INFORMATION: terminus addition to maintain ability of the             |  |
| ; APPLICANT: FitzGerald, David J.  |  | ; OTHER INFORMATION: construct to translocate to cytosol                      |  |
| ; APPLICANT: Mrsny, Randall J.   |  | US-10-490-535-6   |  |
| ; APPLICANT: The Government of the United States of America                  |  | Query Match   |  |
| ; APPLICANT: as represented by The Secretary of the                          |  | Best Local Similarity 100.0%; Score 20; DB 5; Length 4;                       |  |

RESULT 11  
US-10-973-718-9  
; Sequence 9, Application US/10973718  
; Publication No. US20050214304A1  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira H.  
; APPLICANT: Chowdhury, Partha S.  
; APPLICANT: The Government of the United States  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Antibodies, including Fv Molecules, and  
; TITLE OF INVENTION: Mesothelin and Methods for Their Use  
; FILE REFERENCE: 015280-339100US  
; CURRENT APPLICATION NUMBER: US/10/973,718  
; CURRENT FILING DATE: 2004-10-25  
; PRIOR APPLICATION NUMBER: US/09/581,345  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US 60/067,175  
; PRIOR FILING DATE: 1997-12-01  
; PRIOR APPLICATION NUMBER: WO PCT/US98/25270  
; PRIOR FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:carboxyl  
; OTHER INFORMATION: terminus  
US-10-973-718-9  
  
Query Match 100.0%; Score 20; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 REDL 4  
Db 1 REDL 4  
|||  
|||  
  
RESULT 12  
US-11-021-438-19  
; Sequence 19, Application US/11021438  
; Publication No. US20050186214A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, BIN  
; APPLICANT: MARKS, JAMES D.  
; TITLE OF INVENTION: PROSTATE CANCER SPECIFIC INTERNALIZING HUMAN ANTIBODIES  
; FILE REFERENCE: 407T-392710US  
; CURRENT APPLICATION NUMBER: US/11/021,438  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: US 60/532,433  
; PRIOR FILING DATE: 2003-12-23  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 19  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Peptide translocation signal sequence.  
US-11-021-438-19  
  
Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 REDL 4  
Db 1 REDL 4  
|||  
|||

Db 1 REDL 4  
  
RESULT 13  
US-09-480-236-6  
; Sequence 6, Application US/09480236  
; Patent No. US20020142000A1  
; GENERAL INFORMATION:  
; APPLICANT: Digan, Mary Ellen  
; APPLICANT: Lake, Philip  
; APPLICANT: Wright, Richard M.  
; TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor  
; FILE REFERENCE: CGC 4-31157A/USN  
; CURRENT APPLICATION NUMBER: US/09/480,236  
; CURRENT FILING DATE: 2000-01-10  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PE peptide  
US-09-480-236-6  
  
Query Match 100.0%; Score 20; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 REDL 4  
Db 1 REDL 4  
|||  
|||  
  
RESULT 14  
US-09-462-713-11  
; Sequence 11, Application US/09462713  
; Publication No. US20030054012A1  
; GENERAL INFORMATION:  
; APPLICANT: FitzGerald, David J.  
; APPLICANT: Mrsny, Randall J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: Genentech, Inc.  
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens  
; FILE REFERENCE: 015280-361100US  
; CURRENT APPLICATION NUMBER: US/09/462,713  
; CURRENT FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: PCT/US98/14336  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/056,924  
; PRIOR FILING DATE: 1997-07-11  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:endoplasmic  
; OTHER INFORMATION: reticulum (ER) retention sequence  
US-09-462-713-11  
  
Query Match 100.0%; Score 20; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 REDL 4  
Db 1 REDL 4  
|||  
|||  
  
RESULT 15

US-10-112-788-15  
; Sequence 15, Application US/10112788  
; Publication No. US20030077676A1  
; GENERAL INFORMATION:  
; APPLICANT: DENARDO, SALLY  
; APPLICANT: WINTHROP, MICHELLE  
; APPLICANT: DENARDO, GERALD  
; TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING  
; FILE REFERENCE: 309T-000210US  
; CURRENT APPLICATION NUMBER: US/10/112,788  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 60/280,721  
; PRIOR FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 15  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Recombinant translocation peptide  
US-10-112-788-15  
Query Match 100.0%; Score 20; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 REDL 4  
Db 1 REDL 4  
RESULT 16  
US-10-297-337-15  
; Sequence 15, Application US/10297337  
; Publication No. US20040018203A1  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira H.  
; APPLICANT: Tsutsumi, Yasuo  
; APPLICANT: Onda, Masanori  
; APPLICANT: Nagata, Satoshi  
; APPLICANT: Lee, Byungkook  
; APPLICANT: Kreitman, Robert J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: PEGylation of Linkers Improves Antitumor Activity and  
; TITLE OF INVENTION: Reduces Toxicity of Immunoconjugates  
; FILE REFERENCE: 015280-43200US  
; CURRENT APPLICATION NUMBER: US/10/297,337  
; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/211,331  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: US 60/213,804  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: WO PCT/US01/18503  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PE38 C-terminal  
; OTHER INFORMATION: native residues 609-613  
US-10-297-337-15  
Query Match 100.0%; Score 20; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 REDL 4

Db 1 REDL 4  
RESULT 17  
US-10-406-830-23  
; Sequence 23, Application US/10406830  
; Publication No. US20040071696A1  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, GREGORY P.  
; APPLICANT: HORAK, EVA M.  
; APPLICANT: WEINER, LOUIS M.  
; APPLICANT: JAMES, MARKS D.  
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
; FILE REFERENCE: 407T-000410US  
; CURRENT APPLICATION NUMBER: US/10/406,830  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/370,276  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 23  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Translocation signaling sequence.  
US-10-406-830-23  
Query Match 100.0%; Score 20; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 REDL 4  
Db 1 REDL 4  
RESULT 18  
US-10-432-412-21  
; Sequence 21, Application US/10432412  
; Publication No. US20040071731A1  
; GENERAL INFORMATION:  
; APPLICANT: FitzGerald, David J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas  
; TITLE OF INVENTION: Exotoxin A and Type IV Pilin Sequences  
; FILE REFERENCE: 015280-429100US  
; CURRENT APPLICATION NUMBER: US/10/432,412  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/257,877  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic  
; OTHER INFORMATION: reticulum (ER) retention domain in native  
; OTHER INFORMATION: Pseudomonas exotoxin A  
US-10-432-412-21  
Query Match 100.0%; Score 20; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 REDL 4
Db 1 REDL 4

RESULT 19
US-10-659-036-11
; Sequence 11, Application US/10659036
; Publication No. US2005007917A1
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Msnny, Randall J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens for
; TITLE OF INVENTION: Eliciting a Secretory IGA-Mediated Immune Response
; FILE REFERENCE: 015280-361200US
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US 60/056,924
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: WO PCT/US98/14336
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 09/462,713
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention sequence
US-10-659-036-11

Query Match 100.0%; Score 20; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 20
US-10-490-535-7
; Sequence 7, Application US/10490535
; Publication No. US20050118182A1
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Salvatore, Giuliana
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mutated Anti-CD22 Antibodies With Increased Affinity to
; TITLE OF INVENTION: CD22-Expressing Leukemia Cells
; FILE REFERENCE: 015280-438100US
; CURRENT APPLICATION NUMBER: US/10/490,535
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/325,360
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: WO PCT/US02/30316
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT

Query Match 100.0%; Score 20; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 21
US-11-021-438-18
; Sequence 18, Application US/11021438
; Publication No. US20050186214A1
; GENERAL INFORMATION:
; APPLICANT: LIU, BIN
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: PROSTATE CANCER SPECIFIC INTERNALIZING HUMAN ANTIBODIES
; FILE REFERENCE: 407T-392710US
; CURRENT APPLICATION NUMBER: US/11/021.438
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/532,433
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide translocation signal sequence.
US-11-021-438-18

Query Match 100.0%; Score 20; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 22
US-10-122-675-6
; Sequence 6, Application US/10122675
; Publication No. US20030194712A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Li, Weiqun
; APPLICANT: Lu, Henry
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying Polypeptide Factors Interacting
; TITLE OF INVENTION: With RNA
; FILE REFERENCE: 021044-002000US
; CURRENT APPLICATION NUMBER: US/10/122,675
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 40S ribosomal
; OTHER INFORMATION: protein S18 peptide
US-10-122-675-6

Query Match 100.0%; Score 20; DB 4; Length 7;
```

```
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 2 REDL 5

RESULT 23
US-10-137-867-296
; Sequence 236, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 296
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-296

Query Match 100.0%; Score 20; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 5 REDL 8

RESULT 24
US-10-376-121A-33
; Sequence 33, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1..8
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-376-121A-33

Query Match 100.0%; Score 20; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 1 REDL 4

RESULT 25
US-10-133-210-114
; Sequence 114, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLES OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-114

Query Match 100.0%; Score 20; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 3 REDL 6
```

RESULT 26  
US-10-780-321-40  
; Sequence 40, Application US/10780321  
; Publication No. US2004024810A1  
; GENERAL INFORMATION:  
; APPLICANT: Buelow, Roland  
; APPLICANT: Calas, Bernard  
; TITLE OF INVENTION: Cycomodulating Lipophilic Peptides for Modulating Immune System  
; FILE REFERENCE: A-64360-2/TAL/CYO (465840-00087)  
; CURRENT APPLICATION NUMBER: US/10/780,321  
; CURRENT FILING DATE: 2004-02-17  
; PRIOR APPLICATION NUMBER: US 09/028,083  
; PRIOR FILING DATE: 1998-02-28  
; PRIOR APPLICATION NUMBER: US 08/838,916  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 40  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-780-321-40

Query Match 100.0%; Score 20; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 27  
US-09-955-504-29  
; Sequence 29, Application US/09955504  
; Publication No. US20020182702A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies  
; CURRENT APPLICATION NUMBER: US/09/955,504  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 60/234,222  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 09/712,907  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: PCT/US00/14308  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 60/178,717  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/142,930  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/136,388  
; PRIOR FILING DATE: 1999-05-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-955-504-29

Query Match 100.0%; Score 20; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 8 REDL 11  
RESULT 28  
US-10-125-452-29  
; Sequence 29, Application US/10125452  
; Publication No. US20020173640A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies  
; FILE REFERENCE: PT006P2  
; CURRENT APPLICATION NUMBER: US/10/125,452  
; CURRENT FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 09/955,504  
; PRIOR FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 09/712,907  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: PCT/US00/14308  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 60/178,717  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/142,930  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/136,388  
; PRIOR FILING DATE: 1999-05-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-125-452-29

Query Match 100.0%; Score 20; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 8 REDL 11

RESULT 29  
US-10-126-845-4  
; Sequence 4, Application US/10126845  
; Publication No. US20030181367A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Mahony, Daniel J.  
; APPLICANT: Lambkin, Imelda J.  
; APPLICANT: Pinilla, Clemencia  
; APPLICANT: Houghten, Richard  
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM  
; FILE REFERENCE: E1067/20058  
; CURRENT APPLICATION NUMBER: US/10/126,845  
; CURRENT FILING DATE: 2002-10-15  
; NUMBER OF SEQ ID NOS: 119  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: membrane translocating peptide  
US-10-126-845-4

Query Match 100.0%; Score 20; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 16 REDL 19

|           |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |      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|                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |            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            |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |            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            |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |    |
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| US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | 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US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | US-10-126-845-62 | 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US-10-955-656-62
; Sequence 62, Application US/10955656
; Publication No. US20050101762A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: P26,481-A USA
; CURRENT APPLICATION NUMBER: US/10/955,656
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/126,845
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(19)
; OTHER INFORMATION: D form amino acid
US-10-955-656-62

Query Match 100.0%; Score 20; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 16 REDL 19

RESULT 35
US-09-864-761-39759
; Sequence 39759, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39759
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005332.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EST_HUMAN HIT: AI076293.1, EVALU8 1.00e-05
US-09-864-761-39759

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 10 REDL 13

RESULT 36
US-10-136-187-5
; Sequence 5, Application US/10136187
; Publication No. US20030203865A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
; FILE REFERENCE: 226272005300
; CURRENT APPLICATION NUMBER: US/10/136,187
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/287,786
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
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US-10-136-187-5
Query Match      100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      17 REDL 20

RESULT 37
US-10-136-187-9
; Sequence 9, Application US/10136187
; Publication No. US20030203865A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; FILE REFERENCE: 226272005300
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US/10/136,187
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to galactose
US-10-136-187-9

Query Match      100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      17 REDL 20

RESULT 38
US-10-850-873-5
; Sequence 5, Application US/10850873
; Publication No. US20050025821A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; FILE REFERENCE: 226272005300
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/10/136,187
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to galactose
US-10-850-873-5

Query Match      100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      17 REDL 20

RESULT 39
US-10-850-873-9
; Sequence 9, Application US/10850873
; Publication No. US20050025821A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; FILE REFERENCE: 226272005300
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/10/136,187
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to galactose
US-10-850-873-9

Query Match      100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      17 REDL 20

RESULT 40
US-10-690-276-239
; Sequence 239, Application US/10690276
; Publication No. US20050112118A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Incorporated
; APPLICANT: Cimbora, Daniel
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul
; APPLICANT: Mauck, Kimberly
; APPLICANT: Bush, Angie
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS
; FILE REFERENCE: 1834.01
; CURRENT APPLICATION NUMBER: US/10/690,276
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/727,384
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/168,377
US-10-690-276-239
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; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: 60/168,379  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: 60/185,056  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: 10/035,344  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 60/259,571  
; PRIOR FILING DATE: 2001-01-04  
; PRIOR APPLICATION NUMBER: 10/035,343  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 60/259,572  
; PRIOR FILING DATE: 2001-01-04  
; PRIOR APPLICATION NUMBER: 10/099,924  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 60/276,179  
; PRIOR FILING DATE: 2001-03-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 728  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 239  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-690-276-239

Query Match 100.0%; Score 20; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 41  
US-10-302-547-89  
; Sequence 89, Application US/10302547  
; Publication No. US20040142448A1  
; GENERAL INFORMATION:  
; APPLICANT: MURPHY, BRIAN R.  
; APPLICANT: COLLINS, PETER L.  
; APPLICANT: SKIADOPOULOS, MARIO H.  
; APPLICANT: NEWMAN, JASON T.  
; TITLE OF INVENTION: RECOVERY OF RECOMBINANT HUMAN PARAINFLUENZA VIRUS TYPE  
; TITLE OF INVENTION: 1 (HPV1) FROM CDNA AND USE OF RECOMBINANT HPV1 IN  
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AND AS VECTORS TO ELICIT  
; TITLE OF INVENTION: IMMUNE RESPONSES AGAINST PIV AND OTHER HUMAN PATHOGENS  
; FILE REFERENCE: 2303-37-3  
; CURRENT APPLICATION NUMBER: US/10/302,547  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: 60/331,961  
; PRIOR FILING DATE: 2001-11-21  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 89  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Human parainfluenza virus 3  
US-10-302-547-89

Query Match 100.0%; Score 20; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 15 REDL 18

RESULT 42  
US-10-302-547-90  
; Sequence 90, Application US/10302547

; Publication No. US20040142448A1  
; GENERAL INFORMATION:  
; APPLICANT: MURPHY, BRIAN R.  
; APPLICANT: COLLINS, PETER L.  
; APPLICANT: SKIADOPOULOS, MARIO H.  
; APPLICANT: NEWMAN, JASON T.  
; TITLE OF INVENTION: RECOVERY OF RECOMBINANT HUMAN PARAINFLUENZA VIRUS TYPE  
; TITLE OF INVENTION: 1 (HPV1) FROM CDNA AND USE OF RECOMBINANT HPV1 IN  
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AND AS VECTORS TO ELICIT  
; TITLE OF INVENTION: IMMUNE RESPONSES AGAINST PIV AND OTHER HUMAN PATHOGENS  
; FILE REFERENCE: 2303-37-3  
; CURRENT APPLICATION NUMBER: US/10/302,547  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: 60/331,961  
; PRIOR FILING DATE: 2001-11-21  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 90  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Human parainfluenza virus 3  
US-10-302-547-90

Query Match 100.0%; Score 20; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 15 REDL 18

RESULT 43  
US-10-029-386-32550  
; Sequence 32550, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: AROMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 32550  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC002472.3  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.42  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8  
; OTHER INFORMATION: SWISSPROT HIT: O43246, EVALUE 2.00e-06  
US-10-029-386-32550

Query Match 100.0%; Score 20; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 18 REDL 21

RESULT 44  
US-11-155-043-23

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, PRIOR APPLICATION NUMBER: PCT/US01/006662
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006661
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006670
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: US 60/234,687
, PRIOR FILING DATE: 2000-09-21
, PRIOR APPLICATION NUMBER: US 09/608,408
, PRIOR FILING DATE: 2000-06-30
, PRIOR APPLICATION NUMBER: US 09/774,203
, PRIOR FILING DATE: 2001-01-29
, NUMBER OF SEQ ID NOS: 49117
, SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
, SEQ ID NO 37447
, LENGTH: 28
, TYPE: PRT
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: MAP TO AL050342.36
, OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3
, OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.3
, OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9
, OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.5
, OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
, OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.4
, OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
, OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.8
, OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
, OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9
, OTHER INFORMATION: EST_HUMAN HIT: F08485.1, EVALUAE 2.00e-09
, US-09-864-761-37447

Query Match 100.0%; Score 20; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels

Qy 1 REDL 4
Db 18 REDL 21

RESULT 46
US-09-864-761-42724
, Sequence 42724, Application US/09864761
, Patent No. US20020048763A1
, GENERAL INFORMATION:
, APPLICANT: Penn, Sharon G.
, APPLICANT: Rank, David R.
, APPLICANT: Hanzel, David K.
, APPLICANT: Chen, Wensheng
, TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID SEQUENCES AND METHODS OF ANALYSIS BY MICROARRAY
, TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
, FILE REFERENCE: aeomica-X-1
, CURRENT APPLICATION NUMBER: US/09/864,761
, CURRENT FILING DATE: 2001-05-23
, PRIOR APPLICATION NUMBER: US 60/180,312
, PRIOR FILING DATE: 2000-02-04
, PRIOR APPLICATION NUMBER: US 60/207,456
, PRIOR FILING DATE: 2000-05-26
, PRIOR APPLICATION NUMBER: US 09/632,366
, PRIOR FILING DATE: 2000-08-03
, PRIOR APPLICATION NUMBER: GB 24263.6
, PRIOR FILING DATE: 2000-10-04
, PRIOR APPLICATION NUMBER: US 60/236,959
, PRIOR FILING DATE: 2000-09-27
, PRIOR APPLICATION NUMBER: PCT/US01/006666
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006667
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006664
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006669

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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 42724  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL050342.29  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3  
; OTHER INFORMATION: EST\_HUMAN HIT: F08485.1, EVALUATE 2.00e-09  
US-09-864-761-42724

Query Match 100.0%; Score 20; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 18 REDL 21

RESULT 47  
US-10-808-187-236  
; Sequence 236, Application US/10808187  
; Publication No. US2005009009A1  
; GENERAL INFORMATION:  
; APPLICANT: PEIRIS, JOSEPH S. M.  
; APPLICANT: YUEN, KWOK YUNG  
; APPLICANT: POON, LIT MAN  
; APPLICANT: GUAN, YI  
; APPLICANT: CHAN, KWOK HUNG  
; APPLICANT: NICHOLLS, JOHN  
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE  
; FILE REFERENCE: V9661.0078  
; CURRENT APPLICATION NUMBER: US/10/808,187  
; CURRENT FILING DATE: 2004-03-24  
; PRIOR APPLICATION NUMBER: 60/457,031  
; PRIOR FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: 60/457,730  
; PRIOR FILING DATE: 2003-03-26  
; PRIOR APPLICATION NUMBER: 60/459,931  
; PRIOR FILING DATE: 2003-04-02  
; PRIOR APPLICATION NUMBER: 60/460,357  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: 60/461,265  
; PRIOR FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: 60/462,805  
; PRIOR FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: 60/468,139  
; PRIOR FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: 60/464,886

; PRIOR FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: 60/471,200  
; PRIOR FILING DATE: 2003-05-16  
; NUMBER OF SEQ ID NOS: 2476  
; SOFTWARE: PatentIn ver. 3.2  
; SEQ ID NO 236  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Human severe acute respiratory system virus  
US-10-808-187-236

Query Match 100.0%; Score 20; DB 5; Length 28;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 6 REDL 9

RESULT 48  
US-10-807-807-236  
; Sequence 236, Application US/10807807  
; Publication No. US20050181357A1  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, FREDERICK C.  
; APPLICANT: PEIRIS, JOSEPH S. M.  
; APPLICANT: YUEN, KWOK YUNG  
; APPLICANT: POON, LIT MAN  
; APPLICANT: GUAN, YI  
; APPLICANT: CHAN, KWOK HUNG  
; APPLICANT: NICHOLLS, JOHN M.  
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS  
; FILE REFERENCE: V9661.0077  
; CURRENT APPLICATION NUMBER: US/10/807,807  
; CURRENT FILING DATE: 2004-03-24  
; PRIOR APPLICATION NUMBER: 60/457,031  
; PRIOR FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: 60/457,730  
; PRIOR FILING DATE: 2003-03-26  
; PRIOR APPLICATION NUMBER: 60/459,931  
; PRIOR FILING DATE: 2003-04-02  
; PRIOR APPLICATION NUMBER: 60/460,357  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: 60/461,265  
; PRIOR FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: 60/462,805  
; PRIOR FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: 60/464,886  
; PRIOR FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: 60/465,738  
; PRIOR FILING DATE: 2003-04-25  
; PRIOR APPLICATION NUMBER: 60/470,935  
; PRIOR FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 2487  
; SOFTWARE: PatentIn ver. 3.2  
; SEQ ID NO 236  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Human severe acute respiratory system virus  
US-10-807-807-236

Query Match 100.0%; Score 20; DB 5; Length 28;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 6 REDL 9

RESULT 49

```
US-09-932-367A-33
; Sequence 33, Application US/09932367A
; Publication No. US20030027152A1
; GENERAL INFORMATION:
; APPLICANT: RHODES, Simon J.
; APPLICANT: BRIDWELL, Jeanne L.
; APPLICANT: MEIER, Bradley C.
; APPLICANT: PARKER, Gretchen E.
; APPLICANT: PRICE, Jeffrey R.
; APPLICANT: SHOWALTER, Aaron D.
; APPLICANT: SLOOP, Kyle W.
; TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN
; FILE OF INVENTION: LHX3/P-LIM/LIM-3 FACTOR
; FILE REFERENCE: 053884-5003
; CURRENT APPLICATION NUMBER: US/09/932,367A
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/04424
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/121,110
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-932-367A-33

Query Match      100.0%; Score 20; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      26 REDL 29

RESULT 50
US-10-425-115-269508
; Sequence 269508, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 269508
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177387C.1.pep
US-10-425-115-269508

Query Match      100.0%; Score 20; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      22 REDL 25

Search completed: March 20, 2006, 07:55:14
Job time : 64.5 secs
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:53:30 ; Search time 8.5 Seconds  
(without alignments)  
13.470 Million cell updates/sec

Title: US-09-673-707-10  
Perfect score: 20  
Sequence: 1 REDL 4

Scoring table: BLOSUM62  
Gapex 10.0 , Gapex 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

#### Database :

Published Applications\_AA\_New:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
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| 1          | 20    | 100.0       | 4      | 6     | US-10-537-061-12    |
| 2          | 20    | 100.0       | 4      | 7     | US-11-019-027-16    |
| 3          | 20    | 100.0       | 7      | 7     | US-11-096-706-24    |
| 4          | 20    | 100.0       | 8      | 7     | US-11-045-024-4306  |
| 5          | 20    | 100.0       | 8      | 7     | US-11-045-024-9685  |
| 6          | 20    | 100.0       | 8      | 7     | US-11-045-024-12706 |
| 7          | 20    | 100.0       | 11     | 6     | US-10-892-870-3     |
| 8          | 20    | 100.0       | 11     | 6     | US-10-938-690-3     |
| 9          | 20    | 100.0       | 28     | 7     | US-11-004-399-929   |
| 10         | 20    | 100.0       | 37     | 6     | US-10-729-121-15    |
| 11         | 20    | 100.0       | 38     | 6     | US-10-729-121-15    |
| 12         | 20    | 100.0       | 55     | 7     | US-11-140-311-14    |
| 13         | 20    | 100.0       | 55     | 7     | US-11-140-311-15    |
| 14         | 20    | 100.0       | 60     | 6     | US-10-475-075-913   |
| 15         | 20    | 100.0       | 61     | 6     | US-10-934-944-148   |
| 16         | 20    | 100.0       | 61     | 7     | US-11-116-881A-157  |
| 17         | 20    | 100.0       | 72     | 6     | US-10-544-501-8     |
| 18         | 20    | 100.0       | 75     | 7     | US-11-096-568A-4959 |
| 19         | 20    | 100.0       | 82     | 7     | US-11-124-367A-275  |
| 20         | 20    | 100.0       | 82     | 7     | US-11-124-367A-277  |
| 21         | 20    | 100.0       | 82     | 7     | US-11-124-367A-278  |
| 22         | 20    | 100.0       | 82     | 7     | US-11-124-367A-279  |
| 23         | 20    | 100.0       | 99     | 7     | US-11-087-099-6823  |
| 24         | 20    | 100.0       | 100    | 6     | US-10-793-626-2944  |
| 25         | 20    | 100.0       | 112    | 6     | US-10-667-295-226   |
|            |       |             |        |       | Sequence 12, Appl   |
|            |       |             |        |       | Sequence 16, Appl   |
|            |       |             |        |       | Sequence 24, Appl   |
|            |       |             |        |       | Sequence 4306, Ap   |
|            |       |             |        |       | Sequence 9685, Ap   |
|            |       |             |        |       | Sequence 12706, A   |
|            |       |             |        |       | Sequence 3, Appli   |
|            |       |             |        |       | Sequence 929, App   |
|            |       |             |        |       | Sequence 15, Appl   |
|            |       |             |        |       | Sequence 14, Appl   |
|            |       |             |        |       | Sequence 14, Appl   |
|            |       |             |        |       | Sequence 15, Appl   |
|            |       |             |        |       | Sequence 913, App   |
|            |       |             |        |       | Sequence 148, App   |
|            |       |             |        |       | Sequence 157, App   |
|            |       |             |        |       | Sequence 8, Appli   |
|            |       |             |        |       | Sequence 4959, Ap   |
|            |       |             |        |       | Sequence 275, App   |
|            |       |             |        |       | Sequence 277, App   |
|            |       |             |        |       | Sequence 278, App   |
|            |       |             |        |       | Sequence 279, App   |
|            |       |             |        |       | Sequence 6823, Ap   |
|            |       |             |        |       | Sequence 2944, Ap   |
|            |       |             |        |       | Sequence 226, App   |

Sequence 2796, Ap  
Sequence 2804, Ap  
Sequence 2872, Ap  
Sequence 3074, Ap  
Sequence 69, Appl  
Sequence 13950, A  
Sequence 1347, Ap  
Sequence 54, Appl  
Sequence 274, App  
Sequence 428, App  
Sequence 17, Appl  
Sequence 23874, A  
Sequence 193, App  
Sequence 7, Appli  
Sequence 2881, Ap  
Sequence 1646, Ap  
Sequence 273, App  
Sequence 1344, Ap  
Sequence 5557, Ap  
Sequence 170, App  
Sequence 204, App  
Sequence 3632, Ap  
Sequence 6390, Ap  
Sequence 12351, A  
Sequence 352, App  
Sequence 8718, Ap  
Sequence 8516, Ap  
Sequence 144, App  
Sequence 244, App  
Sequence 24753, A  
Sequence 230, App  
Sequence 24752, A  
Sequence 32959, A  
Sequence 36, Appl  
Sequence 579, App  
Sequence 23873, A  
Sequence 3856, Ap  
Sequence 6602, Ap  
Sequence 10256, A  
Sequence 19, Appl  
Sequence 546, App  
Sequence 777, App  
Sequence 804, App  
Sequence 24751, A  
Sequence 3999, Ap  
Sequence 266, App  
Sequence 207, App  
Sequence 165, App  
Sequence 580, App  
Sequence 150, App  
Sequence 238, App  
Sequence 5188, Ap  
Sequence 230, App  
Sequence 803, App  
Sequence 802, App  
Sequence 2823, Ap  
Sequence 204, App  
Sequence 23872, A  
Sequence 2194, Ap  
Sequence 9213, Ap  
Sequence 1344, Ap  
Sequence 167, App  
Sequence 33021, A  
Sequence 10737, A  
Sequence 4302, Ap  
Sequence 7429, Ap  
Sequence 32958, A  
Sequence 7, Appli  
Sequence 10595, A  
Sequence 3876, Ap  
Sequence 33925, A

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| 99  | 20 | 100.0 | 258 | 7 | US-11-096-568A-4301  | Sequence 4301, Ap  |
| 100 | 20 | 100.0 | 263 | 7 | US-11-040-638-2      | Sequence 2, Appli  |
| 101 | 20 | 100.0 | 263 | 7 | US-11-042-889-2      | Sequence 2, Appli  |
| 102 | 20 | 100.0 | 263 | 7 | US-11-096-568A-33924 | Sequence 3, Appli  |
| 103 | 20 | 100.0 | 267 | 7 | US-11-179-363-3      | Sequence 10255, A  |
| 104 | 20 | 100.0 | 268 | 7 | US-11-096-568A-10255 | Sequence 11, Appli |
| 105 | 20 | 100.0 | 269 | 7 | US-11-179-977-11     | Sequence 8151, Ap  |
| 106 | 20 | 100.0 | 269 | 7 | US-11-087-099-8151   | Sequence 4300, Ap  |
| 107 | 20 | 100.0 | 269 | 7 | US-11-096-568A-4300  | Sequence 26985, A  |
| 108 | 20 | 100.0 | 270 | 7 | US-11-096-568A-26985 | Sequence 514, App  |
| 109 | 20 | 100.0 | 270 | 6 | US-10-793-626-514    | Sequence 2274, Ap  |
| 110 | 20 | 100.0 | 270 | 6 | US-10-793-626-2274   | Sequence 1013, Ap  |
| 111 | 20 | 100.0 | 272 | 6 | US-10-853-807A-40    | Sequence 1013, Ap  |
| 112 | 20 | 100.0 | 275 | 6 | US-10-821-234-1013   | Sequence 32957, A  |
| 113 | 20 | 100.0 | 278 | 7 | US-11-096-568A-32957 | Sequence 32923, A  |
| 114 | 20 | 100.0 | 285 | 7 | US-11-096-568A-32923 | Sequence 427, App  |
| 115 | 20 | 100.0 | 287 | 5 | US-09-978-360A-427   | Sequence 792, App  |
| 116 | 20 | 100.0 | 289 | 7 | US-11-055-822-792    | Sequence 416, App  |
| 117 | 20 | 100.0 | 290 | 7 | US-11-082-389-416    | Sequence 3, Appli  |
| 118 | 20 | 100.0 | 292 | 6 | US-10-491-468-3      | Sequence 28, Appli |
| 119 | 20 | 100.0 | 297 | 6 | US-10-510-903-28     | Sequence 339, App  |
| 120 | 20 | 100.0 | 299 | 7 | US-11-156-084-339    | Sequence 15962, A  |
| 121 | 20 | 100.0 | 299 | 7 | US-11-096-568A-15962 | Sequence 8781, Ap  |
| 122 | 20 | 100.0 | 303 | 7 | US-11-087-099-8781   | Sequence 1696, Ap  |
| 123 | 20 | 100.0 | 304 | 7 | US-11-087-099-1696   | Sequence 264, App  |
| 124 | 20 | 100.0 | 305 | 6 | US-10-131-826A-264   | Sequence 1518, Ap  |
| 125 | 20 | 100.0 | 305 | 6 | US-10-821-234-1518   | Sequence 264, App  |
| 126 | 20 | 100.0 | 305 | 6 | US-10-973-1158-264   | Sequence 263, App  |
| 127 | 20 | 100.0 | 310 | 7 | US-11-087-099-263    | Sequence 19670, A  |
| 128 | 20 | 100.0 | 310 | 7 | US-11-096-568A-19670 | Sequence 22341, A  |
| 129 | 20 | 100.0 | 310 | 7 | US-11-096-568A-22341 | Sequence 15961, A  |
| 130 | 20 | 100.0 | 311 | 7 | US-11-096-568A-15961 | Sequence 8002, Ap  |
| 131 | 20 | 100.0 | 312 | 7 | US-11-086-568A-8002  | Sequence 1216, Ap  |
| 132 | 20 | 100.0 | 313 | 6 | US-11-096-568A-1216  | Sequence 6, Appli  |
| 133 | 20 | 100.0 | 313 | 7 | US-11-198-728-6      | Sequence 10, Appli |
| 134 | 20 | 100.0 | 313 | 7 | US-11-198-728-10     | Sequence 18, Appli |
| 135 | 20 | 100.0 | 313 | 7 | US-11-198-728-18     | Sequence 7122, Ap  |
| 136 | 20 | 100.0 | 313 | 7 | US-11-096-568A-7122  | Sequence 874, App  |
| 137 | 20 | 100.0 | 314 | 7 | US-11-087-099-874    | Sequence 11271, A  |
| 138 | 20 | 100.0 | 314 | 7 | US-11-087-099-11271  | Sequence 5725, Ap  |
| 139 | 20 | 100.0 | 315 | 7 | US-11-096-568A-5725  | Sequence 8001, Ap  |
| 140 | 20 | 100.0 | 315 | 7 | US-11-096-568A-8001  | Sequence 28592, A  |
| 141 | 20 | 100.0 | 315 | 7 | US-11-096-568A-28592 | Sequence 2144, Ap  |
| 142 | 20 | 100.0 | 316 | 6 | US-10-467-657-2144   | Sequence 240, App  |
| 143 | 20 | 100.0 | 316 | 7 | US-11-156-084-240    | Sequence 303, App  |
| 144 | 20 | 100.0 | 316 | 7 | US-11-156-084-303    | Sequence 2359, Ap  |
| 145 | 20 | 100.0 | 316 | 7 | US-11-087-099-2359   | Sequence 11, Appli |
| 146 | 20 | 100.0 | 318 | 7 | US-11-012-522-11     | Sequence 5625, Ap  |
| 147 | 20 | 100.0 | 318 | 7 | US-11-096-568A-5625  | Sequence 11060, A  |
| 148 | 20 | 100.0 | 319 | 7 | US-11-098-686-11060  | Sequence 5502, Ap  |
| 149 | 20 | 100.0 | 319 | 7 | US-11-087-099-5502   | Sequence 22650, A  |
| 150 | 20 | 100.0 | 320 | 7 | US-11-096-568A-22650 |                    |

ALIGNMENTS

Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 REDL 4

RESULT 3  
US-10-537-061-12  
; Sequence 12, Application US/10537061  
; Publication No. US20060051359A1  
; GENERAL INFORMATION:  
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
; APPLICANT: HUMAN SERVICES  
; APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH  
; APPLICANT: Pastan, Ira  
; APPLICANT: Onda, Masanori  
; APPLICANT: Cheung, Nai-Kong  
; TITLE OF INVENTION: IN-VIVO CYTOTOXIC ACTIVITIES OF RECOMBINANT IMMUNOTOXIN 8H9  
; TITLE OF INVENTION: (FV)-PE38 AGAINST BREAST CANCER, OSTEOCARCINOMA AND NEUROBLASTOM  
; FILE REFERENCE: 4239-67287-05  
; CURRENT APPLICATION NUMBER: US/10/537,061

CURRENT FILING DATE: 2005-06-01  
PRIOR APPLICATION NUMBER: PCT/US03/038227  
PRIOR FILING DATE: 2003-12-01  
PRIOR APPLICATION NUMBER: US 60/430,305  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 12  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-10-537-061-12

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 1 REDL 4

RESULT 2  
US-11-019-027-16  
; Sequence 16, Application US/11019027  
; Publication No. US20050282181A1  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Wei  
; APPLICANT: SHEN, Wenyan  
; APPLICANT: ZHOU, Hongxing  
; APPLICANT: ZHOU, Chen  
; APPLICANT: COSMAN, David J.  
; APPLICANT: CARTER, Paul  
; APPLICANT: MARTIN, Francis H.  
; TITLE OF INVENTION: METHODS OF IDENTIFYING FUNCTIONAL ANTIBODIES  
; FILE REFERENCE: A-890A  
; CURRENT APPLICATION NUMBER: US/11/019,027  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: 60/605,902  
; PRIOR FILING DATE: 2004-08-31  
; PRIOR APPLICATION NUMBER: 60/531,714  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 16  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: ER localization signal  
US-11-019-027-16

Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 1 REDL 4

RESULT 3  
US-11-096-706-24  
; Sequence 24, Application US/11096706  
; Publication No. US20050245476A1  
; GENERAL INFORMATION:  
; APPLICANT: Sangamo Biosciences, Inc.  
; APPLICANT: Collingwood, Trevor  
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins  
; FILE REFERENCE: 019496-008220US  
; CURRENT APPLICATION NUMBER: US/11/096,706  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 60/560,535



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; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: region)
US-11-096-706-24

Query Match      100.0%; Score 20; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 2 REDL 5

RESULT 4
US-11-045-024-4306
; Sequence 4306, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4306
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4306

Query Match      100.0%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

US-11-045-024-4306
; Sequence 4306, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4306
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4306

Query Match      100.0%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4
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Db 3 REDL 6

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; Sequence 9685, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9685
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9685

Query Match      100.0%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 3 REDL 6

RESULT 6
US-11-045-024-12706
; Sequence 12706, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12706
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12706

Query Match      100.0%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Mon Mar 20 08:51:25 2006

```

; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12706
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
;
US-11-045-024-12706

Query Match      100.0%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
Db      3 REDL 6

RESULT 7
US-10-892-870-3
; Sequence 3, Application US/10892870
; Publication No. US20060014210A1
; GENERAL INFORMATION:
; APPLICANT: Agilent Technologies
; APPLICANT: Boyes, Barry E.
; APPLICANT: Liu, Hongbin E.
; APPLICANT: Nicol, Gordon R.
; TITLE OF INVENTION: Serial Derivatization of Peptides for De Novo Sequencing Using
; FILE REFERENCE: 10040405 KTM7374
; CURRENT APPLICATION NUMBER: US/10/892,870
; CURRENT FILING DATE: 2004-07-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: bovine
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: peptide from cytochrome C (bovine heart)
US-10-892-870-3

Query Match      100.0%; Score 20; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
Db      3 REDL 6

RESULT 8
US-10-938-690-3
; Sequence 3, Application US/10938690
```

```

; Publication No. US20060014293A1
; GENERAL INFORMATION:
; APPLICANT: Agilent Technologies
; APPLICANT: Joyce, Timothy H.
; APPLICANT: Boyes, Barry E.
; APPLICANT: Nicol, Gordon R.
; APPLICANT: Liu, Hongbin
; TITLE OF INVENTION: Lock Mass Ions For Use With Derivatized Peptides for De Novo
; FILE REFERENCE: 10040464-1 KTM7374
; CURRENT APPLICATION NUMBER: US/10/938,690
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 10/892870
; PRIOR FILING DATE: 2004-07-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: bovine
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: peptide from cytochrome C (bovine heart)
US-10-938-690-3

Query Match      100.0%; Score 20; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
Db      3 REDL 6

RESULT 9
US-11-004-399-929
; Sequence 929, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 929
; LENGTH: 28
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399-929

Query Match      100.0%; Score 20; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
Db      6 REDL 9

RESULT 10
US-10-729-121-15
; Sequence 15, Application US/10729121
; Publication No. US20040144397A1
; GENERAL INFORMATION:
```

; APPLICANT: Conkling, Mark  
 ; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE  
 ; FILE REFERENCE: VTOB.033C1  
 ; CURRENT APPLICATION NUMBER: US/10/729,121  
 ; CURRENT FILING DATE: 2003-12-04  
 ; PRIOR APPLICATION NUMBER: 60/297,154  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: PCTUS02/18040  
 ; PRIOR FILING DATE: 2002-06-06  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 15  
 ; LENGTH: 37  
 ; TYPE: PRT  
 ; ORGANISM: Salmonella typhimurium  
 US-10-729-121-15

Query Match 100.0%; Score 20; DB 6; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 5 REDL 8

## RESULT 11

US-10-729-121-14  
 ; Sequence 14, Application US/10729121  
 ; Publication No. US20040144397A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conkling, Mark  
 ; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE  
 ; FILE REFERENCE: VTOB.033C1  
 ; CURRENT APPLICATION NUMBER: US/10/729,121  
 ; CURRENT FILING DATE: 2003-12-04  
 ; PRIOR APPLICATION NUMBER: 60/297,154  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: PCTUS02/18040  
 ; PRIOR FILING DATE: 2002-06-06  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 14  
 ; LENGTH: 38  
 ; TYPE: PRT  
 ; ORGANISM: Nicotiana tabacum  
 US-10-729-121-14

Query Match 100.0%; Score 20; DB 6; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 78;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 5 REDL 8

## RESULT 12

US-11-140-311-14  
 ; Sequence 14, Application US/11140311  
 ; Publication No. US20060035249A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ziermann, Rainer A.  
 ; TITLE OF INVENTION: Means And Methods For Monitoring  
 ; TITLE OF INVENTION: Protease Inhibitor Antiretroviral Therapy And Guiding  
 ; FILE REFERENCE: 11068-154-999  
 ; CURRENT APPLICATION NUMBER: US/11/140,311  
 ; CURRENT FILING DATE: 2005-05-27  
 ; PRIOR APPLICATION NUMBER: 09/874,472

; PRIOR FILING DATE: 2001-06-04  
 ; PRIOR APPLICATION NUMBER: 09/766,344  
 ; PRIOR FILING DATE: 2001-01-19  
 ; PRIOR APPLICATION NUMBER: 09/663,458  
 ; PRIOR FILING DATE: 2000-09-15  
 ; PRIOR APPLICATION NUMBER: 09/591,899  
 ; PRIOR FILING DATE: 2000-06-12  
 ; PRIOR APPLICATION NUMBER: 60/140,483  
 ; PRIOR FILING DATE: 1999-06-22  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 14  
 ; LENGTH: 55  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-11-140-311-14

Query Match 100.0%; Score 20; DB 7; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 11e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 3 REDL 6

## RESULT 13

US-11-140-311-15  
 ; Sequence 15, Application US/11140311  
 ; Publication No. US20060035249A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Parkin, Neil T.  
 ; APPLICANT: Ziermann, Rainer A.  
 ; TITLE OF INVENTION: Means And Methods For Monitoring  
 ; TITLE OF INVENTION: Protease Inhibitor Antiretroviral Therapy And Guiding  
 ; FILE REFERENCE: 11068-154-999  
 ; CURRENT APPLICATION NUMBER: US/11/140,311  
 ; CURRENT FILING DATE: 2005-05-27  
 ; PRIOR APPLICATION NUMBER: 09/874,472  
 ; PRIOR FILING DATE: 2001-06-04  
 ; PRIOR APPLICATION NUMBER: 09/766,344  
 ; PRIOR FILING DATE: 2001-01-19  
 ; PRIOR APPLICATION NUMBER: 09/663,458  
 ; PRIOR FILING DATE: 2000-09-15  
 ; PRIOR APPLICATION NUMBER: 09/591,899  
 ; PRIOR FILING DATE: 2000-06-12  
 ; PRIOR APPLICATION NUMBER: 60/140,483  
 ; PRIOR FILING DATE: 1999-06-22  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 15  
 ; LENGTH: 55  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-11-140-311-15

Query Match 100.0%; Score 20; DB 7; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 3 REDL 6

## RESULT 14

US-10-475-075-913  
 ; Sequence 913, Application US/10475075  
 ; Publication No. US2006003498A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bejanin, Stephanie  
 ; APPLICANT: Tanaka, Hiroaki

```

; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 913
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-475-075-913

```

```

Query Match 100.0%; Score 20; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 REDL 4
    ||||
Db 18 REDL 21

```

```

RESULT 15
US-10-934-944-148
; Sequence 148, Application US/10934944
; Publication No. US20060037096A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Cloning of Cytochrome P450 Genes From Nicotiana
; FILE REFERENCE: 07678/141008
; CURRENT APPLICATION NUMBER: US/10/934,944
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/686,947
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 10/387,346
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 10/340,861
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 10/293,252
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/363,684
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/347,444
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 60/337,684
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-10-934-944-148

```

```

Query Match 100.0%; Score 20; DB 6; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 REDL 4
    ||||
Db 51 REDL 54

```

```

RESULT 16
US-11-116-881A-157
; Sequence 157, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 157
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-157

```

```

Query Match 100.0%; Score 20; DB 7; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 REDL 4
    ||||
Db 51 REDL 54

```

```

RESULT 17
US-10-544-501-8
; Sequence 8, Application US/10544501
; Publication No. US20060037106A1
; GENERAL INFORMATION:
; APPLICANT: Cropdesign N.V.
; TITLE OF INVENTION: Method for modifying plant growth characteristics
; FILE REFERENCE: 4440-13
; CURRENT APPLICATION NUMBER: US/10/544,501
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: EP 03075363.6
; PRIOR FILING DATE: 2003-02-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: peptidase_M24 domain of AtMAP2B
US-10-544-501-8

```

```

Query Match 100.0%; Score 20; DB 6; Length 72;

```

Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 50 REDL 53

## RESULT 18

US-11-096-568A-4959  
; Sequence 4959, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 4959  
; LENGTH: 75  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(75)  
; OTHER INFORMATION: Ceres Seq. ID no. 14306200

US-11-096-568A-4959

Query Match 100.0%; Score 20; DB 7; Length 75;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 69 REDL 72

## RESULT 19

US-11-124-367A-275  
; Sequence 275, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; FILE REFERENCE: CL001519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124,367A  
; CURRENT FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 275  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-124-367A-275

Query Match 100.0%; Score 20; DB 7; Length 82;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 38 REDL 41

## RESULT 20

US-11-124-367A-277  
; Sequence 277, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; FILE REFERENCE: CL001519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124,367A  
; CURRENT FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 277  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-124-367A-277

Query Match 100.0%; Score 20; DB 7; Length 82;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 38 REDL 41

## RESULT 21

US-11-124-367A-278  
; Sequence 278, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; FILE REFERENCE: CL001519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124,367A  
; CURRENT FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 278  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-124-367A-278

Query Match 100.0%; Score 20; DB 7; Length 82;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 38 REDL 41

## RESULT 22

US-11-124-367A-279

```
; SEQ ID NO 2944
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2944

Query Match          100.0%; Score 20; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        ||||
Db       82 REDL 85

RESULT 25
US-10-667-295-226
; Sequence 226, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(112)
; OTHER INFORMATION: Ceres Seq. ID no. 13633592
US-10-667-295-226

Query Match          100.0%; Score 20; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        ||||
Db       17 REDL 20

RESULT 26
US-10-793-626-2796
; Sequence 2796, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2796
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2796
```

```
; Sequence 279, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 279
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-279

Query Match          100.0%; Score 20; DB 7; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        ||||
Db       38 REDL 41

RESULT 23
US-11-087-099-6823
; Sequence 6823, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6823
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Zea mays
US-11-087-099-6823

Query Match          100.0%; Score 20; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
        ||||
Db       87 REDL 90

RESULT 24
US-10-793-626-2944
; Sequence 2944, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
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```
Query Match      100.0%; Score 20; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      90 REDL 93

RESULT 27
US-10-793-626-2804
; Sequence 2804, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2804
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2804

Query Match      100.0%; Score 20; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      90 REDL 93

RESULT 28
US-10-793-626-2872
; Sequence 2872, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2872
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2872

Query Match      100.0%; Score 20; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      90 REDL 93

RESULT 29
US-10-793-626-3074
; Sequence 3074, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3074
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3074

Query Match      100.0%; Score 20; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      90 REDL 93

RESULT 30
US-11-098-686-69
; Sequence 69, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-69

Query Match      100.0%; Score 20; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      40 REDL 43

RESULT 31
US-11-096-568A-13950
; Sequence 13950, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
```

Mon Mar 20 08:51:25 2006

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; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 13950
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(122)
; OTHER INFORMATION: Ceres Seq. ID no. 15220798
US-11-096-568A-13950

Query Match      100.0%; Score 20; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
Db      83 REDL 86

RESULT 32
US-11-051-720-1347
; Sequence 1347, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1347
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1347

Query Match      100.0%; Score 20; DB 7; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
Db      63 REDL 66

RESULT 33
US-11-019-711-54
; Sequence 54, Application US/11019711
; Publication No. US2006009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsbrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgesse, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shionit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Laminin B
; OTHER INFORMATION: Domain Consensus Sequence
US-11-019-711-54

Query Match      100.0%; Score 20; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
Db      89 REDL 92

RESULT 34
US-11-124-367A-274
; Sequence 274, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 274

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; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-274

Query Match      100.0%; Score 20; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      108 REDL 111
      |||||

RESULT 35
US-11-082-389-428
; Sequence 428, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 428
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-428

Query Match      100.0%; Score 20; DB 7; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      124 REDL 127
      |||||

RESULT 36
US-10-667-295-17
; Sequence 17, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
```

```
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(134)
; OTHER INFORMATION: Ceres Seq. ID no. 12474811
US-10-667-295-17

Query Match      100.0%; Score 20; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      39 REDL 42
      |||||

RESULT 37
US-11-096-568A-23874
; Sequence 23874, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23874
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(141)
; OTHER INFORMATION: Ceres Seq. ID no. 12416018
US-11-096-568A-23874

Query Match      100.0%; Score 20; DB 7; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      113 REDL 116
      |||||

RESULT 38
US-10-485-517-193
; Sequence 193, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: E100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
```

; PRIOR APPLICATION NUMBER: GB 0200349.9  
; PRIOR FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 424  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 193  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-10-485-517-193

Query Match 100.0%; Score 20; DB 6; Length 146;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 137 REDL 140

RESULT 39

US-11-118-855-7  
; Sequence 7, Application US/11118855  
; Publication No. US20050266457A1  
; GENERAL INFORMATION:  
; APPLICANT: Kumar, Mohan  
; APPLICANT: Palli, Subba Reddy  
; TITLE OF INVENTION: Mutant Receptors and Their Use in a Nuclear Receptor-Based  
; FILE REFERENCE: A01508-US  
; CURRENT APPLICATION NUMBER: US/11/118,855  
; CURRENT FILING DATE: 2005-04-28  
; PRIOR APPLICATION NUMBER: US 60/567,294  
; PRIOR FILING DATE: 2004-04-30  
; PRIOR APPLICATION NUMBER: US 60/609,424  
; PRIOR FILING DATE: 2004-09-13  
; NUMBER OF SEQ ID NOS: 176  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 147  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-11-118-855-7

Query Match 100.0%; Score 20; DB 7; Length 147;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 74 REDL 77

RESULT 40

US-11-072-512-2881  
; Sequence 2881, Application US/11072512  
; Publication No. US20060029945A1  
; GENERAL INFORMATION:  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: SUGIYAMA, TOMOYASU  
; APPLICANT: OTSUKI, TETSUJI  
; APPLICANT: WAKAMATSU, AI  
; APPLICANT: SATO, HIROYUKI  
; APPLICANT: ISHII, SHIZUKO  
; APPLICANT: YAMAMOTO, JUN-ICHI  
; APPLICANT: ISONO, YUUKO  
; APPLICANT: HIO, YURI  
; APPLICANT: OTSUKA, KAORU  
; APPLICANT: NAGAI, KEIICHI  
; APPLICANT: IRIE, RYOTARO  
; APPLICANT: TAMECHIKA, ICHIRO  
; APPLICANT: SEKI, NAOHICO  
; APPLICANT: YOSHIKAWA, TSUTOMU  
; APPLICANT: OTSUKA, MOTOKYUKI

; APPLICANT: NAGAHARI, KENJI  
; APPLICANT: MASUHO, YASUHIKO  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: 084335-0191  
; CURRENT APPLICATION NUMBER: US/11/072,512  
; CURRENT FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: US 60/350,978  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: JP 2001-379298  
; PRIOR FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2881  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-072-512-2881

Query Match 100.0%; Score 20; DB 7; Length 149;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 25 REDL 28

RESULT 41

US-10-821-234-1646  
; Sequence 1646, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Grain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: Pt\_SEQ\_genes Version 1.0  
; SEQ ID NO 1646  
; LENGTH: 152  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1646

Query Match 100.0%; Score 20; DB 6; Length 152;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 108 REDL 111

RESULT 42

US-11-124-367A-273  
; Sequence 273, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; FILE REFERENCE: Fibrosis Methods of Detection and Uses Thereof  
; FILE REFERENCE: CLO01519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124,367A  
; CURRENT FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07

; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 273  
; LENGTH: 152  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-124-367A-273

Query Match 100.0%; Score 20; DB 7; Length 152;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 108 REDL 111

RESULT 43  
US-10-821-234-1344  
; Sequence 1344, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1344  
; LENGTH: 154  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1344

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Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
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Db 74 REDL 77

RESULT 44  
US-11-087-099-5557  
; Sequence 5557, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 5557  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-11-087-099-5557

Query Match 100.0%; Score 20; DB 7; Length 157;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
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Qy 1 REDL 4  
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Db 105 REDL 108

RESULT 45  
US-10-467-657-170  
; Sequence 170, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 170  
; LENGTH: 164  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-170

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
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Db 62 REDL 65

RESULT 46  
US-10-467-657-204  
; Sequence 204, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 204  
; LENGTH: 164  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-204

Query Match 100.0%; Score 20; DB 6; Length 164;  
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||  
Db 62 REDL 65

RESULT 47

; TITLE OF INVENTION: Nucleic Acids, and Methods of Use

; FILE REFERENCE: P-LJ 5144  
; CURRENT APPLICATION NUMBER: US/10/057,813  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: US 09/770,219  
; PRIOR FILING DATE: 2001-01-25  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-057-813-2

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Db 163 REDL 166

RESULT 50

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; Sequence 12351, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 12351  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(168)  
; OTHER INFORMATION: Ceres Seq. ID no. 13664315  
US-11-096-568A-12351

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 28 REDL 31

Search completed: March 20, 2006, 07:53:54  
Job time : 8.5 secs

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; Sequence 3632, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 3632  
; LENGTH: 164  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-3632

Query Match 100.0%; Score 20; DB 6; Length 164;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
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Db 62 REDL 65

RESULT 48

US-10-467-657-6390  
; Sequence 6390, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 6390  
; LENGTH: 164  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6390

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 62 REDL 65

RESULT 49

US-10-057-813-2  
; Sequence 2, Application US/10057813  
; Publication No. US20060035359A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Okada, Kazuya  
; TITLE OF INVENTION: Survivin-Binding Proteins, Encoding

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:52:41 ; Search time 401.5 Seconds  
(without alignments)  
13.768 Million cell updates/sec

Title: US-09-673-707-10  
Perfect score: 20  
Sequence: 1 REDL 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID                 | Description       |
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| 1          | 20    | 100.0         | 4      | 1  | PCT-US02-30316-6   | Sequence 6, Appli |
| 2          | 20    | 100.0         | 4      | 1  | PCT-US03-18373-31  | Sequence 31, Appl |
| 3          | 20    | 100.0         | 4      | 1  | PCT-US03-18373A-31 | Sequence 31, Appl |
| 4          | 20    | 100.0         | 4      | 1  | PCT-US03-38227-12  | Sequence 12, Appl |
| 5          | 20    | 100.0         | 4      | 1  | PCT-US03-39476-6   | Sequence 6, Appli |
| 6          | 20    | 100.0         | 4      | 1  | PCT-US98-05710-11  | Sequence 11, Appl |
| 7          | 20    | 100.0         | 4      | 9  | US-07-992-900-4    | Sequence 4, Appli |
| 8          | 20    | 100.0         | 4      | 9  | US-07-992-900A-4   | Sequence 4, Appli |
| 9          | 20    | 100.0         | 4      | 13 | US-08-331-396A-52  | Sequence 52, Appl |
| 10         | 20    | 100.0         | 4      | 13 | US-08-331-396C-52  | Sequence 52, Appl |
| 11         | 20    | 100.0         | 4      | 13 | US-08-331-396D-52  | Sequence 52, Appl |
| 12         | 20    | 100.0         | 4      | 21 | US-09-153-803-3    | Sequence 3, Appli |
| 13         | 20    | 100.0         | 4      | 22 | US-09-250-056B-6   | Sequence 6, Appli |
| 14         | 20    | 100.0         | 4      | 24 | US-09-410-362F-79  | Sequence 79, Appl |
| 15         | 20    | 100.0         | 4      | 24 | US-09-462-682-12   | Sequence 12, Appl |
| 16         | 20    | 100.0         | 4      | 24 | US-09-462-713-12   | Sequence 12, Appl |
| 17         | 20    | 100.0         | 4      | 24 | US-09-480-236-7    | Sequence 7, Appli |
| 18         | 20    | 100.0         | 4      | 26 | US-09-673-707-10   | Sequence 10, Appl |
| 19         | 20    | 100.0         | 4      | 26 | US-09-684-599A-5   | Sequence 5, Appli |
| 20         | 20    | 100.0         | 4      | 27 | US-09-743-173-1    | Sequence 1, Appli |
| 21         | 20    | 100.0         | 4      | 27 | US-09-763-393-15   | Sequence 15, Appl |
| 22         | 20    | 100.0         | 4      | 29 | US-09-979-539-7    | Sequence 7, Appli |
| 23         | 20    | 100.0         | 4      | 30 | US-10-092-640-27   | Sequence 27, Appl |
| 24         | 20    | 100.0         | 4      | 31 | US-10-112-788-16   | Sequence 16, Appl |
| 25         | 20    | 100.0         | 4      | 31 | US-10-130-393-10   | Sequence 10, Appl |
| 26         | 20    | 100.0         | 4      | 32 | US-10-297-337-16   | Sequence 16, Appl |
| 27         | 20    | 100.0         | 4      | 33 | US-10-363-233-7    | Sequence 7, Appli |
| 28         | 20    | 100.0         | 4      | 34 | US-10-406-830-24   | Sequence 24, Appl |
| 29         | 20    | 100.0         | 4      | 34 | US-10-432-412-23   | Sequence 23, Appl |
| 30         | 20    | 100.0         | 4      | 34 | US-10-432-412-23   | Sequence 23, Appl |
| 31         | 20    | 100.0         | 4      | 34 | US-10-490-535-6    | Sequence 6, Appli |
| 32         | 20    | 100.0         | 4      | 35 | US-10-537-061-12   | Sequence 12, Appl |
| 33         | 20    | 100.0         | 4      | 36 | US-10-659-036-12   | Sequence 12, Appl |
| 34         | 20    | 100.0         | 4      | 39 | US-10-973-718-9    | Sequence 9, Appli |
| 35         | 20    | 100.0         | 4      | 40 | US-11-019-027-16   | Sequence 16, Appl |
| 36         | 20    | 100.0         | 4      | 40 | US-11-021-438-19   | Sequence 19, Appl |
| 37         | 20    | 100.0         | 4      | 42 | US-11-253-869-79   | Sequence 79, Appl |
| 38         | 20    | 100.0         | 4      | 42 | US-11-254-185-79   | Sequence 79, Appl |
| 39         | 20    | 100.0         | 4      | 44 | US-60-042-056-11   | Sequence 11, Appl |
| 40         | 20    | 100.0         | 5      | 1  | PCT-US00-29080-5   | Sequence 5, Appli |
| 41         | 20    | 100.0         | 5      | 1  | PCT-US02-30316-7   | Sequence 7, Appli |
| 42         | 20    | 100.0         | 5      | 1  | PCT-US03-10630A-4  | Sequence 4, Appli |
| 43         | 20    | 100.0         | 5      | 1  | PCT-US03-10630A-4  | Sequence 4, Appli |
| 44         | 20    | 100.0         | 5      | 1  | PCT-US98-05710-10  | Sequence 10, Appl |
| 45         | 20    | 100.0         | 5      | 12 | US-08-224-831-32   | Sequence 32, Appl |
| 46         | 20    | 100.0         | 5      | 12 | US-08-224-831A-32  | Sequence 32, Appl |
| 47         | 20    | 100.0         | 5      | 13 | US-08-331-396A-53  | Sequence 53, Appl |
| 48         | 20    | 100.0         | 5      | 13 | US-08-331-396C-53  | Sequence 53, Appl |
| 49         | 20    | 100.0         | 5      | 13 | US-08-331-396D-53  | Sequence 53, Appl |
| 50         | 20    | 100.0         | 5      | 21 | US-09-153-803-2    | Sequence 2, Appli |
| 51         | 20    | 100.0         | 5      | 21 | US-09-172-006-46   | Sequence 46, Appl |
| 52         | 20    | 100.0         | 5      | 22 | US-09-247-139-33   | Sequence 33, Appl |
| 53         | 20    | 100.0         | 5      | 22 | US-09-247-139-37   | Sequence 37, Appl |
| 54         | 20    | 100.0         | 5      | 22 | US-09-250-056B-5   | Sequence 5, Appli |
| 55         | 20    | 100.0         | 5      | 24 | US-09-410-362F-78  | Sequence 78, Appl |

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| 57  | 20 | 100.0 | 20 | 100.0 | 11  | 39 | US-10-938-690-3    | Sequence 3, Appli  |
| 58  | 20 | 100.0 | 20 | 100.0 | 14  | 1  | PCT-US98-05710-5   | Sequence 5, Appli  |
| 59  | 20 | 100.0 | 20 | 100.0 | 14  | 1  | PCT-US98-23061-8   | Sequence 8, Appli  |
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| 61  | 20 | 100.0 | 20 | 100.0 | 14  | 14 | US-08-433-613-7    | Sequence 7, Appli  |
| 62  | 20 | 100.0 | 20 | 100.0 | 14  | 26 | US-09-623-931D-10  | Sequence 10, Appli |
| 63  | 20 | 100.0 | 20 | 100.0 | 14  | 27 | US-09-742-148B-7   | Sequence 7, Appli  |
| 64  | 20 | 100.0 | 20 | 100.0 | 14  | 44 | US-60-042-056-5    | Sequence 7, Appli  |
| 65  | 20 | 100.0 | 20 | 100.0 | 15  | 27 | US-09-786-635A-53  | Sequence 53, Appli |
| 66  | 20 | 100.0 | 20 | 100.0 | 15  | 27 | US-09-786-635C-53  | Sequence 53, Appli |
| 67  | 20 | 100.0 | 20 | 100.0 | 15  | 27 | US-09-786-635D-53  | Sequence 53, Appli |
| 68  | 20 | 100.0 | 20 | 100.0 | 15  | 41 | US-11-154-939-5497 | Sequence 5497, Ap  |
| 69  | 20 | 100.0 | 20 | 100.0 | 15  | 41 | US-11-167-575-5497 | Sequence 5497, Ap  |
| 70  | 20 | 100.0 | 20 | 100.0 | 15  | 50 | US-60-651-509-1874 | Sequence 1874, Ap  |
| 71  | 20 | 100.0 | 20 | 100.0 | 15  | 50 | US-60-687-846-1508 | Sequence 1508, Ap  |
| 72  | 20 | 100.0 | 20 | 100.0 | 16  | 9  | US-07-944-143-16   | Sequence 16, Appl  |
| 73  | 20 | 100.0 | 20 | 100.0 | 16  | 9  | US-07-944-143A-16  | Sequence 16, Appl  |
| 74  | 20 | 100.0 | 20 | 100.0 | 16  | 9  | US-07-944-143B-16  | Sequence 16, Appl  |
| 75  | 20 | 100.0 | 20 | 100.0 | 17  | 13 | US-08-324-163-4    | Sequence 4, Appli  |
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| 80  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 81  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
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| 83  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 84  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 85  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 86  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 87  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
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| 89  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 90  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
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| 97  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 98  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 99  | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 100 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 101 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 102 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 103 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 104 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 105 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 106 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 107 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 108 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 109 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 110 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 111 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 112 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 113 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 114 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 115 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 116 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 117 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 118 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 119 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 120 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 121 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 122 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 123 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 124 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 125 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 126 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 127 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 128 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 129 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 130 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 131 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 132 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 133 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 134 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 135 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 136 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 137 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 138 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 139 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 140 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 141 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 142 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 143 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 144 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 145 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 146 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 147 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 148 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 149 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 150 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 151 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 152 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 153 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 154 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 155 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 156 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 157 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 158 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 159 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 160 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 161 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 162 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 163 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 164 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 165 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 166 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 167 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 168 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 169 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 170 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 171 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 172 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 173 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 174 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 175 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 176 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 177 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 178 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 179 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 180 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 181 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 182 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 183 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 184 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 185 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 186 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 187 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 188 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 189 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 190 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 191 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 192 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 193 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 194 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 195 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 196 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 197 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 198 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 199 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 200 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 201 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 202 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 203 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 204 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 205 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 206 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 207 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 208 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 209 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 210 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 211 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 212 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 213 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 214 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 215 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 216 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 217 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 218 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 219 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 220 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 221 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 222 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 223 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 224 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 225 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 226 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 227 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 228 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 229 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
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| 231 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 232 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 233 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
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| 235 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 236 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 237 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 238 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 239 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 240 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 241 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 242 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |
| 243 | 20 | 100.0 | 20 | 100.0 |     |    |                    |                    |

```
; APPLICANT: Numata, Yoshito
; APPLICANT: Santora, Kenneth
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert
; APPLICANT: Sinha, Abhishek
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Anti-CD30 Stalk and Anti-CD30 Antibodies Suitable for
; TITLE OF INVENTION: Use in Immunotoxins
; FILE REFERENCE: 015280-464100PC
; CURRENT APPLICATION NUMBER: PCT/US03/18373
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: US 60/387,293
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/411,032
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Pseudomonas
; OTHER INFORMATION: exotoxin (PE) carboxyl terminus addition
PCT-US03-18373-31

Query Match          100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 3
PCT-US03-18373A-31
; Sequence 31, Application PC/TUS0318373A
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Nagata, Satoshi
; APPLICANT: Onda, Masanori
; APPLICANT: Numata, Yoshito
; APPLICANT: Santora, Kenneth
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert
; APPLICANT: Sinha, Abhishek
; APPLICANT: as represented by The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Anti-CD30 Stalk and Anti-CD30 Antibodies Suitable for
; TITLE OF INVENTION: Use in Immunotoxins
; FILE REFERENCE: 015280-464100PC
; CURRENT APPLICATION NUMBER: PCT/US03/18373A
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: US 60/387,293
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/411,032
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Pseudomonas
; OTHER INFORMATION: exotoxin (PE) carboxyl terminus addition
PCT-US03-18373A-31

Query Match          100.0%; Score 20; DB 1; Length 4;
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; APPLICANT: Numata, Yoshito
; APPLICANT: Santora, Kenneth
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert
; APPLICANT: Sinha, Abhishek
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Anti-CD30 Stalk and Anti-CD30 Antibodies Suitable for
; TITLE OF INVENTION: Use in Immunotoxins
; FILE REFERENCE: 015280-464100PC
; CURRENT APPLICATION NUMBER: PCT/US03/18373
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: US 60/387,293
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/411,032
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Pseudomonas
; OTHER INFORMATION: exotoxin (PE) carboxyl terminus addition
PCT-US03-18373A-31

Query Match          100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 3
PCT-US03-18373A-31
; Sequence 31, Application PC/TUS0318373A
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Nagata, Satoshi
; APPLICANT: Onda, Masanori
; APPLICANT: Numata, Yoshito
; APPLICANT: Santora, Kenneth
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert
; APPLICANT: Sinha, Abhishek
; APPLICANT: as represented by The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Anti-CD30 Stalk and Anti-CD30 Antibodies Suitable for
; TITLE OF INVENTION: Use in Immunotoxins
; FILE REFERENCE: 015280-464100PC
; CURRENT APPLICATION NUMBER: PCT/US03/18373A
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: US 60/387,293
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/411,032
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Pseudomonas
; OTHER INFORMATION: exotoxin (PE) carboxyl terminus addition
PCT-US03-18373A-31

Query Match          100.0%; Score 20; DB 1; Length 4;
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Query Match          100.0%; Score 20; DB 1; Length 4;
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|          |   |         |              |          |            |    |        |    |      |    |
|----------|---|---------|--------------|----------|------------|----|--------|----|------|----|
|          | Best Local Similarity   | 100.0%; | Pred. No.    | 7.2e+06; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|          | Matches   | 4;      | Conservative | 0;       |            |    |        |    |      |    |
| QY       | 1 REDL 4  |         |              |          |            |    |        |    |      |    |
|          |   |         |              |          |            |    |        |    |      |    |
| Db       | 1 REDL 4  |         |              |          |            |    |        |    |      |    |
|          |   |         |              |          |            |    |        |    |      |    |
| RESULT 6 |   |         |              |          |            |    |        |    |      |    |
|          | PCT-US98-05710-11   |         |              |          |            |    |        |    |      |    |
|          | ; Sequence 11, Application PC/TUS9805710                                      |         |              |          |            |    |        |    |      |    |
|          | ; GENERAL INFORMATION:  |         |              |          |            |    |        |    |      |    |
|          | ; APPLICANT:  |         |              |          |            |    |        |    |      |    |
|          | ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USING                      |         |              |          |            |    |        |    |      |    |
|          | ; TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS |         |              |          |            |    |        |    |      |    |
|          | ; TITLE OF INVENTION: CELL MEMBRANES  |         |              |          |            |    |        |    |      |    |
|          | ; NUMBER OF SEQUENCES: 13   |         |              |          |            |    |        |    |      |    |
|          | ; COMPUTER READABLE FORM:   |         |              |          |            |    |        |    |      |    |
|          | ; MEDIUM TYPE: Floppy disk  |         |              |          |            |    |        |    |      |    |
|          | ; COMPUTER: IBM PC compatible   |         |              |          |            |    |        |    |      |    |
|          | ; OPERATING SYSTEM: PC-DOS/MS-DOS   |         |              |          |            |    |        |    |      |    |
|          | ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)                        |         |              |          |            |    |        |    |      |    |
|          | ; CURRENT APPLICATION DATA:   |         |              |          |            |    |        |    |      |    |
|          | ; FILING DATE: PCT/US98/05710   |         |              |          |            |    |        |    |      |    |
|          | ; CLASSIFICATION:   |         |              |          |            |    |        |    |      |    |
|          | ; PRIOR APPLICATION DATA:   |         |              |          |            |    |        |    |      |    |
|          | ; APPLICATION NUMBER: US 60/042,056   |         |              |          |            |    |        |    |      |    |
|          | ; FILING DATE: 26-MAR-1997  |         |              |          |            |    |        |    |      |    |
|          | ; INFORMATION FOR SEQ ID NO: 11:  |         |              |          |            |    |        |    |      |    |
|          | ; SEQUENCE CHARACTERISTICS:   |         |              |          |            |    |        |    |      |    |
|          | ; LENGTH: 4 amino acids   |         |              |          |            |    |        |    |      |    |
|          | ; TYPE: amino acid  |         |              |          |            |    |        |    |      |    |
|          | ; STRANDEDNESS:   |         |              |          |            |    |        |    |      |    |
|          | ; TOPOLOGY: linear  |         |              |          |            |    |        |    |      |    |
|          | ; PCT-US98-05710-11   |         |              |          |            |    |        |    |      |    |
|          | Query Match   | 100.0%; | Score 20;    | DB 1;    | Length 4;  |    |        |    |      |    |
|          | Best Local Similarity   | 100.0%; | Pred. No.    | 7.2e+06; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|          | Matches   | 4;      | Conservative | 0;       |            |    |        |    |      |    |
| QY       | 1 REDL 4  |         |              |          |            |    |        |    |      |    |
|          |   |         |              |          |            |    |        |    |      |    |
| Db       | 1 REDL 4  |         |              |          |            |    |        |    |      |    |
|          |   |         |              |          |            |    |        |    |      |    |
| RESULT 7 |   |         |              |          |            |    |        |    |      |    |
|          | US-07-992-900A-4  |         |              |          |            |    |        |    |      |    |
|          | ; Sequence 4, Application US/07992900   |         |              |          |            |    |        |    |      |    |
|          | ; GENERAL INFORMATION:  |         |              |          |            |    |        |    |      |    |
|          | ; APPLICANT: DRAPER, ROCKFORD K.  |         |              |          |            |    |        |    |      |    |
|          | ; APPLICANT: CHAUDRY, G. JILANI   |         |              |          |            |    |        |    |      |    |
|          | ; TITLE OF INVENTION: POTENT AND SPECIFIC CHEMICALLY-CONJUGATED               |         |              |          |            |    |        |    |      |    |
|          | ; TITLE OF INVENTION: IMMUNOTOXINS  |         |              |          |            |    |        |    |      |    |
|          | ; NUMBER OF SEQUENCES: 5  |         |              |          |            |    |        |    |      |    |
|          | ; CORRESPONDENCE ADDRESS:   |         |              |          |            |    |        |    |      |    |
|          | ; ADDRESSEE: ARNOLD, WHITE & DURKEE   |         |              |          |            |    |        |    |      |    |
|          | ; STREET: P.O. BOX 4433   |         |              |          |            |    |        |    |      |    |
|          | ; CITY: HOUSTON   |         |              |          |            |    |        |    |      |    |
|          | ; STATE: TEXAS  |         |              |          |            |    |        |    |      |    |
|          | ; COUNTRY: USA  |         |              |          |            |    |        |    |      |    |
|          | ; ZIP: 77210  |         |              |          |            |    |        |    |      |    |
|          | ; COMPUTER READABLE FORM:   |         |              |          |            |    |        |    |      |    |
|          | ; MEDIUM TYPE: FLOPPY DISK  |         |              |          |            |    |        |    |      |    |
|          | ; COMPUTER: IBM PC COMPATIBLE   |         |              |          |            |    |        |    |      |    |
|          | ; OPERATING SYSTEM: PC-DOS/MS-DOS   |         |              |          |            |    |        |    |      |    |
|          | ; SOFTWARE: WORDPERFECT 5.1   |         |              |          |            |    |        |    |      |    |
|          | ; CURRENT APPLICATION DATA:   |         |              |          |            |    |        |    |      |    |
|          | ; APPLICATION NUMBER: US/07/992,900   |         |              |          |            |    |        |    |      |    |
|          | ; FILING DATE: 19921216   |         |              |          |            |    |        |    |      |    |
|          | ; CLASSIFICATION: 530   |         |              |          |            |    |        |    |      |    |
|          | ; ATTORNEY/AGENT INFORMATION:   |         |              |          |            |    |        |    |      |    |
|          | ; NAME: HODGINS, DANIEL S.  |         |              |          |            |    |        |    |      |    |
|          | Query Match   | 100.0%; | Score 20;    | DB 9;    | Length 4;  |    |        |    |      |    |
|          | Best Local Similarity   | 100.0%; | Pred. No.    | 7.2e+06; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|          | Matches   | 4;      | Conservative | 0;       |            |    |        |    |      |    |
| Qy       | 1 REDL 4  |         |              |          |            |    |        |    |      |    |



```
; Sequence 52, Application US/08331396A
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira H.
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: TUMOR-SPECIFIC ANTIBODY FRAGMENTS,
; TITLE OF INVENTION: FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Steuart Street tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.396A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-396A-52

Query Match 100.0%; Score 20; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 10
US-08-331-396C-52
; Sequence 52, Application US/08331396C
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Lee, Byungkook
; TITLE OF INVENTION: Humanized Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```

```
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.396C
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-396C-52

Query Match 100.0%; Score 20; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 11
US-08-331-396D-52
; Sequence 52, Application US/08331396D
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Lee, Byungkook
; TITLE OF INVENTION: Humanized Tumor-Specific Antibody
; TITLE OF INVENTION: Fragments, Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.396D
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
```

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; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA: US 07/596,289
; APPLICATION NUMBER: 12-OCT-1990
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-331-396D-52

```

```

Query Match      100.0%; Score 20; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

```

```

Qy      1 REDL 4
Db      1 REDL 4

```

```

RESULT 12
US-09-153-803-3
; Sequence 3, Application US/09153803
; GENERAL INFORMATION:
; APPLICANT: WEICHSSELBAUM, RALPH R.
; APPLICANT: SEETHARAM, SARA
; APPLICANT: KUFE, DONALD W.
; APPLICANT: PASTAN, IRA
; TITLE OF INVENTION: COMBINATION OF CHIMERIC EXOTOXIN AND THERAPEUTIC
; TITLE OF INVENTION: RADIATION
; FILE REFERENCE: ARSB:514
; CURRENT APPLICATION NUMBER: US/09/153,803
; CURRENT FILING DATE: 1998-09-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-153-803-3

```

```

Query Match      100.0%; Score 20; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

```

```

Qy      1 REDL 4
Db      1 REDL 4

```

```

RESULT 13
US-09-250-056B-6
; Sequence 6, Application US/09250056B
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Poul, Marie A
; TITLE OF INVENTION: INTERNALIZING ERB2 ANTIBODIES
; FILE REFERENCE: 2500.116US3 Internalizing ErbB2 Ab
; CURRENT APPLICATION NUMBER: US/09/250,056B
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/082,953

```

```

; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:: translocation
; OTHER INFORMATION: sequence
US-09-250-056B-6

```

```

Query Match      100.0%; Score 20; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

```

```

Qy      1 REDL 4
Db      1 REDL 4

```

```

RESULT 14
US-09-410-362F-79
; Sequence 79, Application US/09410362F
; GENERAL INFORMATION:
; APPLICANT: CRAIK, CHARLES S.
; APPLICANT: TAKEUCHI, TOSHIHIKO
; APPLICANT: SCHUMAN, MARC
; TITLE OF INVENTION: MEMBRANE TYPE SERINE PROTEASE 1 (MT-SPI) AND USES THEREOF
; FILE REFERENCE: 28644-701.201
; CURRENT APPLICATION NUMBER: US/09/410,362F
; CURRENT FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Endoplasmic refention sequence
US-09-410-362F-79

```

```

Query Match      100.0%; Score 20; DB 24; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

```

```

Qy      1 REDL 4
Db      1 REDL 4

```

```

RESULT 15
US-09-462-682-12
; Sequence 12, Application US/09462682
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary,
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens
; FILE REFERENCE: 015280-310100US
; CURRENT APPLICATION NUMBER: US/09/462,682
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/052,375
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: WO PCT/US98/14341
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention sequence
US-09-462-682-12

Query Match          100.0%; Score 20; DB 24; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 16
US-09-462-713-12
; Sequence 12, Application US/09462713
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Mrsny, Randall J.
; APPLICANT: The Government of the United States of America
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens
; TITLE OF INVENTION: for Eliciting a Secretory IGA-Mediated Immune Response
; FILE REFERENCE: 015280-361100US
; CURRENT APPLICATION NUMBER: US/09/462.713
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: PCT/US98/14336
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/056,924
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention sequence
US-09-462-713-12

Query Match          100.0%; Score 20; DB 24; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 17
US-09-480-236-7
; Sequence 7, Application US/09480236
; GENERAL INFORMATION:
; APPLICANT: Digan, Mary Ellen
; APPLICANT: Lake, Philip
; APPLICANT: Wright, Richard M.
; TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor
; FILE REFERENCE: CGC 4-31157A/USN
; CURRENT APPLICATION NUMBER: US/09/480.236
; CURRENT FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PE peptide
US-09-480-236-7

Query Match          100.0%; Score 20; DB 24; Length 4;
```

```
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 18
US-09-673-707-10
; Sequence 10, Application US/09673707
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Bera, Tapan K.
; APPLICANT: Kennedy, Paul E.
; APPLICANT: Berger, Edward A.
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Immunotoxin Directed Against the HIV-1
; TITLE OF INVENTION: gp120 Envelope Glycoprotein
; FILE REFERENCE: 015280-356100US
; CURRENT APPLICATION NUMBER: US/09/673,707
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: WO PCT/US99/12909
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: US 60/088,860
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: carboxy
; OTHER INFORMATION: terminal sequence of Pseudomonas exotoxin (PE)
; OTHER INFORMATION: endoplasmic retention sequence
US-09-673-707-10

Query Match          100.0%; Score 20; DB 26; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 1 REDL 4

RESULT 19
US-09-684-599A-5
; Sequence 5, Application US/09684599A
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Chang, Kai
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; and Methods and Kits for Targeting the Antigen
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/684,599A  
; FILING DATE: 05-Oct-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/215,035  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: WO PCT/US97/00224  
; FILING DATE: 03-JAN-1997  
; APPLICATION NUMBER: US 60/010,166  
; FILING DATE: 05-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Faris, Susan K.  
; REGISTRATION NUMBER: 41,739  
; REFERENCE/DOCKET NUMBER: 015280-259110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-684-599A-5

Query Match 100.0%; Score 20; DB 26; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|  
|  
|  
|  
Db 1 REDL 4

RESULT 20  
US-09-743-173-1  
; Sequence 1, Application US/09743173  
; GENERAL INFORMATION:  
; APPLICANT: Seveso, Michael  
; APPLICANT: O'Mahony, Daniel J.  
; APPLICANT: Page, David T.  
; TITLE OF INVENTION: Enhanced Delivery of Nucleic Acid-Based Drugs  
; FILE REFERENCE: P24,376-A USA  
; CURRENT APPLICATION NUMBER: US/09/743,173  
; CURRENT FILING DATE: 2001-01-05  
; CURRENT APPLICATION NUMBER: PCT/GB00/01726  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: US 60/132,603  
; PRIOR FILING DATE: 1999-05-05  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: endosome escape motif  
US-09-743-173-1

Query Match 100.0%; Score 20; DB 27; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|  
|  
|  
|  
Db 1 REDL 4

RESULT 21  
US-09-763-393-15  
; Sequence 15, Application US/09763393

; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America as  
; APPLICANT: represented by the Secretary of the Department of Health and  
; APPLICANT: Human Services  
; APPLICANT: Pastan, Ira  
; APPLICANT: Brinkmann, Ulrich  
; APPLICANT: Vasmatazis, George  
; APPLICANT: Lee, Byungkook  
; TITLE OF INVENTION: PAGE-4, an X-Linked GAGE-Like Gene Expressed in Normal and  
; TITLE OF INVENTION: Neoplastic Prostate, Testis and Uterus, and Uses Therefor  
; FILE REFERENCE: 4239-61541-01  
; CURRENT APPLICATION NUMBER: US/09/763,393  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: PCT/US99/20046  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: US 60/098,993  
; PRIOR FILING DATE: 1998-09-01  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 15  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Carboxyl terminus  
US-09-763-393-15

Query Match 100.0%; Score 20; DB 27; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|  
|  
|  
|  
Db 1 REDL 4

RESULT 22  
US-09-979-539-7  
; Sequence 7, Application US/09979539  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Chowdhury, Partha S.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Immunoconjugates Having High Binding Affinity  
; FILE REFERENCE: 015280-395100US  
; CURRENT APPLICATION NUMBER: US/09/979,539  
; CURRENT FILING DATE: 2002-02-26  
; PRIOR APPLICATION NUMBER: US 60/160,071  
; PRIOR FILING DATE: 1999-05-27  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14829  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequence  
; OTHER INFORMATION: addition at carboxyl terminus to maintain ability  
; OTHER INFORMATION: to translocate into the cytosol  
US-09-979-539-7

Query Match 100.0%; Score 20; DB 29; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|  
|  
|  
|  
Db 1 REDL 4

```
RESULT 23
US-10-092-640-27
; Sequence 27, Application US/10092640
; GENERAL INFORMATION:
; APPLICANT: Markle, James D.
; TITLE OF INVENTION: Novel High Affinity Human Antibodies to
; Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quine Intellectual Property Law Group P.C.
; STREET: 2033 Clement Ave. Suite 200
; CITY: Alameda
; STATE: California
; COUNTRY: USA
; ZIP: 94501
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/092,640
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; APPLICATION NUMBER: US 09/315,574
; FILING DATE: 20-MAY-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-092-640-27

Query Match 100.0%; Score 20; DB 30; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 1 REDL 4

RESULT 24
US-10-112-788-16
; Sequence 16, Application US/10112788
; GENERAL INFORMATION:
; APPLICANT: DENARDO, SALLY
; APPLICANT: WINTHROP, MICHELLE
; APPLICANT: DENARDO, GERALD
; TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING
; FILE REFERENCE: 309T-000210US
; CURRENT APPLICATION NUMBER: US/10/112,788
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/280,721
```

```
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant translocation peptide
US-10-112-788-16

Query Match 100.0%; Score 20; DB 31; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 1 REDL 4

RESULT 25
US-10-130-393-10
; Sequence 10, Application US/10130393
; GENERAL INFORMATION:
; APPLICANT: Puri, Raj K.
; APPLICANT: Oshima, Yasuo
; APPLICANT: Joshi, Bharat H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Modulating IL-13 Activity Using Mutated IL-13 Molecules
; FILE REFERENCE: 015280-409100US
; CURRENT APPLICATION NUMBER: US/10/130,393
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/165,236
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: WO PCT/US00/31044
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; TYPE: PRT
; LENGTH: 4
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: retention sequence
US-10-130-393-10

Query Match 100.0%; Score 20; DB 31; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
Db 1 REDL 4

RESULT 26
US-10-297-337-16
; Sequence 16, Application US/10297337
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Tsutsumi, Yasuo
; APPLICANT: Onda, Masanori
; APPLICANT: Nagata, Satoshi
; APPLICANT: Lee, Byungkook
; APPLICANT: Kreitman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: PEGylation of Linkers Improves Antitumor Activity and
```

US-10-406-830-24  
; TITLE OF INVENTION: Reduces Toxicity of Immunoconjugates  
; FILE REFERENCE: 015280-423200US  
; CURRENT APPLICATION NUMBER: US/10/297,337  
; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/211,331  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: US 60/213,804  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: WO PCT/US01/18503  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:C-terminal  
; OTHER INFORMATION: variation to maintain ability of construct to  
; OTHER INFORMATION: translocate to cytosol  
US-10-297-337-16

Query Match 100.0%; Score 20; DB 32; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 27  
US-10-363-233-7  
; Sequence 7, Application US/10363233  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira H.  
; APPLICANT: Liu, Xiu Fen  
; APPLICANT: Bera, Tapan K.  
; APPLICANT: Lee, Byungkook  
; APPLICANT: Eglund, Kristi A.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: XAGE-1, a Gene Expressed in Multiple Cancers, and Uses  
; TITLE OF INVENTION: Thereof  
; FILE REFERENCE: 015280-420100US  
; CURRENT APPLICATION NUMBER: US/10/363,233  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: US 60/229,684  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: WO PCT/US01/27258  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Pseudomonas  
; OTHER INFORMATION: exotoxin carboxy terminus addition  
US-10-363-233-7

Query Match 100.0%; Score 20; DB 33; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 28

US-10-406-830-24  
; Sequence 24, Application US/10406830  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, GREGORY P.  
; APPLICANT: HORAK, EVA M.  
; APPLICANT: WEINER, LOUIS M.  
; APPLICANT: JAMES, MARKS D.  
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 407T-000410US  
; CURRENT APPLICATION NUMBER: US/10/406,830  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/370,276  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Translocation signaling sequence.  
US-10-406-830-24

Query Match 100.0%; Score 20; DB 34; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 29  
US-10-432-412-22  
; Sequence 22, Application US/10432412  
; GENERAL INFORMATION:  
; APPLICANT: Fitzgerald, David J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; APPLICANT: A Chimeric Protein Comprising Non-Toxic Pseudomonas  
; TITLE OF INVENTION: Exotoxin A and Type IV Pilin Sequences  
; FILE REFERENCE: 015280-429100US  
; CURRENT APPLICATION NUMBER: US/10/432,412  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/257,877  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:endoplasmic  
; OTHER INFORMATION: reticulum (ER) retention domain  
US-10-432-412-22

Query Match 100.0%; Score 20; DB 34; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 30  
US-10-432-412-23  
; Sequence 23, Application US/10432412

GENERAL INFORMATION:  
; APPLICANT: FitzGerald, David J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas  
; TITLE OF INVENTION: Exotoxin A and Type IV Pilin Sequences  
; FILE REFERENCE: 015280-429100US  
; CURRENT APPLICATION NUMBER: US/10/432,412  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/257,877  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic  
; OTHER INFORMATION: reticulum (ER) retention domain  
US-10-432-412-23

Query Match 100.0%; Score 20; DB 34; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 31  
US-10-490-535-6  
; Sequence 6, Application US/10490535  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira H.  
; APPLICANT: Salvatore, Giuliana  
; APPLICANT: Beers, Richard  
; APPLICANT: Kreitman, Robert J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Mutated Anti-CD22 Antibodies With Increased Affinity to  
; TITLE OF INVENTION: CD22-Expressing Leukemia Cells  
; FILE REFERENCE: 015280-438100US  
; CURRENT APPLICATION NUMBER: US/10/490,535  
; CURRENT FILING DATE: 2004-03-24  
; PRIOR APPLICATION NUMBER: US 60/325,360  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: WO PCT/US02/30316  
; PRIOR FILING DATE: 2002-09-25  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: carboxyl  
; OTHER INFORMATION: terminus addition to maintain ability of the  
; OTHER INFORMATION: construct to translocate to cytosol  
US-10-490-535-6

Query Match 100.0%; Score 20; DB 34; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 32  
US-10-537-061-12  
; Sequence 12, Application US/10537061  
; GENERAL INFORMATION:  
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
; APPLICANT: HUMAN SERVICES  
; APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH  
; APPLICANT: Pastan, Ira  
; APPLICANT: Onda, Masanori  
; APPLICANT: Cheung, Nai-Kong  
; TITLE OF INVENTION: IN-VIVO CYTOTOXIC ACTIVITIES OF RECOMBINANT IMMUNOTOXIN 8H9  
; FILE REFERENCE: 4239-67287-05  
; CURRENT APPLICATION NUMBER: US/10/537,061  
; CURRENT FILING DATE: 2005-06-01  
; PRIOR APPLICATION NUMBER: PCT/US03/038227  
; PRIOR FILING DATE: 2003-12-01  
; PRIOR APPLICATION NUMBER: US 60/430,305  
; PRIOR FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-10-537-061-12

Query Match 100.0%; Score 20; DB 35; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

RESULT 33  
US-10-659-036-12  
; Sequence 12, Application US/10659036  
; GENERAL INFORMATION:  
; APPLICANT: FitzGerald, David J.  
; APPLICANT: Mrsny, Randall J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; APPLICANT: Genentech, Inc.  
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens for  
; TITLE OF INVENTION: Eliciting a Secretory IgA-Mediated Immune Response  
; FILE REFERENCE: 015280-361200US  
; CURRENT APPLICATION NUMBER: US/10/659,036  
; CURRENT FILING DATE: 2003-09-09  
; PRIOR APPLICATION NUMBER: US 60/056,924  
; PRIOR FILING DATE: 1997-07-11  
; PRIOR APPLICATION NUMBER: WO PCT/US98/14336  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 09/462,713  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic  
; OTHER INFORMATION: reticulum (ER) retention sequence  
US-10-659-036-12

Query Match 100.0%; Score 20; DB 36; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;





```
RESULT 38
US-11-254-185-79
; Sequence 79, Application US/11254185
; GENERAL INFORMATION:
; APPLICANT: CRAIK, CHARLES S.
; APPLICANT: TAKEUCHI, TOSHIHIKO
; APPLICANT: SCHUMAN, MARC
; TITLE OF INVENTION: MT-SP1 SERINE PROTEASE
; FILE REFERENCE: 28644-701.302
; CURRENT APPLICATION NUMBER: US/11/254.185
; CURRENT FILING DATE: 2005-10-18
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Endoplasmic refention sequence
US-11-254-185-79

Query Match      100.0%; Score 20; DB 42; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      1 REDL 4

RESULT 39
US-60-042-056-11
; Sequence 11, Application US/60042056
; GENERAL INFORMATION:
; APPLICANT: Draper, Rockford
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USING
; TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSP:072P21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-60-042-056-11

Query Match      100.0%; Score 20; DB 44; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      1 REDL 4

RESULT 40
PCT-US00-29080-5
; Sequence 5, Application PC/TUS0029080
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Mresny, Randall J.
; APPLICANT: McKee, Marian
; APPLICANT: Daugherty, Ann
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Delivery of Proteins Across Polar Epithelial Cell
; TITLE OF INVENTION: Layers
; FILE REFERENCE: 015280-378100PC
; CURRENT APPLICATION NUMBER: PCT/US00/29080
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,923
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum retention sequence
PCT-US00-29080-5

Query Match      100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      1 REDL 4

RESULT 41
PCT-US02-30316-7
; Sequence 7, Application PC/TUS0230316
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Salvatore, Giuliana
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mutated Anti-CD22 Antibodies With Increased Affinity to
; TITLE OF INVENTION: CD22-Expressing Leukemia Cells
; FILE REFERENCE: 015280-438100PC
; CURRENT APPLICATION NUMBER: PCT/US02/30316
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/325,360
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-terminal
; OTHER INFORMATION: native sequence
```

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PCT-US02-30316-7
Query Match          100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      1 REDL 4
      ||||
      ||||

RESULT 42
PCT-US03-10630-4
; Sequence 4, Application PC/TUS0310630
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
; TITLE OF INVENTION: COLON TUMOR SPECIFIC BINDING PEPTIDES
; FILE REFERENCE: 38509-0015
; CURRENT APPLICATION NUMBER: PCT/US03/10630
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/369,850
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; TYPE: PRT
; LENGTH: 5
; ORGANISM: Pseudomonas sp.
PCT-US03-10630-4

Query Match          100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      1 REDL 4
      ||||
      ||||

RESULT 43
PCT-US03-10630A-4
; Sequence 4, Application PC/TUS0310630A
; GENERAL INFORMATION:
; APPLICANT: Kimberly A. Kelly
; APPLICANT: David A. Jones
; TITLE OF INVENTION: COLON TUMOR SPECIFIC BINDING PEPTIDES
; FILE REFERENCE: 38509-0015US1
; CURRENT APPLICATION NUMBER: PCT/US03/10630A
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: PCT/US03/10630
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/369,850
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
PCT-US03-10630A-4

Query Match          100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      1 REDL 4
      ||||
      ||||

RESULT 44
PCT-US98-05710-10
; Sequence 10, Application PC/TUS9805710
; GENERAL INFORMATION:
; APPLICANT: METHODS AND COMPOSITIONS FOR USING
; TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
; TITLE OF INVENTION: CELL MEMBRANES
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/05710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,056
; FILING DATE: 26-MAR-1997
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US98-05710-10

Query Match          100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      1 REDL 4
      ||||
      ||||

RESULT 45
US-08-224-831-32
; Sequence 32, Application US/08224831
; GENERAL INFORMATION:
; APPLICANT: Morgan, Charles A.
; TITLE OF INVENTION: RECEPTOR MODULATING AGENTS AND METHODS
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,831
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 930063.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-224-831-32

```

Query Match 100.0%; Score 20; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

## RESULT 46

US-08-224-831A-32  
; Sequence 32, Application US/08224831A  
; GENERAL INFORMATION:  
; APPLICANT: Morgan, A. Charles  
; TITLE OF INVENTION: RECEPTOR MODULATING AGENTS AND METHODS  
; TITLE OF INVENTION: RELATED THERETO  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/224,831A  
; FILING DATE: 08-APR-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Deehr, Manya S.  
; REGISTRATION NUMBER: 37,120  
; REFERENCE/DOCKET NUMBER: 930063.402  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; TELEX: 3723836 SEEDANBERRY  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-224-831A-32

Query Match 100.0%; Score 20; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

## RESULT 47

US-08-331-396A-53  
; Sequence 53, Application US/08331396A  
; GENERAL INFORMATION:  
; APPLICANT: PASTAN, Ira H.  
; APPLICANT: BENHAR, Itai  
; APPLICANT: PADLAN, Eduardo A.  
; APPLICANT: JUNG, Sun-Hee  
; APPLICANT: LEE, Byungkook  
; TITLE OF INVENTION: TUMOR-SPECIFIC ANTIBODY FRAGMENTS,  
; TITLE OF INVENTION: FUSION PROTEINS, AND USES THEREOF  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew  
; STREET: Steuart Street Tower, One Market Plaza

CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,396A  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-126-1-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-331-396A-53

Query Match 100.0%; Score 20; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 1 REDL 4

## RESULT 48

US-08-331-396C-53  
; Sequence 53, Application US/08331396C  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Benhar, Itai  
; APPLICANT: Padlan, Eduardo A.  
; APPLICANT: Jung, Sun-Hee  
; APPLICANT: Lee, Byungkook  
; TITLE OF INVENTION: Humanized Tumor-Specific Antibody Fragments,  
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,396C  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA: US 07/596,289
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-396C-53

Query Match 100.0%; Score 20; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 REDL 4

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; Sequence 2, Application US/09153803
; GENERAL INFORMATION:
; APPLICANT: WEICHSELBAUM, RALPH R.
; APPLICANT: SEETHARAM, SARA
; APPLICANT: KUFE, DONALD W.
; APPLICANT: PASTAN, IRA
; TITLE OF INVENTION: COMBINATION OF CHIMERIC EXOTOXIN AND THERAPEUTIC
; FILE REFERENCE: ARSB:514
; CURRENT APPLICATION NUMBER: US/09/153,803
; CURRENT FILING DATE: 1998-09-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
; US-09-153-803-2

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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 REDL 4

Search completed: March 20, 2006, 08:10:49
Job time : 404.5 secs
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; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA: US 07/596,289
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-396C-53

Query Match 100.0%; Score 20; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 1 REDL 4

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; Sequence 53, Application US/08331396D
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Lee, Byungkook
; TITLE OF INVENTION: Humanized Tumor-Specific Antibody
; TITLE OF INVENTION: Fragments, Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,396D
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:52:40 ; Search time 17.5 Seconds  
(without alignments)  
21.955 Million cell updates/sec

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Perfect score: 20  
Sequence: 1 REDL 4

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Gapop 10.0 , Gapext 0.5

Searched: 443638 seqs, 96052105 residues

Total number of hits satisfying chosen parameters: 443638

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 79 | 20 | 100.0 | 126 | 7 US-11-360-355-15842  | Sequence 15842, A |
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ALIGNMENTS

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; GENERAL INFORMATION:  
; APPLICANT: DENARDO, SALLY J.  
; APPLICANT: DENARDO, RODNEY  
; APPLICANT: BALHORN, GERALD I.  
; TITLE OF INVENTION: SELECTIVE HIGH-AFFINITY POLYDENTATE LIGANDS AND METHODS OF MAKING  
; TITLE OF INVENTION: SUCH  
; FILE REFERENCE: 309T-3005100S  
; CURRENT APPLICATION NUMBER: US/11/055,181  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,444  
; PRIOR FILING DATE: 2004-02-09  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.3

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Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 REDL 4  
  
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; Sequence 24, Application US/11154103  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, GREGORY P.  
; APPLICANT: HORAK, EVA M.  
; APPLICANT: WEINER, LOUIS M.  
; APPLICANT: JAMES, MARKS D.  
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 407T-000420US  
; CURRENT APPLICATION NUMBER: US/11/154,103  
; CURRENT FILING DATE: 2005-06-15  
; PRIOR APPLICATION NUMBER: US 60/370,276  
; PRIOR FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: US10/406,830  
; PRIOR FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 57  
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; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Translocation signaling sequence.  
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Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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; Sequence 22, Application US/10432412A  
; GENERAL INFORMATION:  
; APPLICANT: FitzGerald, David J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas  
; TITLE OF INVENTION: Exotoxin A and Type IV Pilin Sequences  
; FILE REFERENCE: 015280-429100US  
; CURRENT APPLICATION NUMBER: US/10/432,412A  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/257,877  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22

```
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention domain
US-10-432-412A-22

Query Match      100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      1 REDL 4

RESULT 4
US-11-055-181-4
; Sequence 4, Application US/11055181
; GENERAL INFORMATION:
; APPLICANT: DENARDO, SALLY J.
; APPLICANT: DENARDO, GERALD L.
; APPLICANT: BALHORN, RODNEY
; TITLE OF INVENTION: SELECTIVE HIGH-AFFINITY POLYDENTATE LIGANDS AND METHODS OF MAKING
; FILE REFERENCE: 309t-300510US
; CURRENT APPLICATION NUMBER: US/11/055,181
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,444
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic translocation signaling sequence.
US-11-055-181-4

Query Match      100.0%; Score 20; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      1 REDL 4

RESULT 5
US-11-154-103-23
; Sequence 23, Application US/11154103
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
```

```
; FEATURE:
; OTHER INFORMATION: Translocation signaling sequence.
US-11-154-103-23

Query Match      100.0%; Score 20; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      1 REDL 4

RESULT 6
US-11-344-466-7
; Sequence 7, Application US/11344466
; GENERAL INFORMATION:
; APPLICANT: Fey, Georg H
; APPLICANT: Peipp, Matthias
; APPLICANT: Schwemmlin, Michael
; TITLE OF INVENTION: CD19-Specific Immunotoxin and Treatment Method
; FILE REFERENCE: 59849-8005
; CURRENT APPLICATION NUMBER: US/11/344,466
; CURRENT FILING DATE: 2006-01-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic transport sequence
US-11-344-466-7

Query Match      100.0%; Score 20; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
Db      1 REDL 4

RESULT 7
US-10-432-412A-21
; Sequence 21, Application US/10432412A
; GENERAL INFORMATION:
; APPLICANT: FitzGerald, David J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas
; FILE REFERENCE: Exotoxin A and type IV Pilin Sequences
; FILE REFERENCE: 015280-429100US
; CURRENT APPLICATION NUMBER: US/10/432,412A
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/257,877
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum (ER) retention domain in native
; OTHER INFORMATION: Pseudomonas exotoxin A
US-10-432-412A-21

Query Match      100.0%; Score 20; DB 6; Length 5;
```

Best Local Similarity 100.0%; Pred. No. 4e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 REDL 4  
    ||||  
Db 1 REDL 4

RESULT 8  
US-10-110-880-5  
; Sequence 5, Application US/10110880  
; GENERAL INFORMATION:  
; APPLICANT: FitzGerald, David J.  
; APPLICANT: Miesny, Randall J.  
; APPLICANT: McKee, Marian  
; APPLICANT: Daugherty, Ann  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; APPLICANT: Genentech, Inc.  
; TITLE OF INVENTION: Delivery of Proteins Across Polar Epithelial Cell  
; FILE REFERENCE: Layers  
; FILE REFERENCE: 015280-378100US  
; CURRENT APPLICATION NUMBER: US/10/110,880  
; CURRENT FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: US 60/160,923  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: WO PCT/US00/29080  
; PRIOR FILING DATE: 2000-10-18  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic  
; OTHER INFORMATION: reticulum retention sequence  
US-10-110-880-5

Query Match 100.0%; Score 20; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 REDL 4  
    ||||  
Db 1 REDL 4

RESULT 9  
US-60-772-986-4665  
; Sequence 4665, Application US/60772986  
; GENERAL INFORMATION:  
; APPLICANT: Dunker, A. Keith  
; APPLICANT: Uversky, Vladimir N.  
; APPLICANT: Cheng, Yugong  
; APPLICANT: Le Gall, Tanguy  
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF  
; TITLE OF INVENTION: INTERACTION WITHIN HUMAN PROTEINS AND USSES THEREFOR  
; FILE REFERENCE: 670098.405P1  
; CURRENT APPLICATION NUMBER: US/60/772,986  
; CURRENT FILING DATE: 2006-02-14  
; NUMBER OF SEQ ID NOS: 24337  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4665  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-772-986-4665

Query Match 100.0%; Score 20; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Best Local Similarity 100.0%; Pred. No. 4e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 REDL 4

Db 2 REDL 5

RESULT 10  
US-60-772-986-5174  
; Sequence 5174, Application US/60772986  
; GENERAL INFORMATION:  
; APPLICANT: Dunker, A. Keith  
; APPLICANT: Uversky, Vladimir N.  
; APPLICANT: Cheng, Yugong  
; APPLICANT: Le Gall, Tanguy  
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF  
; TITLE OF INVENTION: INTERACTION WITHIN HUMAN PROTEINS AND USES THEREFOR  
; FILE REFERENCE: 670098.405P1  
; CURRENT APPLICATION NUMBER: US/60/772,986  
; CURRENT FILING DATE: 2006-02-14  
; NUMBER OF SEQ ID NOS: 24337  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5174  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-772-986-5174

Query Match 100.0%; Score 20; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 REDL 4  
    ||||  
Db 4 REDL 7

RESULT 11  
US-08-838-916J-35  
; Sequence 35, Application US/08838916J  
; GENERAL INFORMATION:  
; APPLICANT: Buelow, Roland  
; APPLICANT: Grassy, Gerald  
; APPLICANT: Calais, Bernard  
; TITLE OF INVENTION: Cytomodulating Lipophilic Peptides for Inhibiting Lymphocyte  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: A-64360  
; CURRENT APPLICATION NUMBER: US/08/838,916J  
; CURRENT FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 35  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-838-916J-35

Query Match 100.0%; Score 20; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 36; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 REDL 4  
    ||||  
Db 1 REDL 4

RESULT 12  
US-10-560-069-794  
; Sequence 794, Application US/10560069  
; GENERAL INFORMATION:  
; APPLICANT: KENT, Stephen J.  
; TITLE OF INVENTION: Immunomodulating compositions, uses therefor and processes for  
; TITLE OF INVENTION: production  
; FILE REFERENCE: 21415-0021.01-US



```

; CURRENT APPLICATION NUMBER: US/10/560,069
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: PCT/AU2004/000775
; PRIOR FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: 2003902875
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 2004901589
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 2232
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 794
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: HIV-1 pol peptide 1
US-10-560-069-794

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```

Query Match      100.0%; Score 20; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 REDL 4
    ||||
Db 3 REDL 6

```

```

RESULT 13
US-11-303-372-4
; Sequence 4, Application US/11303372
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
; FILE REFERENCE: P26,481-A USA
; CURRENT APPLICATION NUMBER: US/11/303,372
; CURRENT FILING DATE: 2005-12-16
; PRIOR APPLICATION NUMBER: US/10/955,656
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/126,845
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-11-303-372-4

```

```

Query Match      100.0%; Score 20; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 REDL 4
    ||||
Db 16 REDL 19

```

```

RESULT 14
US-11-303-372-62
; Sequence 62, Application US/11303372
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.

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; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: P26,481-A USA
; CURRENT APPLICATION NUMBER: US/11/303,372
; CURRENT FILING DATE: 2005-12-16
; PRIOR APPLICATION NUMBER: US/10/955,656
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/126,845
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(19)
; OTHER INFORMATION: D form amino acid
US-11-303-372-62

```

```

Query Match      100.0%; Score 20; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 REDL 4
    ||||
Db 16 REDL 19

```

```

RESULT 15
US-60-772-986-9495
; Sequence 9495, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tanguy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; TITLE OF INVENTION: INTERACTION WITHIN HUMAN PROTEINS AND USES THEREFOR
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9495
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-9495

```

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Query Match      100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 REDL 4
    ||||
Db 15 REDL 18

```

```

RESULT 16
US-60-772-986-12177
; Sequence 12177, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith

```

```
; APPLICANT: Uvertsky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tanguy
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12177
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-12177

Query Match      100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 6 REDL 9

RESULT 17
US-11-004-399A-929
; Sequence 929, Application US/11004399A
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399A
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 929
; LENGTH: 28
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399A-929

Query Match      100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 6 REDL 9

RESULT 18
US-10-561-506-100
; Sequence 100, Application US/10561506
; GENERAL INFORMATION:
; APPLICANT: MEINKE, ANDREAS
; APPLICANT: NAGY, ESZTER
; APPLICANT: WINKLER, BIRGIT
; TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENS
; FILE REFERENCE: SONN:085US
; CURRENT APPLICATION NUMBER: US/10/561,506
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: PCT/EP2004/006460
; PRIOR FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: EP03450148.6
; PRIOR FILING DATE: 2003-06-17
```

```
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-561-506-100

Query Match      100.0%; Score 20; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 3 REDL 6

RESULT 19
US-11-285-537-15
; Sequence 15, Application US/11285537
; GENERAL INFORMATION:
; APPLICANT: Conkling, Mark
; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
; FILE REFERENCE: VTOB.033C1C1
; CURRENT APPLICATION NUMBER: US/11/285,537
; CURRENT FILING DATE: 2005-11-22
; PRIOR APPLICATION NUMBER: 11/077,752
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 10/729,121
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCTUS02/18040
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/297,154
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-11-285-537-15

Query Match      100.0%; Score 20; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 5 REDL 8

RESULT 20
US-10-729-121-15
; Sequence 15, Application US/10729121
; GENERAL INFORMATION:
; APPLICANT: Conkling, Mark
; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
; FILE REFERENCE: VTOB.033C1
; CURRENT APPLICATION NUMBER: US/10/729,121
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/297,154
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: PCTUS02/18040
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 37
```

```
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-729-121-15

Query Match      100.0%; Score 20; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 5 REDL 8

RESULT 21
US-60-734-556-19
; Sequence 19, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; TITLE OF INVENTION: Diseases and Methods Therefor
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-60-734-556-19

Query Match      100.0%; Score 20; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 34 REDL 37

RESULT 22
US-60-734-556-20
; Sequence 20, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; TITLE OF INVENTION: Diseases and Methods Therefor
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-60-734-556-20

Query Match      100.0%; Score 20; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 34 REDL 37

RESULT 23
US-11-285-537-14
; Sequence 14, Application US/11285537
; GENERAL INFORMATION:
; APPLICANT: Li, Yonghe
; APPLICANT: Bu, Guojun
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; TITLE OF INVENTION: Diseases and Methods Therefor
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
```

```
; APPLICANT: Conkling, Mark
; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
; FILE REFERENCE: VTOB.033C1C1
; CURRENT APPLICATION NUMBER: US/11/285,537
; CURRENT FILING DATE: 2005-11-22
; PRIOR APPLICATION NUMBER: 11/077,752
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 10/729,121
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCTUS02/18040
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/297,154
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-285-537-14

Query Match      100.0%; Score 20; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 5 REDL 8

RESULT 24
US-10-729-121-14
; Sequence 14, Application US/10729121
; GENERAL INFORMATION:
; APPLICANT: Conkling, Mark
; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
; FILE REFERENCE: VTOB.033C1
; CURRENT APPLICATION NUMBER: US/10/729,121
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/297,154
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: PCTUS02/18040
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-10-729-121-14

Query Match      100.0%; Score 20; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 5 REDL 8

RESULT 25
US-60-734-556-23
; Sequence 23, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; TITLE OF INVENTION: Diseases and Methods Therefor
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
```

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; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Mus musculus
US-60-734-556-23

Query Match          100.0%; Score 20; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
DB      43 REDL 46

RESULT 26
US-60-734-556-16
; Sequence 16, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; TITLE OF INVENTION: Diseases and Methods Therefor
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-734-556-16

Query Match          100.0%; Score 20; DB 8; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
DB      44 REDL 47

RESULT 27
US-11-360-355-145914
; Sequence 145914, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 145914
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_72337; Strand=+; Position=1
; OTHER INFORMATION: -85,212-281
US-11-360-355-145914

Query Match          100.0%; Score 20; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
DB      16 REDL 19

RESULT 29
US-60-734-556-4
; Sequence 4, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; TITLE OF INVENTION: Diseases and Methods Therefor
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Mus musculus
US-60-734-556-4

Query Match          100.0%; Score 20; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
DB      16 REDL 19

RESULT 28
US-60-732-162-738
; Sequence 738, Application US/60732162
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Faquin, Bruno
; APPLICANT: Fournier, Helene
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Debrus, Sophie
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Little, Randall D
; APPLICANT: Keith, Tim
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease
; FILE REFERENCE: 059908-5010-PR
; CURRENT APPLICATION NUMBER: US/60/732,162
; CURRENT FILING DATE: 2005-11-02
; NUMBER OF SEQ ID NOS: 4417
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 738
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homosapiens
US-60-732-162-738

Query Match          100.0%; Score 20; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
DB      16 REDL 19

RESULT 29
US-60-734-556-4
; Sequence 4, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; TITLE OF INVENTION: Diseases and Methods Therefor
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Mus musculus
US-60-734-556-4

Query Match          100.0%; Score 20; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 REDL 4
DB      16 REDL 19
```

```
Db          51 REDL 54

RESULT 30
US-60-734-556-5
; Sequence 5, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Mus musculus
US-60-734-556-5

Query Match      100.0%; Score 20; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      51 REDL 54

RESULT 31
US-60-734-556-8
; Sequence 8, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-60-734-556-8

Query Match      100.0%; Score 20; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      51 REDL 54

RESULT 32
US-60-734-556-3
; Sequence 3, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3

Query Match      100.0%; Score 20; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      51 REDL 54

RESULT 33
US-60-734-556-6
; Sequence 6, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-60-734-556-6

Query Match      100.0%; Score 20; DB 8; Length 55;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      52 REDL 55

RESULT 34
US-60-734-556-7
; Sequence 7, Application US/60734556
; GENERAL INFORMATION:
; APPLICANT: Bu, Guojun
; APPLICANT: Li, Yonghe
; TITLE OF INVENTION: Oligopeptides for Treatment of Osteoporosis and Other Bone
; FILE REFERENCE: 60005161-0190
; CURRENT APPLICATION NUMBER: US/60/734,556
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Pongo pygmaeus
US-60-734-556-7

Query Match      100.0%; Score 20; DB 8; Length 55;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 REDL 4
      ||||
Db      52 REDL 55

RESULT 35
US-11-360-355-126856
; Sequence 126856, Application US/11360355
```

```
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 126856
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_53279; Strand=-; Position=1
; OTHER INFORMATION: -16,232-431
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit_ID=NP_872170.1; Match_level="QueryCoverage
; OTHER INFORMATION: =100%, HitCoverage=6%, E-value=4e-11, Identity=46%"; Hit description
; OTHER INFORMATION: =ankyrim and patatin family member (5V188) [Caenorhabditis elegans
; OTHER INFORMATION: emb|CAD54162.1| Hypothetical protein W
US-11-360-355-126856

Query Match 100.0%; Score 20; DB 7; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 REDL 4
Db 2 REDL 5

RESULT 36
US-11-360-355-149183
; Sequence 149183, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 149183
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_75606; Strand=-; Position=1
; OTHER INFORMATION: -85,643-773
US-11-360-355-149183

Query Match 100.0%; Score 20; DB 7; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;
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```
Qy 1 REDL 4
Db 15 REDL 18

RESULT 37
US-10-276-817B-11417
; Sequence 11417, Application US/10276817B
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: US/10/276,817B
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US01/14827
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 11417
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(72)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-276-817B-11417

Query Match 100.0%; Score 20; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 REDL 4
Db 7 REDL 10

RESULT 38
US-10-953-349-28331
; Sequence 28331, Application US/10953349
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28331
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-28331

Query Match 100.0%; Score 20; DB 6; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 REDL 4
Db 59 REDL 62

RESULT 39
US-10-953-349-18313
; Sequence 18313, Application US/10953349
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
```

; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 18313  
; LENGTH: 75  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-18313

Query Match 100.0%; Score 20; DB 6; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
DB 69 REDL 72

RESULT 40  
US-10-953-349-31993  
; Sequence 31993, Application US/10953349  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 31993  
; LENGTH: 75  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-953-349-31993

Query Match 100.0%; Score 20; DB 6; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
DB 23 REDL 26

RESULT 41  
US-11-360-355-133143  
; Sequence 133143, Application US/11360355  
; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey  
; APPLICANT: Du, Zijing  
; APPLICANT: Guo, Liang  
; APPLICANT: Kovalic, David  
; APPLICANT: Lu, Maolong  
; APPLICANT: McCarter, James  
; APPLICANT: Miller, Nancy  
; APPLICANT: Williams, Deryck  
; APPLICANT: Vaudin, Mark  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS  
; FILE REFERENCE: 38-21(53885)  
; CURRENT APPLICATION NUMBER: US/11/360,355  
; CURRENT FILING DATE: 2006-02-24  
; NUMBER OF SEQ ID NOS: 171306  
; SEQ ID NO 133143  
; LENGTH: 78  
; TYPE: PRT  
; ORGANISM: Heterodera glycines  
; FEATURE:  
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID\_59566; Strand=-; Position=1

; OTHER INFORMATION: -192,251-295  
; FEATURE:  
; OTHER INFORMATION: Homolog annotation: Hit ID=AAP80600.1; Match level="QueryCovera  
; OTHER INFORMATION: =98%, HitCoverage=21%, E-value=3e-32, Identity=87%", Hit descri  
; OTHER INFORMATION: =putative alpha-tubulin [Oikopleura dioica]  
US-11-360-355-133143

Query Match 100.0%; Score 20; DB 7; Length 78;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
DB 52 REDL 55

RESULT 42  
US-10-461-673-14945  
; Sequence 14945, Application US/10461673  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Zhou, Ping  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Xue, Aidong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Wang, Yonghong  
; APPLICANT: Wang, Zhi Wei  
; APPLICANT: Goodrich, Ryle W.  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Ujwal, Manusha L.  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Chen, Rui-Hong  
; APPLICANT: Ghosh, Malabika  
; APPLICANT: Weng, Gezhi  
; APPLICANT: Haley-Vicente, Dana  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 823  
; CURRENT APPLICATION NUMBER: US/10/461,673  
; CURRENT FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: PCT/US02/29964  
; PRIOR FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: US 10/245,014  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 60/323,739  
; PRIOR FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: PCT/US02/29636  
; PRIOR FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: US 10/245,817  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 60/323,349  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: PCT/US02/29001  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: US 10/243,552  
; PRIOR FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 60/322,511  
; PRIOR FILING DATE: 2001-09-13  
; PRIOR APPLICATION NUMBER: PCT/US02/25485  
; PRIOR FILING DATE: 2002-08-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 17116  
; SOFTWARE: Pf FL\_genes Version 6.0  
; SEQ ID NO 14945  
; LENGTH: 79  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-461-673-14945

Query Match 100.0%; Score 20; DB 6; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 60 REDL 63

RESULT 43

US-10-498-451-991  
; Sequence 991, Application US/10498451

; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Wang, Jian-rui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Ghosh, Malabika  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Goodrich, Kyle W.  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Weng, Gezhi  
; APPLICANT: Xu, Chongjun  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Drmanac, Radoje T  
; TITLE OF INVENTION: Novel Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 820/PCT  
; CURRENT APPLICATION NUMBER: US/10/498,451  
; CURRENT FILING DATE: 2004-05-09  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: US 60/339,739  
; PRIOR FILING DATE: 2002-04-22  
; PRIOR APPLICATION NUMBER: US 60/339,453  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: US 60/365,384  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: US 60/365,091  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: US 60/372,615  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 60/376,045  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 60/372,381  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3134  
; SOFTWARE: pt\_FL\_genes Version 6.0  
; SEQ ID NO 991  
; LENGTH: 79  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-498-451-991

Query Match 100.0%; Score 20; DB 6; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 60 REDL 63

RESULT 44

US-11-360-355-162235  
; Sequence 162235, Application US/11360355

; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey  
; APPLICANT: Du, Zijiang  
; APPLICANT: Guo, Liang  
; APPLICANT: Kovalic, David  
; APPLICANT: Lu, Maolong  
; APPLICANT: McCarter, James  
; APPLICANT: Miller, Nancy  
; APPLICANT: Williams, Deryck  
; APPLICANT: Vaudin, Mark  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS  
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF  
; FILE REFERENCE: 38-21(53885)  
; CURRENT APPLICATION NUMBER: US/11/360,355  
; CURRENT FILING DATE: 2006-02-24  
; NUMBER OF SEQ ID NOS: 171306  
; SEQ ID NO 162235  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Heterodera glycines  
; FEATURE:  
; OTHER INFORMATION: Coding regions on vcdna: vcdna=seqID\_88658; Strand=+; Position=3

US-11-360-355-162235

Query Match 100.0%; Score 20; DB 7; Length 86;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 49 REDL 52

RESULT 45

US-11-360-355-171301  
; Sequence 171301, Application US/11360355

; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey  
; APPLICANT: Du, Zijiang  
; APPLICANT: Guo, Liang  
; APPLICANT: Kovalic, David  
; APPLICANT: Lu, Maolong  
; APPLICANT: McCarter, James  
; APPLICANT: Miller, Nancy  
; APPLICANT: Williams, Deryck  
; APPLICANT: Vaudin, Mark  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS  
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF  
; FILE REFERENCE: 38-21(53885)  
; CURRENT APPLICATION NUMBER: US/11/360,355  
; CURRENT FILING DATE: 2006-02-24  
; NUMBER OF SEQ ID NOS: 171306  
; SEQ ID NO 171301  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Heterodera glycines  
; FEATURE:  
; OTHER INFORMATION: Coding regions on vcdna: vcdna=seqID\_97724; Strand=+; Position=3

US-11-360-355-171301

Query Match 100.0%; Score 20; DB 7; Length 86;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 REDL 4  
Db 49 REDL 52

## RESULT 46

US-11-360-355-123353  
; Sequence 123353, Application US/11360355  
; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey  
; APPLICANT: Du, Zijiang  
; APPLICANT: Guo, Liang  
; APPLICANT: Kovalic, David  
; APPLICANT: Lu, Maolong  
; APPLICANT: McCarter, James  
; APPLICANT: Miller, Nancy  
; APPLICANT: Williams, Deryck  
; APPLICANT: Vaudin, Mark  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS  
; FILE REFERENCE: 38-21(53885)  
; CURRENT APPLICATION NUMBER: US/11/360,355  
; CURRENT FILING DATE: 2006-02-24  
; NUMBER OF SEQ ID NOS: 171306  
; SEQ ID NO 123353  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Heterodera glycines  
; NAME/KEY: misc feature  
; LOCATION: (60)..(60)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (67)..(67)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
; FEATURE:  
; OTHER INFORMATION: Homolog annotation: Hit ID=AA24580.1; Match level="QueryCoverage  
; OTHER INFORMATION: =96%, HitCoverage=53%, E-value=8e-24, Identity=65%", Hit descrip  
; OTHER INFORMATION: =ADP/ATP translocase [Heterodera glycines]  
; FEATURE:  
; OTHER INFORMATION: Gene Ontology: Biological process=embryogenesis and morphogenesis  
; FEATURE:  
; OTHER INFORMATION: Essential gene: C elegans homolog=t27E9.1a; Phenotype=Emb  
; FEATURE:  
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID\_49776; Strand=+; Position=2-  
; US-11-360-355-123353

Query Match 100.0%; Score 20; DB 7; Length 87;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 70 REDL 73

## RESULT 47

US-11-360-355-158402  
; Sequence 158402, Application US/11360355  
; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey  
; APPLICANT: Du, Zijiang  
; APPLICANT: Guo, Liang  
; APPLICANT: Kovalic, David  
; APPLICANT: Lu, Maolong  
; APPLICANT: McCarter, James  
; APPLICANT: Miller, Nancy  
; APPLICANT: Williams, Deryck  
; APPLICANT: Vaudin, Mark  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS

; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF  
; FILE REFERENCE: 38-21(53885)  
; CURRENT APPLICATION NUMBER: US/11/360,355  
; CURRENT FILING DATE: 2006-02-24  
; NUMBER OF SEQ ID NOS: 171306  
; SEQ ID NO 158402  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Heterodera glycines  
; FEATURE:  
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID\_84825; Strand=-; Position=1  
; OTHER INFORMATION: -156,213-323  
; US-11-360-355-158402

Query Match 100.0%; Score 20; DB 7; Length 88;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 47 REDL 50

## RESULT 48

US-11-360-355-150094  
; Sequence 150094, Application US/11360355  
; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey  
; APPLICANT: Du, Zijiang  
; APPLICANT: Guo, Liang  
; APPLICANT: Kovalic, David  
; APPLICANT: Lu, Maolong  
; APPLICANT: McCarter, James  
; APPLICANT: Miller, Nancy  
; APPLICANT: Williams, Deryck  
; APPLICANT: Vaudin, Mark  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS  
; FILE REFERENCE: 38-21(53885)  
; CURRENT APPLICATION NUMBER: US/11/360,355  
; CURRENT FILING DATE: 2006-02-24  
; NUMBER OF SEQ ID NOS: 171306  
; SEQ ID NO 150094  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Heterodera glycines  
; FEATURE:  
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID\_76517; Strand=-; Position=1  
; OTHER INFORMATION: -112,479-636  
; US-11-360-355-150094

Query Match 100.0%; Score 20; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 6 REDL 9

## RESULT 49

US-10-461-673-10208  
; Sequence 10208, Application US/10461673  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Zhou, Ping  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhao, Qing A.

Mon Mar 20 08:51:25 2006

```

; APPLICANT: Xue, Aidong
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Zhi Wei
; APPLICANT: Yang, Yonghong
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Wang, Dunrui
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Ujwal, Manusha L.
; APPLICANT: Ma, Yunding
; APPLICANT: Chen, Rui-Hong
; APPLICANT: Ghosh, Malabika
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Dmanahac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 823
; CURRENT APPLICATION NUMBER: US/10/461,673
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: PCT/US02/29964
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/245,014
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: PCT/US02/29636
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 10/245,817
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/323,349
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: PCT/US02/29001
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 10/243,552
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/322,511
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: PCT/US02/25485
; PRIOR FILING DATE: 2002-08-09
; Remaining Prior Application data removed - See File Wrapper
; NUMBER OF SEQ ID NOS: 17116
; SOFTWARE: pt_Fl_genes Version 6.0
; SEQ ID NO 10208
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; PS-10-461-673-10208

```

|                       |         |                    |       |            |
|-----------------------|---------|--------------------|-------|------------|
| Query Match           | 100.0%; | Score 20;          | DB 6; | Length 93; |
| Best Local Similarity | 100.0%; | Pred. No. 4.6e+02; |       |            |
| Mismatches            | 0;      | Mismatches         | 0;    | Indels     |
| 4: Conservative       | 0;      | Indels             | 0;    | Gaps       |

Qy 1 REDL 4  
78 REDL 81

RESULT 50  
US-11-360-355-148045  
; Sequence 148045, Application US/11360355  
; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey  
; APPLICANT: Du, Zijiang  
; APPLICANT: Guo, Liang  
; APPLICANT: Kovalic, David  
; APPLICANT: Lu, Maolong  
; APPLICANT: McCarter, James  
; APPLICANT: Miller, Nancy  
; APPLICANT: Williams, Deryck  
; APPLICANT: Vaudin, Mark  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS  
; FILE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF  
; FILE REFERENCE: 38-21(53885)

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:59 ; Search time 15 Seconds  
(without alignments)  
25.658 Million cell updates/sec

Title: US-09-673-707-10

Perfect score: 20

Sequence: 1 REDL 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : PIR\_80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 20    | 100.0       | 27     | 4     | probable 2.8K prot  |
| 2          | 20    | 100.0       | 35     | 2     | lignin peroxidase   |
| 3          | 20    | 100.0       | 50     | 2     | tubulin alpha chain |
| 4          | 20    | 100.0       | 51     | 2     | ribosomal protein   |
| 5          | 20    | 100.0       | 53     | 2     | tubulin alpha chain |
| 6          | 20    | 100.0       | 59     | 2     | nblA protein - Syn  |
| 7          | 20    | 100.0       | 67     | 2     | 14-3-3 protein iso  |
| 8          | 20    | 100.0       | 73     | 2     | hypothetical prote  |
| 9          | 20    | 100.0       | 78     | 1     | cytochrome c551 -   |
| 10         | 20    | 100.0       | 79     | 2     | D-alanyl carrier p  |
| 11         | 20    | 100.0       | 81     | 2     | probable plasmid s  |
| 12         | 20    | 100.0       | 83     | 2     | hypothetical prote  |
| 13         | 20    | 100.0       | 84     | 2     | hypothetical prote  |
| 14         | 20    | 100.0       | 85     | 2     | probable involveme  |
| 15         | 20    | 100.0       | 85     | 2     | hypothetical prote  |
| 16         | 20    | 100.0       | 88     | 2     | hypothetical prote  |
| 17         | 20    | 100.0       | 91     | 2     | probable secreted   |
| 18         | 20    | 100.0       | 91     | 2     | conserved hypothet  |
| 19         | 20    | 100.0       | 95     | 2     | acyl carrier prote  |
| 20         | 20    | 100.0       | 97     | 2     | translation initia  |
| 21         | 20    | 100.0       | 98     | 2     | tubulin alpha chain |
| 22         | 20    | 100.0       | 98     | 2     | hypothetical prote  |
| 23         | 20    | 100.0       | 100    | 2     | hypothetical prote  |
| 24         | 20    | 100.0       | 102    | 2     | probable periplasm  |
| 25         | 20    | 100.0       | 103    | 2     | phage-related, Zn   |
| 26         | 20    | 100.0       | 104    | 1     | CCBO                |
| 27         | 20    | 100.0       | 104    | 1     | cytochrome c - bov  |
| 28         | 20    | 100.0       | 104    | 1     | cytochrome c [vali  |
| 29         | 20    | 100.0       | 104    | 1     | cytochrome c - com  |

cytochrome c [vali  
cytochrome c - she  
cytochrome c, test  
cytochrome c, test  
hypothetical prote  
hypothetical prote  
glutaredoxin-like  
hypothetical prote  
pectin degradation  
hypothetical prote  
unknown protein en  
hypothetical prote  
glutaredoxin-like  
transcription regu  
transcription regu  
Whcy protein - Ara  
gas-vesicle operon  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
serum amyloid prot  
serum amyloid pr  
translation repres  
hypothetical prote  
partial transposas  
conserved hypothet  
thioredoxin N-2 -  
hypothetical prote  
probable deoxycyti  
partial transposas  
hypothetical prote  
polyketide synthas  
hypothetical prote  
ribosomal protein  
30S ribosomal prot  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable flagellar  
transcription regu  
hypothetical prote  
probable esterase  
hypothetical prote  
very hypothetical  
probable transcrip  
tropenin I beta -  
tropenin I alpha -  
hypothetical prote  
hypothetical prote  
conserved hypothet  
hypothetical prote  
hypothetical prote  
hypothetical prote  
kilB protein - Str  
ribosomal protein  
conserved hypothet  
conserved hypothet  
ribosomal protein  
ribosomal protein  
ribosomal protein  
ribosomal protein  
hypothetical prote  
hypothetical prote  
probable lyase - S  
translation initia

103 20 100.0 153 2 AF1334  
104 20 100.0 153 2 AE1705  
105 20 100.0 153 2 I39827  
106 20 100.0 153 2 S52083  
107 20 100.0 153 2 E71526  
108 20 100.0 153 2 C90405  
109 20 100.0 154 1 A31486  
110 20 100.0 154 1 FIHUA  
111 20 100.0 154 2 T27228  
112 20 100.0 154 2 F90394  
113 20 100.0 155 1 D6197  
114 20 100.0 155 2 T46546  
115 20 100.0 155 2 T00134  
116 20 100.0 156 1 W6WL41  
117 20 100.0 156 2 F70027  
118 20 100.0 157 2 S25479  
119 20 100.0 158 2 A90085  
120 20 100.0 161 1 UBURAL  
121 20 100.0 161 2 C82272  
122 20 100.0 161 2 E72339  
123 20 100.0 162 1 Z3B8L7  
124 20 100.0 162 1 Z3B8L7  
125 20 100.0 162 1 C69424  
126 20 100.0 162 2 G90288  
127 20 100.0 163 2 A43259  
128 20 100.0 163 2 S32867  
129 20 100.0 164 2 C35216  
130 20 100.0 164 2 F75616  
131 20 100.0 164 2 S74709  
132 20 100.0 166 1 B64019  
133 20 100.0 166 2 D86026  
134 20 100.0 167 2 E90329  
135 20 100.0 168 2 T36405  
136 20 100.0 169 2 D79928  
137 20 100.0 171 2 D83443  
138 20 100.0 171 2 T46342  
139 20 100.0 172 2 D82194  
140 20 100.0 172 2 A28713  
141 20 100.0 172 2 AB1806  
142 20 100.0 172 2 AB1434  
143 20 100.0 172 2 A35145  
144 20 100.0 172 2 D90346  
145 20 100.0 173 2 T24720  
146 20 100.0 173 2 A72714  
147 20 100.0 173 2 AG3559  
148 20 100.0 173 2 A82413  
149 20 100.0 173 2 JC5610  
150 20 100.0 174 2 AI1274

ALIGNMENTS

RESULT 1  
JE0015  
probable 2.8K protein pseudogene - cucumber mosaic virus (strain D)  
A:Status: translation not shown; conceptual translation of pseudogene  
A:Molecule type: genomic RNA  
A:Residues: 1-27 <RIC>  
A:Cross-references: UNIPROT:Q89492; UNIPARC:UPI00000F7E7F  
R:Kaper, J.M.; Tounsgiant, M.E.; Steen, M.T.  
Virology 163, 284-292, 1988  
A:Title: Cucumber mosaic virus-associated RNA 5. XI. Comparison of 14 CARNA 5 variants  
A:Reference number: JE0018; MUID:88179532; PMID:3354198  
A:Accession: PS0286

A:Status: translation not shown; conceptual translation of pseudogene  
A:Molecule type: genomic RNA  
A:Residues: 1-27 <KAP>  
A:Cross-references: UNIPARC:UPI00000F7E7F; GB:M20350; NID:G331658; PIDN:AAA46385.1; PID  
A:Note: this sequence is found in strain D and isolates Sq10, Ch20, X2nt3, X7, X12 and  
C:Genetics:  
A:Map position: segment 5  
C:Keywords: pseudogene  
Query Match 100.0%; Score 20; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 REDL 4  
DB 11 REDL 14

RESULT 2

S29728  
lignin peroxidase (EC 1.11.1.-) 12 - white-rot fungus (Trametes versicolor) (fragment)  
C:Species: Trametes versicolor (white-rot fungus)  
C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 12-Jul-2004  
C:Accession: S29728  
R:Johansson, T.; Welinder, K.G.; Nyman, P.O.  
Arch. Biochem. Biophys. 300, 57-62, 1993  
A:Title: Isozymes of lignin peroxidase and manganese(II) peroxidase from the white-rot  
ions.  
A:Reference number: S29724; MUID:93143365; PMID:8424691  
A:Accession: S29728  
A:Molecule type: protein  
A:Residues: 1-35 <JOH>  
A:Cross-references: UNIPROT:Q9UQY7; UNIPARC:UPI0000069C2A  
A:Experimental source: strain PRL 572  
C:Function:  
A:Description: involved in degradation of lignin and certain xenobiotics  
C:Superfamily: peroxidase  
C:Keywords: extracellular protein; heme; oxidoreductase

Query Match 100.0%; Score 20; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
DB 22 REDL 25

RESULT 3

S36687  
tubulin alpha chain - Blepharisma japonicum (fragment)  
C:Species: Blepharisma japonicum  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: S36687  
R:Liang, A.; Heckmann, K.  
Naturwissenschaften 80, 225-226, 1993  
A:Title: Blepharisma uses UAA as a termination codon.  
A:Reference number: S36687; MUID:93288144; PMID:7685500  
A:Accession: S36687  
A:Molecule type: mRNA  
A:Residues: 1-50 <LIA>  
A:Cross-references: UNIPROT:Q08628; UNIPARC:UPI000013699B; GB:S623518; NID:G385736; PID  
C:Genetics:  
A:Genetic code: SGC9  
C:Superfamily: tubulin  
C:Keywords: heterodimer; microtubule

Query Match 100.0%; Score 20; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
DB 11 REDL 14

Db 19 REDL 22

## RESULT 4

C61510

ribosomal protein S18, cytosolic - African clawed frog (fragment)

C;Species: Xenopus laevis (African clawed frog)

C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004

C;Accession: C61510

R;Grossberger, D.; Flajnik, M.; Marcuz, A.

Comp. Biochem. Physiol. B 98, 127-133, 1991

A;Title: Ribosomal and chromosomal protein cDNA clones of Xenopus laevis thymus isolated

A;Reference number: A61510; MUID:91284580; PMID:2060276

A;Accession: C61510

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-51 <GRO>

A;Cross-references: UNIPROT:Q7LZL4; UNIPARC:UPI00001772A1

C;Superfamily: ribosomal protein S13/S18

Query Match 100.0%; Score 20; DB 2; Length 51;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 7 REDL 10

## RESULT 5

S71388

tubulin alpha chain - Giardia lamblia (fragments)

C;Species: Giardia lamblia

C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 31-Dec-2004

C;Accession: S71388

R;Weber, K.; Schneider, A.; Mueller, N.; Plessmann, U.

FEBS Lett. 393, 27-30, 1996

A;Title: Polyglycylation of tubulin in the diplomonad Giardia lamblia, one of the oldest

A;Reference number: S71388; MUID:96397523; PMID:8804417

A;Accession: S71388

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-29;30-53 <WEB>

A;Cross-references: UNIPROT:Q9U014; UNIPARC:UPI0000177562; UNIPARC:UPI0000177563

C;Keywords: heterodimer; microtubule

Query Match 100.0%; Score 20; DB 2; Length 53;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 21 REDL 24

## RESULT 6

S42636

nblA protein - Synechococcus sp. (strain PCC 7942)

C;Species: Synechococcus sp.

A;Variety: PCC 7942

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S42636

R;Collier, J.L.; Grossman, A.R.

EMBO J. 13, 1039-1047, 1994

A;Title: A small polypeptide triggers complete degradation of light-harvesting phycobil

A;Reference number: S42636; MUID:94178246; PMID:8131738

A;Accession: S42636

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-59 <COL>

A;Cross-references: UNIPROT:P35087; UNIPARC:UPI000012FDBC; GB:U05044; GB:U00671; NID:g45

A;Experimental source: PCC 7942

Query Match 100.0%; Score 20; DB 2; Length 59;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 30 REDL 33

## RESULT 7

S53754

14-3-3 protein isoform epsilon - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004

C;Accession: S53754

R;Jones, D.H.A.; Martin, H.; Madrazo, J.; Robinson, K.A.; Nielsen, P.; Roseboom, P.H.;

J. Mol. Biol. 245, 375-384, 1995

A;Title: Expression and structural analysis of 14-3-3 proteins.

A;Reference number: S53753; MUID:95139067; PMID:7837270

A;Accession: S53754

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-67 <JON>

A;Cross-references: UNIPROT:Q7M312; UNIPARC:UPI00001758B5

C;Superfamily: 14-3-3 protein

Query Match 100.0%; Score 20; DB 2; Length 67;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 4 REDL 7

## RESULT 8

D90287

hypothetical protein SSO7675 [imported] - Sulfolobus solfataricus transposon ISC1316

C;Species: Sulfolobus solfataricus

C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C;Accession: D90287

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: D90287

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-73 <KUR>

A;Cross-references: UNIPROT:Q97YK4; UNIPARC:UPI0000064402; GB:AE006641; NID:g13814523;

C;Genetics:

A;Gene: SSO7675

Query Match 100.0%; Score 20; DB 2; Length 73;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 10 REDL 13

## RESULT 9

CCER51

cytochrome c551 - Ectothiorhodospira halophila

C;Species: Ectothiorhodospira halophila

C;Date: 30-Nov-1979 #sequence\_revision 30-Nov-1979 #text\_change 09-Jul-2004

C;Accession: S38755; A00115

R;Ambler, R.P.; Meyer, T.E.; Kamen, M.D.

Arch. Biochem. Biophys. 306, 83-93, 1993

A;Title: Amino acid sequences of cytochromes c-551 from the halophilic purple phototrop



Qy 1 REDL 4  
|||||  
Db 46 REDL 49

RESULT 14  
T39536  
probable involvement in cytochrome oxidase assembly - fission yeast (Schizosaccharomyces  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T39536  
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.  
submitted to the EMBL Data Library, February 1998  
A:Reference number: 221862  
A:Accession: T39536  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-85 <WOO>  
A:Cross-references: UNIPROT:O42921; UNIPARC:UPI000006B7BF; EMBL:AL021748; PIDN:CAA16867.  
A:Experimental source: strain 972h-; cosmid c16A3  
C:Genetics:  
A:Gene: SPDB:SPBC16A3.16  
A:Map position: 2  
A:Introns: 57/3

Query Match 100.0%; Score 20; DB 2; Length 85;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||||  
Db 9 REDL 12

RESULT 15  
T26542  
hypothetical protein Y19D2B.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26542  
R:White, S.  
submitted to the EMBL Data Library, June 1998  
A:Reference number: Z20227  
A:Accession: T26542  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-85 <WIL>  
A:Cross-references: UNIPROT:Q9XXH2; UNIPARC:UPI000007EA87; EMBL:AL023832; PIDN:CAA19475.  
A:Experimental source: clone Y19D2B  
C:Genetics:  
A:Gene: CESP:Y19D2B.1  
A:Map position: 2  
A:Introns: 42/2

Query Match 100.0%; Score 20; DB 2; Length 85;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||||  
Db 57 REDL 60

RESULT 16  
F83979  
hypothetical protein BH2638 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: F83979  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: F83979  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-88 <STO>  
A:Cross-references: UNIPROT:Q9K9K7; UNIPARC:UPI000013BEA1; GB:AP001516; GB:BA000004; N  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH2638

Query Match 100.0%; Score 20; DB 2; Length 88;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||||  
Db 36 REDL 39

RESULT 17  
AE0547  
probable secreted protein [imported] - Salmonella enterica subsp. enterica serovar Typhi  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AE0547  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra  
; S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AE0547  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-91 <PAR>  
A:Cross-references: UNIPARC:UPI000005A269; GB:AL513382; PIDN:CAD08821.1; PID:gi6501635  
C:Genetics:  
A:Gene: STY0398  
C:Superfamily: conserved hypothetical protein b3238

Query Match 100.0%; Score 20; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||||  
Db 55 REDL 58

RESULT 18  
E83483  
conserved hypothetical protein PAI298 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: E83483  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; L  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Liu  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: E83483  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-91 <STO>  
A:Cross-references: UNIPROT:Q9I446; UNIPARC:UPI00000C52F9; GB:AE004559; GB:AE004091; NI  
A:Experimental source: strain PA01  
C:Genetics:  
A:Superfamily: hypothetical protein b2105

Query Match 100.0%; Score 20; DB 2; Length 91;

|  |   |                                |                          |            |         |
|--|---|--------------------------------|--------------------------|------------|---------|
| Best Local Similarity  | 100.0%;   | Pred. No. 3.6e+02;             | Mismatches 0;            | Indels 0;  | Gaps 0; |
| Matches  | 4;  | Conservative                   | 0;                       |            |         |
| QY   | 1 REDL 4  |                                |                          |            |         |
| DB   | 76 REDL 79  |                                |                          |            |         |
| RESULT 19  |   |                                |                          |            |         |
| A47030   |   |                                |                          |            |         |
| acyl carrier protein - Saccharopolyspora erythraea                       |   |                                |                          |            |         |
| C:Species:   | Saccharopolyspora erythraea   |                                |                          |            |         |
| C:Date:  | 03-May-1994   | #sequence_revision 03-May-1994 | #text_change 09-Jul-2004 |            |         |
| C:Accession:   | A47030; S00186  |                                |                          |            |         |
| R:Revill, W.P.; Leadlay, P.F.  |   |                                |                          |            |         |
| J. Bacteriol.  | 173, 4379-4385, 1991  |                                |                          |            |         |
| A:Title:   | Cloning, characterization, and high-level expression in Escherichia coli of the |                                |                          |            |         |
| sis.   |   |                                |                          |            |         |
| A:Reference number:  | A47030; MUID:91294181; PMID:2066335   |                                |                          |            |         |
| A:Accession:   | A47030  |                                |                          |            |         |
| A:Status:  | preliminary   |                                |                          |            |         |
| A:Molecule type:   | DNA   |                                |                          |            |         |
| A:Residues:  | 1-95 <REV>  |                                |                          |            |         |
| A:Cross-references:  | UNIPROT:P11830; UNIPARC:UPI0000125383; GB:M64477; NID:G152677; PIDN:            |                                |                          |            |         |
| R:Hale, R.S.; Jordan, K.N.; Leadlay, P.F.                                |   |                                |                          |            |         |
| FEBS Lett.   | 224, 133-136, 1987  |                                |                          |            |         |
| A:Title:   | A small, discrete acyl carrier protein is involved in de novo fatty acid biosyn |                                |                          |            |         |
| A:Reference number:  | S00186; MUID:88055578; PMID:3315744   |                                |                          |            |         |
| A:Accession:   | S00186  |                                |                          |            |         |
| A:Molecule type:   | protein   |                                |                          |            |         |
| A:Residues:  | 1-31,'X',33-44,'X',46 <HAL>   |                                |                          |            |         |
| A:Cross-references:  | UNIPARC:UPI0000177FC6   |                                |                          |            |         |
| A:Note:  | the source is designated as Streptomyces erythraeus                             |                                |                          |            |         |
| C:Comment:   | This protein is the carrier of the growing fatty acid chain in fatty acid syn   |                                |                          |            |         |
| C:Superfamily:   | acyl/peptidyl carrier protein; acyl carrier protein homology                    |                                |                          |            |         |
| C:Keywords:  | carrier protein; fatty acid biosynthesis; lipid metabolism; phosphopantethei    |                                |                          |            |         |
| F:4-75/Domain:   | acyl carrier protein homology <ACP>   |                                |                          |            |         |
| F:39/Binding site:   | phosphopantetheine (Ser) (covalent) #status predicted                           |                                |                          |            |         |
| Query Match  | 100.0%;   | Score 20;                      | DB 2;                    | Length 95; |         |
| Best Local Similarity  | 100.0%;   | Pred. No. 3.8e+02;             | Mismatches 0;            | Indels 0;  | Gaps 0; |
| Matches  | 4;  | Conservative                   | 0;                       |            |         |
| QY   | 1 REDL 4  |                                |                          |            |         |
| DB   | 32 REDL 35  |                                |                          |            |         |
| RESULT 20  |   |                                |                          |            |         |
| B42156   |   |                                |                          |            |         |
| translation initiation factor eIF-5A II [validated] - chicken (fragment) |   |                                |                          |            |         |
| C:Species:   | Gallus gallus (chicken)   |                                |                          |            |         |
| C:Date:  | 07-Apr-1994   | #sequence_revision 07-Apr-1994 | #text_change 18-Aug-2000 |            |         |
| C:Accession:   | B42156  |                                |                          |            |         |
| R:Wolff, E.C.; Kinzy, T.G.; Merrick, W.C.; Park, M.H.                    |   |                                |                          |            |         |
| J. Biol. Chem.   | 267, 6107-6113, 1992  |                                |                          |            |         |
| A:Title:   | Two isoforms of eIF-5A in chick embryo. Isolation, activity, and comparison of  |                                |                          |            |         |
| A:Reference number:  | A42156; MUID:92210582; PMID:1556119   |                                |                          |            |         |
| A:Accession:   | B42156  |                                |                          |            |         |
| A:Status:  | preliminary   |                                |                          |            |         |
| A:Molecule type:   | protein   |                                |                          |            |         |
| A:Residues:  | 1-97 <WOL>  |                                |                          |            |         |
| A:Cross-references:  | UNIPARC:UPI00001782DA   |                                |                          |            |         |
| C:Superfamily:   | translation initiation factor eIF-5A  |                                |                          |            |         |
| C:Keywords:  | hypusine; protein biosynthesis  |                                |                          |            |         |
| F:26/Modified site:  | N6-(4-amino-2-hydroxybutyl)lysine (Lys) #status experimental                    |                                |                          |            |         |
| Query Match  | 100.0%;   | Score 20;                      | DB 2;                    | Length 97; |         |
| Best Local Similarity  | 100.0%;   | Pred. No. 3.9e+02;             | Mismatches 0;            | Indels 0;  | Gaps 0; |
| Matches  | 4;  | Conservative                   | 0;                       |            |         |
| QY   | 1 REDL 4  |                                |                          |            |         |
| DB   | 32 REDL 35  |                                |                          |            |         |

|  |  |                                |                          |            |         |
|--|--|--------------------------------|--------------------------|------------|---------|
| Db   | 85 REDL 88   |                                |                          |            |         |
| RESULT 21  |  |                                |                          |            |         |
| I57601   |  |                                |                          |            |         |
| tubulin alpha chain isotype H2-alpha - human (fragment)                                  |  |                                |                          |            |         |
| C:Species:   | Homo sapiens (man)   |                                |                          |            |         |
| C:Date:  | 02-Jul-1996  | #sequence_revision 02-Jul-1996 | #text_change 09-Jul-2004 |            |         |
| C:Accession:   | I57601   |                                |                          |            |         |
| R:Villasante, A.; Wang, D.; Dobner, P.; Dolph, P.; Lewis, S.A.; Cowan, N.J.              |  |                                |                          |            |         |
| Mol. Cell. Biol.   | 6, 2409-2419, 1986   |                                |                          |            |         |
| A:Title:   | Six mouse alpha-tubulin mRNAs encode five distinct isotypes: Testis-specific e |                                |                          |            |         |
| A:Reference number:  | I57601; MUID:87064538; PMID:3785200  |                                |                          |            |         |
| A:Accession:   | I57601   |                                |                          |            |         |
| A:Status:  | preliminary; translated from GB/EMBL/DDBJ                                      |                                |                          |            |         |
| A:Molecule type:   | DNA  |                                |                          |            |         |
| A:Residues:  | 1-98 <RES>   |                                |                          |            |         |
| A:Cross-references:  | UNIPROT:Q15670; UNIPARC:UPI00000706A3; GB:K03460; NID:G340016; PIDN:           |                                |                          |            |         |
| C:Superfamily:   | tubulin  |                                |                          |            |         |
| Query Match  | 100.0%;  | Score 20;                      | DB 2;                    | Length 98; |         |
| Best Local Similarity  | 100.0%;  | Pred. No. 3.9e+02;             | Mismatches 0;            | Indels 0;  | Gaps 0; |
| Matches  | 4;   | Conservative                   | 0;                       |            |         |
| QY   | 1 REDL 4   |                                |                          |            |         |
| DB   | 70 REDL 73   |                                |                          |            |         |
| RESULT 22  |  |                                |                          |            |         |
| B95323   |  |                                |                          |            |         |
| hypothetical protein SMA0894 [imported] - Sinorhizobium meliloti (strain 1021) magaplas  |  |                                |                          |            |         |
| C:Species:   | Sinorhizobium meliloti   |                                |                          |            |         |
| C:Date:  | 24-Aug-2001  | #sequence_revision 24-Aug-2001 | #text_change 09-Jul-2004 |            |         |
| C:Accession:   | B95323   |                                |                          |            |         |
| R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow  |  |                                |                          |            |         |
| .; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C  |  |                                |                          |            |         |
| Proc. Natl. Acad. Sci. U.S.A.  | 98, 9883-9886, 2001  |                                |                          |            |         |
| A:Title:   | Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo |                                |                          |            |         |
| A:Reference number:  | A95262; MUID:21396509; PMID:11481432   |                                |                          |            |         |
| A:Accession:   | B95323   |                                |                          |            |         |
| A:Status:  | preliminary  |                                |                          |            |         |
| A:Molecule type:   | DNA  |                                |                          |            |         |
| A:Residues:  | 1-98 <KUR>   |                                |                          |            |         |
| A:Cross-references:  | UNIPROT:Q92ZJ5; UNIPARC:UPI00000C80E3; GB:AE006469; PIDN:AAK65148.1            |                                |                          |            |         |
| A:Experimental source:   | strain 1021, megaplasmid pSymA   |                                |                          |            |         |
| R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, |  |                                |                          |            |         |
| pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F   |  |                                |                          |            |         |
| L.; Hyman, R.W.; Jones, T.   |  |                                |                          |            |         |
| Science  | 293, 668-672, 2001   |                                |                          |            |         |
| A:Authors:   | Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lela      |                                |                          |            |         |
| hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. |  |                                |                          |            |         |
| A:Title:   | The composite genome of the legume symbiont Sinorhizobium meliloti.            |                                |                          |            |         |
| A:Reference number:  | A96039; MUID:21368234; PMID:11474104   |                                |                          |            |         |
| A:Contents:  | annotation   |                                |                          |            |         |
| C:Genetics:  |  |                                |                          |            |         |
| A:Gene:  | SMA0894  |                                |                          |            |         |
| A:Genome:  | plasmid  |                                |                          |            |         |
| Query Match  | 100.0%;  | Score 20;                      | DB 2;                    | Length 98; |         |
| Best Local Similarity  | 100.0%;  | Pred. No. 3.9e+02;             | Mismatches 0;            | Indels 0;  | Gaps 0; |
| Matches  | 4;   | Conservative                   | 0;                       |            |         |
| QY   | 1 REDL 4   |                                |                          |            |         |
| DB   | 22 REDL 25   |                                |                          |            |         |
| RESULT 23  |  |                                |                          |            |         |
| S69860   |  |                                |                          |            |         |
| hypothetical protein YML116w-a - Yeast (Saccharomyces cerevisiae)                        |  |                                |                          |            |         |
| C:Species:   | Saccharomyces cerevisiae   |                                |                          |            |         |
| C:Date:  | 23-Aug-1996  | #sequence_revision 06-Sep-1996 | #text_change 05-Nov-1999 |            |         |



C;Accession: S69860  
R;Skelton, J.; Churcher, C.M.  
submitted to the EMBL Data Library, May 1995  
A;Reference number: S53954  
A;Accession: S69860  
A;Molecule type: DNA  
A;Residues: 1-100 <SK>  
A;Cross-references: UNIPARC:UPI00001683B6; EMBL:Z49210; GSPDB:GN00013; MIPS:YML116w-a  
C;Genetics:  
A;Gene: MIPS:YML116w-a  
A;Map position: 13L  
C;Superfamily: Sacharomyces hypothetical protein YML116w-a

Query Match 100.0%; Score 20; DB 2; Length 100;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 11 REDL 14

#### RESULT 24

C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 12-Jul-2004

C;Accession: C71091

R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: C71091

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-102 <KAW>

A;Cross-references: UNIPROT:Q58720; UNIPARC:UPI00006682A; GB:AP000004; NID:G3236131; PI

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A;Gene: PH0992

Query Match 100.0%; Score 20; DB 2; Length 102;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 58 REDL 61

#### RESULT 25

A97134

phage-related, Zn finger domain containing protein [imported] - Clostridium acetobutylic

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 31-Dec-2004

C;Accession: A97134

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: A97134

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-103 <KUR>

A;Cross-references: UNIPROT:Q97HW0; UNIPARC:UPI00000CA348; GB:AE001437; PIDN:AAK79860.1;

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC1897

C;Superfamily: HNH endonuclease, phi-105 (gp19) type

Query Match 100.0%; Score 20; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 54 REDL 57

#### RESULT 26

CCBO

Cytochrome c - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 31-Dec-2004

C;Accession: A92022; A00007

R;Nakashima, T.; Higa, H.; Matubara, H.; Benson, A.; Yasunobu, K.T.

J. Biol. Chem. 241, 1166-1177, 1966

A;Title: The amino acid sequence of bovine heart cytochrome c.

A;Reference number: A92022; MUID:66132521; PMID:5933874

A;Accession: A92022

A;Molecule type: protein

A;Residues: 1-104 <NAK>

A;Cross-references: UNIPROT:P00006; UNIPARC:UPI0000128B9A

R;Tsunabawa, S.; Narita, K.

J. Biochem. 92, 607-613, 1982

A;Title: Micro-identification of amino-terminal acetyl amino acids in proteins.

A;Reference number: A61297; MUID:83056735; PMID:6754709

C;Contents: annotation; acetylation

C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology

C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metallo

F;4-98/Domain: cytochrome c homology <CYC>

F;1/Modified site: acetylated amino end (Gly) #status experimental

F;14,17/Binding site: heme (Cys) (covalent) #status predicted

F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 104;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 91 REDL 94

#### RESULT 27

CCHO

Cytochrome c [validated] - horse

C;Species: Equus caballus (domestic horse)

C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 31-Dec-2004

C;Accession: A00005; S59487

R;Margoliash, E.; Smith, E.L.; Kreil, G.; Tuppy, H.

Nature 192, 1125-1127, 1961

A;Title: The complete amino-acid sequence.

A;Reference number: A93145

A;Accession: A00005

A;Molecule type: protein

A;Residues: 1-104 <MAR>

A;Cross-references: UNIPROT:P00004; UNIPARC:UPI000011054E

R;Theodorakis, J.L.; Arnes, L.G.; Margoliash, E.

Biochim. Biophys. Acta 1252, 114-125, 1995

A;Title: beta-Thiopropionyl cytochromes c modified at lysyl residues: preparation and c

A;Reference number: S59487; MUID:96001350; PMID:7548153

A;Accession: S59487

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10;11-18;19-26;27-34;38-47;50-54;55-58;60-67;68-74;75-82;83-97;98-104 <TH

A;Cross-references: UNIPARC:UPI0000171C7B; UNIPARC:UPI0000171C7C; UNIPARC:UPI0000171C7D

C82; UNIPARC:UPI0000171C83; UNIPARC:UPI0000171C84; UNIPARC:UPI0000171C85; UNIPARC:UPI0000171C86

R;Luo, Y.; Brayer, G.D.

submitted to the Brookhaven Protein Data Bank, August 1994

A;Reference number: A52805; PDB:1HRC

A;Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 1-104

R;Dickerson, R.E.; Takano, T.; Eisenberg, D.; Kallai, O.B.; Samson, L.; Cooper, A.; Max

J. Biol. Chem. 246, 1511-1533, 1971  
A;Title: Ferricytochrome c. I. General features of the horse and bonito proteins at 2.8  
A;Reference number: A92076; MUID:71116428; PMID:5545094  
A;Contents: annotation; X-ray crystallography, 2.8 angstroms  
C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology  
C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metallopro  
F;4-98/Domain: cytochrome c homology <CYC>  
F;1/Modified site: acetylated amino end (Gly) #status experimental  
F;14,17/Binding site: heme (Cys) (covalent) #status experimental  
F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status experimental

Query Match 100.0%; Score 20; DB 1; Length 104;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
|||||  
Db 91 REDL 94

RESULT 28  
CCHOD  
cytochrome c - donkey (tentative sequence)  
C;Species: Equus asinus (donkey)  
C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 31-Dec-2004  
C;Accession: A00006  
R;Wlasek, O.F.; Margoliaash, E.  
J. Biol. Chem. 252, 830-834, 1977  
A;Title: Transmision of the cytochrome c structural gene in horse-donkey crosses.  
A;Reference number: A92217; MUID:77118552; PMID:190219  
A;Accession: A00006  
A;Molecule type: protein  
A;Residues: 1-104 <WAL>  
A;Cross-references: UNIPROT:P00005; UNIPARC:UPI0000128BB1  
A;Note: compositions of chymotryptic peptides and the sequence of residues 47-48 were de  
A;Note: mules and hinnies are heterozygous, having equal amounts of horse and donkey cy  
C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology  
C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metallopro  
F;4-98/Domain: cytochrome c homology <CYC>  
F;1/Modified site: acetylated amino end (Gly) #status predicted  
F;14,17/Binding site: heme (Cys) (covalent) #status predicted  
F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 104;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
|||||  
Db 91 REDL 94

RESULT 29  
CCHOZ  
cytochrome c - common zebra (tentative sequence)  
C;Species: Equus burchelli, Equus quagga (common zebra, plains zebra)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 31-Dec-2004  
C;Accession: A91330; A00006  
R;Guertler, L.; Horstmann, H.J.  
FBBS Lett. 18, 106-108, 1971  
A;Title: Zur Primaerstruktur des Cytochromes c des Steppenzebras (Equus quagga boehmi).  
A;Reference number: A91330  
A;Accession: A91330  
A;Molecule type: protein  
A;Residues: 1-104 <GUE>  
A;Cross-references: UNIPROT:P00005; UNIPARC:UPI0000128BB1  
A;Note: the amino acid composition and the sequence of residues 40-48 were determined  
C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology  
C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metallopro  
F;4-98/Domain: cytochrome c homology <CYC>  
F;1/Modified site: acetylated amino end (Gly) #status predicted  
F;14,17/Binding site: heme (Cys) (covalent) #status predicted  
F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 104;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
|||||  
Db 91 REDL 94

RESULT 30  
CCPG  
cytochrome c [validated] - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 31-Dec-2004  
C;Accession: A00007  
R;Stewart, J.W.; Margoliaash, E.  
Can. J. Biochem. 43, 1187-1206, 1965  
A;Title: The primary structure of the cytochrome c from various organs of the hog.  
A;Reference number: A90743; MUID:66072936; PMID:5855656  
A;Accession: A00007  
A;Molecule type: protein  
A;Residues: 1-104 <STE>  
A;Cross-references: UNIPROT:P00006; UNIPARC:UPI0000128B9A  
C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology  
C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metallo  
F;4-98/Domain: cytochrome c homology <CYC>  
F;1/Modified site: acetylated amino end (Gly) #status experimental  
F;14,17/Binding site: heme (Cys) (covalent) #status experimental  
F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 104;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
|||||  
Db 91 REDL 94

RESULT 31  
CCSH  
cytochrome c - sheep (tentative sequence)  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 31-Dec-2004  
C;Accession: A91454; A00007  
R;Smith, E.L.; Margoliaash, E.  
Fed. Proc. 23, 1243-1247, 1964  
A;Title: Evolution of cytochrome c.  
A;Reference number: A91454  
A;Accession: A91454  
A;Molecule type: protein  
A;Residues: 1-104 <SMI>  
A;Cross-references: UNIPROT:P00006; UNIPARC:UPI0000128B9A  
A;Note: amino acid compositions and mobilities of tryptic and chymotryptic peptides we  
C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology  
C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metall  
F;4-98/Domain: cytochrome c homology <CYC>  
F;1/Modified site: acetylated amino end (Gly) #status predicted  
F;14,17/Binding site: heme (Cys) (covalent) #status predicted  
F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 104;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
|||||  
Db 91 REDL 94

RESULT 32  
CCWST  
cytochrome c - common zebra (tentative sequence)  
C;Species: Equus burchelli, Equus quagga (common zebra, plains zebra)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 31-Dec-2004  
C;Accession: A91330; A00006  
R;Guertler, L.; Horstmann, H.J.  
FBBS Lett. 18, 106-108, 1971  
A;Title: Zur Primaerstruktur des Cytochromes c des Steppenzebras (Equus quagga boehmi).  
A;Reference number: A91330  
A;Accession: A91330  
A;Molecule type: protein  
A;Residues: 1-104 <GUE>  
A;Cross-references: UNIPROT:P00005; UNIPARC:UPI0000128BB1  
A;Note: the amino acid composition and the sequence of residues 40-48 were determined  
C;Superfamily: cytochrome c/cytochrome c2; cytochrome c homology  
C;Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metallopro  
F;4-98/Domain: cytochrome c homology <CYC>  
F;1/Modified site: acetylated amino end (Gly) #status predicted  
F;14,17/Binding site: heme (Cys) (covalent) #status predicted  
F;18,80/Binding site: heme iron (His, Met) (axial ligands) #status predicted

cytochrome c, testis-specific [validated] - mouse  
N:Alternate names: cytochrome c  
C:Species: Mus musculus (house mouse)  
C>Date: 24-Apr-1984 #sequence revision 30-Sep-1991 #text\_change 31-Dec-2004  
C:Accession: B28160; A00012; I48313  
R:Virbasius, J.V.; Scarpulla, R.C.  
J. Biol. Chem. 263, 6791-6796, 1988  
A:Title: Structure and expression of rodent genes encoding the testis-specific cytochrome c  
A:Reference number: A28160; MUID:88198250; PMID:2834389  
A:Accession: B28160  
A:Molecule type: mRNA  
A:Residues: 1-105 <VR>  
A:Cross-references: UNIPROT:P00015; UNIPARC:UPI0000022AAF; GB:M20625; NID:g192875; PIDN:R192875, B.  
Eur. J. Biochem. 55, 167-183, 1975  
A:Title: Change of cytochrome c structure during development of the mouse.  
A:Reference number: A00012; MUID:76022386; PMID:240690  
A:Accession: A00012  
A:Molecule type: protein  
A:Residues: 2-57, 'IV', 60-61, 'ZZ', 64-66, 'Z', 68-69, 'ZB', 72-105 <HEN>  
A:Cross-references: UNIPARC:UPI0000171C87  
A:Experimental source: strain BALB/c  
R:Hake, L.E.; Alcivar, A.A.; Hecht, N.B.  
Development 110, 249-257, 1990  
A:Title: Changes in mRNA length accompany translational regulation of the somatic and testis-specific cytochrome c2  
A:Reference number: I48313; MUID:91184013; PMID:1964409  
A:Accession: I48313  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-105 <RES>  
A:Cross-references: UNIPARC:UPI0000022AAF; EMBL:X55771; NID:g288155; PIDN:CAA39293.1; PIDN:CAA39293.1; PI  
C:Comment: Mammalian testis contains two forms of cytochrome c, one identical with the embryonic form and the other with the adult form.  
C:Superfamily: cytochrome c/cytochrome c2: cytochrome c homology  
C:Keywords: blocked amino end; chromoprotein; electron transfer; heme; iron; metalloprotein  
F:2-105/Product: cytochrome c, testis-specific #status experimental <MAT>  
F:5-99/Domain: cytochrome c homology <CYC>  
F:72/Modified site: blocked amino end (Gly) (in mature form) (probably acetylated) #status experimental  
F:15.18/Binding site: heme (Cys) (covalent) #status experimental  
F:19.81/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 105;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 92 REDL 95

RESULT 33  
CCRTT  
Cytochrome c, testis-specific - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text\_change 31-Dec-2004  
C:Accession: A28160  
R:Virbasius, J.V.; Scarpulla, R.C.  
J. Biol. Chem. 263, 6791-6796, 1988  
A:Title: Structure and expression of rodent genes encoding the testis-specific cytochrome c  
A:Reference number: A28160; MUID:88198250; PMID:2834389  
A:Accession: A28160  
A:Molecule type: DNA; mRNA  
A:Residues: 1-105 <VR>  
A:Cross-references: UNIPROT:P10715; UNIPARC:UPI0000167AA4; GB:M20627; GB:M20628; NID:g20627, B.  
C:Comment: Mammalian testis contains two forms of cytochrome c, one identical to the form found in the adult testis and the other with the embryonic form.  
C:Genetics: 57/1  
A:Introns: 57/1  
C:Superfamily: cytochrome c/cytochrome c2: cytochrome c homology  
C:Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metalloprotein  
F:2-105/Product: cytochrome c, testis-specific #status predicted <MAT>  
F:5-99/Domain: cytochrome c homology <CYC>  
F:72/Modified site: acetylated amino end (Gly) (in mature form) #status predicted

F:15.18/Binding site: heme (Cys) (covalent) #status predicted  
F:19.81/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 1; Length 105;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 92 REDL 95

RESULT 34  
A72465  
Hypothetical protein APE2364 - Aeropyrum pernix (strain K1)  
C:Species: Aeropyrum pernix  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: A72465  
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999  
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix  
A:Reference number: A72450; MUID:99310339; PMID:10382966  
A:Accession: A72465  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-106 <KAW>  
A:Cross-references: UNIPROT:Q9Y9C3; UNIPARC:UPI000005E2FD; DDBJ:AP000064; NID:g5105945  
A:Experimental source: strain K1  
C:Genetics:  
C:Superfamily: Aeropyrum pernix hypothetical protein APE2364

Query Match 100.0%; Score 20; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 31 REDL 34

RESULT 35  
AD0106  
Hypothetical protein YP00865 [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AD0106  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AD0106  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-106 <KUR>  
A:Cross-references: UNIPROT:Q8ZHM6; UNIPARC:UPI00000DC736; GB:AL590842; PIDN:CAC89711.  
C:Genetics:  
A:Gene: YP00865

Query Match 100.0%; Score 20; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 46 REDL 49

RESULT 36  
E71634

glutaredoxin-like protein grlA (grxC2) RP745 - Rickettsia prowazekii  
 C/Species: Rickettsia prowazekii  
 C/Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 05-Oct-2004  
 C/Accession: E71634  
 R/Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichertz-Ponten, T.; Alemark, U.  
 Nature 396, 133-140, 1998  
 A/Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
 A/Reference number: A71630; MUID:99039499; PMID:9823893  
 A/Accession: E71634  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-107 <AND>  
 A/Cross-references: UNIPROT:O05957; UNIPARC:UPI000012BAE8; GB:AJ235273; GB:AJ235269; NID  
 A/Experimental source: strain Madrid E  
 C/Genetics:  
 A/Gene: grxC2; RP745  
 C/Superfamily: monothiol glutaredoxin

Query Match 100.0%; Score 20; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 REDL 4  
 ||||  
 Db 61 REDL 64

RESULT 37  
 G71149  
 hypothetical protein PH0409 - Pyrococcus horikoshii  
 C/Species: Pyrococcus horikoshii  
 C/Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 12-Jul-2004  
 C/Accession: G71149  
 F/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
 M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
 DNA Res. 5, 55-76, 1998  
 A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
 A/Reference number: A71000; MUID:98344137; PMID:9679194  
 A/Accession: G71149  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-107 <KAW>  
 A/Cross-references: UNIPROT:O58146; UNIPARC:UPI0000062DE4; GB:AP000002; NID:G3236129; PI  
 A/Experimental source: strain OT3  
 A/Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 C/Genetics:  
 A/Gene: PH0409

Query Match 100.0%; Score 20; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 REDL 4  
 ||||  
 Db 24 REDL 27

RESULT 38  
 H83711  
 pectin degradation protein kdgF [imported] - Bacillus halodurans (strain C-125)  
 C/Species: Bacillus halodurans  
 C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C/Accession: H83711  
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fuji, F.; Hira  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A/Reference number: A83650; MUID:20512582; PMID:11058132  
 A/Accession: H83711  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-108 <STO>  
 A/Cross-references: UNIPROT:Q9KFI3; UNIPARC:UPI00000C38D0; GB:AP001508; GB:BA000004; NID  
 A/Experimental source: strain C-125

C/Genetics:  
 A/Gene: kdgF  
 C/Superfamily: involved in pectin degradation

Query Match 100.0%; Score 20; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 REDL 4  
 ||||  
 Db 98 REDL 101

RESULT 39  
 H90875  
 hypothetical protein ECs1976 [imported] - Escherichia coli (strain O157:H7, substrain R  
 C/Species: Escherichia coli  
 C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
 C/Accession: H90875  
 R/Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 gatawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
 A/Reference number: A99629; MUID:21156231; PMID:11258796  
 A/Accession: H90875  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-108 <HAY>  
 A/Cross-references: UNIPROT:Q8X2M1; UNIPARC:UPI00000D2AA1; GB:BA000007; PIDN:BA835399.1  
 A/Experimental source: strain O157:H7, substrain RMD 050952  
 C/Genetics:  
 A/Gene: ECs1976  
 C/Superfamily: uncharacterized conserved protein

Query Match 100.0%; Score 20; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 REDL 4  
 ||||  
 Db 83 REDL 86

RESULT 40  
 F85691  
 unknown protein encoded by prophage CP-933X [imported] - Escherichia coli (strain O157  
 C/Species: Escherichia coli  
 C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C/Accession: F85691  
 R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh  
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodac  
 Nature 409, 529-533, 2001  
 A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A/Reference number: A85480; MUID:21074935; PMID:11206551  
 A/Accession: F85691  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-108 <STO>  
 A/Cross-references: UNIPROT:Q8X4P1; UNIPARC:UPI00000D0DA4; GB:AE005174; NID:gl2514831;  
 A/Experimental source: strain O157:H7, substrain EDL933  
 C/Genetics:  
 A/Gene: Z1901  
 C/Superfamily: uncharacterized conserved protein

Query Match 100.0%; Score 20; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 REDL 4  
 ||||  
 Db 83 REDL 86

```
RESULT 41
A99822
hypothetical protein ECs1545 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: A99822
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A99822
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <HAY>
A:Cross-references: UNIPROT:Q8X4P1; UNIPARC:UPI00000D0DA4; GB:BA000007; PIDN:BA034968.1;
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs1545
C:Superfamily: uncharacterized conserved protein
Query Match 100.0%; Score 20; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;
Qy 1 REDL 4
Db 83 REDL 86
RESULT 42
D97843
glutaredoxin-like protein grla [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004
C:Accession: D97843
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: D97843
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <KUR>
A:Cross-references: UNIPROT:Q92GH5; UNIPARC:UPI00000C0BF5; GB:AE006914; PIDN:AAL03686.1;
C:Genetics:
A:Gene: grxC2
C:Superfamily: monothiol glutaredoxin
Query Match 100.0%; Score 20; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;
Qy 1 REDL 4
Db 65 REDL 68
RESULT 43
T35131
transcription regulator - Streptomyces coelicolor (fragment)
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T35131
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21568
A:Accession: T35131
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-111 <SEE>
A:Cross-references: UNIPROT:Q8CJQ4; UNIPARC:UPI000017AE11; EMBL:AL022268; PIDN:CAA18347.
A:Experimental source: strain A3(2)
```

## C:Genetics:

A:Gene: SCORDB:SC4H2.32

Query Match 100.0%; Score 20; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 90 REDL 93

## RESULT 44

AE2039

transcription regulator alr1867 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C:Accession: AE2039

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE2039

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-112 &lt;KUR&gt;

A:Cross-references: UNIPROT:Q8YVW6; UNIPARC:UPI00000CE231; GB:BA000019; PIDN:BA073566.

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr1867

C:Superfamily: arsenical resistance operon repressor

Query Match 100.0%; Score 20; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 81 REDL 84

## RESULT 45

S00006

Whey protein - Arabian camel

C:Species: Camelus dromedarius (Arabian camel)

C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004

C:Accession: S00006

R:Beq, O.U.; von Bahr-Lindstroem, H.; Zaidi, Z.H.; Joernvall, H.

FEBS Lett. 216, 270-274, 1987

A:Title: Characterization of a heterogeneous camel milk whey non-casein protein.

A:Reference number: S00006; MUID:87219156; PMID:3495459

A:Accession: S00006

A:Molecule type: protein

A:Residues: 1-112 &lt;BSG&gt;

A:Cross-references: UNIPROT:P15522; UNIPARC:UPI00001797D0

A:Note: the sequence Ala-Ala-Gln-Val-Glu-Ile was also found for residues 4-9

C:Comment: N-terminal fragments derived from both mature protein variants were also fo

C:Keywords: milk

Query Match 100.0%; Score 20; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4

Db 17 REDL 20

## RESULT 46

JQ1128

gas-vesicle operon protein gvpK - Halobacterium salinarum plasmids pHH1 and pNRC100

C;Species: Halobacterium salinarum  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 31-Jan-2000  
C;Accession: JQ1128; S15190  
R;Jones, J.G.; Young, D.C.; DasSarma, S.  
Gene 102, 117-122, 1991  
A;Title: Structure and organization of the gas vesicle gene cluster on the Halobacterium  
A;Reference number: JQ1122; MUID:91323716; PMID:1864501  
A;Accession: JQ1128  
A;Molecule type: DNA  
A;Residues: 1-113 <JON>  
A;Cross-references: UNIPARC:UPI000012BE37; GB:M58557; NID:g150406; PID:g455299  
A;Experimental source: strain NRC-1, plasmid pNRC100  
A;Genetics: NRC  
A;Note: the source is designated as Halobacterium halobium  
R;Horne, M.; Englert, C.; Wimmer, C.; Pfeifer, F.  
Mol. Microbiol. 5, 1159-1174, 1991  
A;Title: A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis in  
A;Reference number: S15183; MUID:92065812; PMID:1956294  
A;Accession: S15190  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-113 <HOR>  
A;Cross-references: UNIPARC:UPI000012BE37; EMBL:X55648; NID:g43516; PID:g43524  
A;Experimental source: plasmid pPH1  
A;Genetics: PHH  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1990  
C;Genetics: <NRC>  
A;Gene: gvpK  
A;Genome: plasmid pNRC100  
C;Genetics: <PHH>  
A;Gene: gvpK  
A;Genome: plasmid pPH1

Query Match 100.0%; Score 20; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 80 REDL 83

RESULT 47  
T08234  
gas-vesicle operon protein gvpK - Halobacterium sp. (strain NRC-1) plasmid pNRC100  
N;Alternate names: hypothetical protein H0228  
C;Species: Halobacterium sp.  
A;Variety: strain NRC-1  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
R;Ng, W.V.; Ciufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;  
Genome Res. 8, 1131-1141, 1998  
A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or m  
A;Reference number: Z16408; MUID:99063795; PMID:9847077  
A;Accession: T08234  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-113 <NGW>  
A;Cross-references: UNIPROT:P24375; UNIPARC:UPI000012BE37; EMBL:AF016485; NID:g2822278;  
A;Experimental source: strain NRC-1  
C;Genetics:  
A;Gene: gvpK; HALOSP:H0228  
A;Genome: plasmid pNRC100

Query Match 100.0%; Score 20; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 80 REDL 83

RESULT 48  
G83746  
hypothetical protein BH0775 [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C;Accession: G83746  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: G83746  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-113 <STO>  
A;Cross-references: UNIPROT:Q9KES4; UNIPARC:UPI00000C39AB; GB:BA0001509; GB:BA0000004; NI  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: BH0775

Query Match 100.0%; Score 20; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 72 REDL 75

RESULT 49  
G95059  
hypothetical protein SP0514 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: G95059  
R;Tettelein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei  
on, J.D.; Hickey, E.K.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, S.  
nson, T.; Hickay, L.A.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: G95059  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-115 <KUR>  
A;Cross-references: UNIPROT:Q97S74; UNIPARC:UPI0000051481; GB:AE005672; PIDN:AAK74672.1  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP0514

Query Match 100.0%; Score 20; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
Db 79 REDL 82

RESULT 50  
E83395  
hypothetical protein PA1995 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Li  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Liu  
; Lozy, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: E83395

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-118 <STO>  
A:Cross-references: UNIPROT:Q9I2B4; UNIPARC:UPI000000C554A; GB:AE004626; GB:AE004091; NID  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA1995

Query Match 100.0%; Score 20; DB 2; Length 118;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|  
|  
|  
|  
Db 17 REDL 20

Search completed: March 20, 2006, 07:50:44  
Job time : 18 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:50 ; Search time 147.5 Seconds  
(without alignments)  
19.133 Million cell updates/sec

Title: US-09-673-707-10  
Perfect score: 20  
Sequence: 1 REDL 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID        | Description         |
|------------|-------|-------------|--------|--------------|---------------------|
| 1          | 20    | 100.0       | 27     | Q89492_9BROM | Q89492 cucumber mo  |
| 2          | 20    | 100.0       | 29     | Q86Lm9_9METZ | Q86Lm9 spongilla s  |
| 3          | 20    | 100.0       | 30     | Q4YF88_PLABE | Q4YF88 plasmodium   |
| 4          | 20    | 100.0       | 31     | Q4KA34_PSEF5 | Q4KA34 pseudomonas  |
| 5          | 20    | 100.0       | 32     | Q86Lp0_9METZ | Q86Lp0 acarusus sp. |
| 6          | 20    | 100.0       | 34     | Q95LA6_PIG   | Q95LA6 sus scrofa   |
| 7          | 20    | 100.0       | 35     | Q9UQV7_TRAVE | Q9UQV7 trametres ve |
| 8          | 20    | 100.0       | 35     | Q570E3_ARATH | Q570E3 arabidopsis  |
| 9          | 20    | 100.0       | 35     | Q5NQJ6_ZYMMO | Q5NQJ6 zymomonas m  |
| 10         | 20    | 100.0       | 36     | Q9QW57_9MURI | Q9QW57 mus sp. hes  |
| 11         | 20    | 100.0       | 38     | Q56Y22_ARATH | Q56Y22 arabidopsis  |
| 12         | 20    | 100.0       | 39     | Q19688_HUMAN | Q19688 homo sapien  |
| 13         | 20    | 100.0       | 39     | Q61645_APLCA | Q61645 aplysia cal  |
| 14         | 20    | 100.0       | 39     | Q8MTM6_9DIPT | Q8MTM6 culicoides   |
| 15         | 20    | 100.0       | 39     | Q74264_9HIVI | Q74264 human immun  |
| 16         | 20    | 100.0       | 41     | Q9UW29_9PEZI | Q9UW29 ceratocysti  |
| 17         | 20    | 100.0       | 41     | Q8CH67_MOUSE | Q8CH67 mus musculu  |
| 18         | 20    | 100.0       | 45     | Q8WMC5_PONPY | Q8WMC5 pongo pygma  |
| 19         | 20    | 100.0       | 45     | Q8WN16_HYLLX | Q8WN16 hylobates k  |
| 20         | 20    | 100.0       | 45     | Q84U15_9ASPA | Q84U15 dendrobium   |
| 21         | 20    | 100.0       | 46     | Q8GT46_ANOGA | Q8GT46 anopheles g  |
| 22         | 20    | 100.0       | 46     | Q8WNH3_CERAE | Q8WNH3 cercopithe   |
| 23         | 20    | 100.0       | 47     | Q87Z84_PSESM | Q87Z84 pseudomonas  |
| 24         | 20    | 100.0       | 49     | Q4GXQ0_9COLE | Q4GXQ0 eucinetus s  |
| 25         | 20    | 100.0       | 49     | Q7YQ54_PHOSS | Q7YQ54 phocoena si  |
| 26         | 20    | 100.0       | 49     | Q7YQ55_PHOSS | Q7YQ55 phocoena si  |
| 27         | 20    | 100.0       | 49     | Q7YQ56_PHOSS | Q7YQ56 phocoena si  |
| 28         | 20    | 100.0       | 49     | Q7YQ57_PHOSS | Q7YQ57 phocoena si  |
| 29         | 20    | 100.0       | 49     | Q7YQ58_PHOSS | Q7YQ58 phocoena si  |
| 30         | 20    | 100.0       | 49     | Q7YQ59_PHOSS | Q7YQ59 phocoena si  |
| 31         | 20    | 100.0       | 49     | Q7YQ60_PHOSS | Q7YQ60 phocoena si  |

|     |    |       |    |   |              |                    |
|-----|----|-------|----|---|--------------|--------------------|
| 32  | 20 | 100.0 | 49 | 2 | Q4ZR70_PSESY | Q4ZR70 pseudomonas |
| 33  | 20 | 100.0 | 50 | 1 | TBA_BLEJA    | Q8628 blepharisma  |
| 34  | 20 | 100.0 | 50 | 2 | Q4XG11_PLACH | Q4XG11 plasmodium  |
| 35  | 20 | 100.0 | 50 | 2 | Q7ZT89_CARAU | Q7ZT89 carassius a |
| 36  | 20 | 100.0 | 51 | 2 | Q64BT2_PARCH | Q64BT2 uncultured  |
| 37  | 20 | 100.0 | 51 | 2 | Q8NFP0_HUMAN | Q8NFP0 homo sapien |
| 38  | 20 | 100.0 | 51 | 2 | Q7LZL4_XENLA | Q7LZL4 xenopus lae |
| 39  | 20 | 100.0 | 52 | 2 | Q8MZQ7_9DIPT | Q8MZQ7 drosophila  |
| 40  | 20 | 100.0 | 52 | 2 | Q58LK4_9CAUD | Q58LK4 cyanophaga  |
| 41  | 20 | 100.0 | 52 | 2 | Q5XY22_BORGA | Q5XY22 borrelia ga |
| 42  | 20 | 100.0 | 54 | 2 | Q96XL7_SULTO | Q96XL7 sulfolobus  |
| 43  | 20 | 100.0 | 54 | 2 | Q9GLJ2_PIG   | Q9GLJ2 sus scrofa  |
| 44  | 20 | 100.0 | 54 | 2 | Q94KJ8_PINTA | Q94KJ8 pinus taeda |
| 45  | 20 | 100.0 | 54 | 2 | Q69433_9BACI | Q69433 exiguobacte |
| 46  | 20 | 100.0 | 54 | 2 | Q69233_BACCE | Q69233 bacillus ce |
| 47  | 20 | 100.0 | 55 | 2 | Q5QLQ2_ORYSA | Q5QLQ2 oryza sativ |
| 48  | 20 | 100.0 | 55 | 2 | Q8F9J9_LEPIN | Q8F9J9 leptospira  |
| 49  | 20 | 100.0 | 56 | 2 | Q5E042_VIBFI | Q5E042 vibrio fisc |
| 50  | 20 | 100.0 | 57 | 2 | Q4HAV9_9DEIO | Q4HAV9 deinococcus |
| 51  | 20 | 100.0 | 58 | 2 | Q7MJF3_VIBVY | Q7MJF3 vibrio vuln |
| 52  | 20 | 100.0 | 59 | 1 | NBLA_SYNP7   | P35087 synechococc |
| 53  | 20 | 100.0 | 59 | 2 | Q5TUH5_ANOGA | Q5TUH5 anopheles g |
| 54  | 20 | 100.0 | 59 | 2 | Q8SZB9_DROME | Q8SZB9 drosophila  |
| 55  | 20 | 100.0 | 60 | 2 | Q4X9Z2_PLACH | Q4X9Z2 plasmodium  |
| 56  | 20 | 100.0 | 60 | 2 | Q653Q0_ORYSA | Q653Q0 oryza sativ |
| 57  | 20 | 100.0 | 62 | 2 | Q8WME7_PONPY | Q8WME7 pongo pygma |
| 58  | 20 | 100.0 | 62 | 2 | Q8WNI7_HYLLX | Q8WNI7 hylobates k |
| 59  | 20 | 100.0 | 63 | 2 | Q8WNH4_CERAE | Q8WNH4 cercopithe  |
| 60  | 20 | 100.0 | 63 | 2 | Q9XSB0_BOVIN | Q9XSB0 bos taurus  |
| 61  | 20 | 100.0 | 63 | 2 | Q65EM4_BACLD | Q65EM4 bacillus li |
| 62  | 20 | 100.0 | 64 | 2 | Q8VT56_STRMU | Q8VT56 streptococc |
| 63  | 20 | 100.0 | 64 | 2 | Q5N0L5_SYNP6 | Q5N0L5 synechococc |
| 64  | 20 | 100.0 | 64 | 2 | Q4RA80_TETNG | Q4RA80 tetraodon n |
| 65  | 20 | 100.0 | 64 | 2 | Q7L431_9HIVI | Q7L431 human immun |
| 66  | 20 | 100.0 | 66 | 1 | RL29_SILPO   | Q51W50 silicibacte |
| 67  | 20 | 100.0 | 66 | 2 | Q77FS8_9CAUD | Q77FS8 streptococc |
| 68  | 20 | 100.0 | 66 | 2 | Q9MBY4_9CAUD | Q9MBY4 streptococc |
| 69  | 20 | 100.0 | 66 | 2 | Q6Y072_ONYPE | Q6Y072 onion yello |
| 70  | 20 | 100.0 | 66 | 2 | Q9QW45_9MURI | Q9QW45 rattus sp.  |
| 71  | 20 | 100.0 | 67 | 2 | Q647X2_9ARCH | Q647X2 uncultured  |
| 72  | 20 | 100.0 | 67 | 2 | Q7M312_SHEEP | Q7M312 ovis aries  |
| 73  | 20 | 100.0 | 67 | 2 | Q9XJU6_9CAUD | Q9XJU6 streptococc |
| 74  | 20 | 100.0 | 67 | 2 | Q9F2D2_SALTY | Q9F2D2 salmonella  |
| 75  | 20 | 100.0 | 67 | 2 | Q9AN11_BRAJA | Q9AN11 bradyrhizob |
| 76  | 20 | 100.0 | 68 | 2 | Q5P601_AZOSE | Q5P601 azoarcus sp |
| 77  | 20 | 100.0 | 68 | 2 | Q9IF22_9HIVI | Q9IF22 human immun |
| 78  | 20 | 100.0 | 69 | 2 | Q01723_BRAFL | Q01723 branchiosto |
| 79  | 20 | 100.0 | 69 | 2 | Q9JN70_BACCE | Q9JN70 bacillus ce |
| 80  | 20 | 100.0 | 69 | 2 | Q9IF24_9HIVI | Q9IF24 human immun |
| 81  | 20 | 100.0 | 69 | 2 | Q71476_9HIVI | Q71476 human immun |
| 82  | 20 | 100.0 | 71 | 2 | Q5Y1B6_9Z2Z2 | Q5Y1B6 uncultured  |
| 83  | 20 | 100.0 | 71 | 2 | Q66L18_XENLA | Q66L18 xenopus lae |
| 84  | 20 | 100.0 | 72 | 2 | Q52UL4_BOVIN | Q52UL4 bos taurus  |
| 85  | 20 | 100.0 | 72 | 2 | Q4UK11_RICPE | Q4UK11 rickettsia  |
| 86  | 20 | 100.0 | 72 | 2 | Q9IF04_9HIVI | Q9IF04 human immun |
| 87  | 20 | 100.0 | 73 | 2 | Q97YK4_SULSO | Q97YK4 sulfolobus  |
| 88  | 20 | 100.0 | 73 | 2 | Q50014_MYCLE | Q50014 mycobacteri |
| 89  | 20 | 100.0 | 73 | 2 | Q4MMB8_BACCE | Q4MMB8 bacillus ce |
| 90  | 20 | 100.0 | 74 | 2 | Q7S2A0_NEUCR | Q7S2A0 neurospora  |
| 91  | 20 | 100.0 | 74 | 2 | Q9IF06_9HIVI | Q9IF06 drosophila  |
| 92  | 20 | 100.0 | 74 | 2 | Q5V382_HALMA | Q5V382 haloarcula  |
| 93  | 20 | 100.0 | 75 | 2 | Q84K97_9ASPA | Q84K97 crocus sati |
| 94  | 20 | 100.0 | 75 | 2 | Q82QL9_STRAW | Q82QL9 streptomyc  |
| 95  | 20 | 100.0 | 75 | 2 | Q8VKG6_MYCTU | Q8VKG6 mycobacteri |
| 96  | 20 | 100.0 | 76 | 2 | Q5YVR1_NOCFA | Q5YVR1 nocardia fa |
| 97  | 20 | 100.0 | 76 | 2 | Q81X92_BACAN | Q81X92 bacillus an |
| 98  | 20 | 100.0 | 76 | 2 | Q4RCC9_TETNG | Q4RCC9 tetraodon n |
| 99  | 20 | 100.0 | 76 | 2 | Q528F0_ORYSA | Q528F0 oryza sativ |
| 100 | 20 | 100.0 | 77 | 2 | Q9RLF4_PLARU | Q9RLF4 planktothri |
| 101 | 20 | 100.0 | 77 | 2 | Q4NPF2_9MICC | Q4NPF2 arthrobacte |
| 102 | 20 | 100.0 | 77 | 2 | Q7M6V4_MOUSE | Q7M6V4 mus musculu |
| 103 | 20 | 100.0 | 77 | 2 | Q91F25_GVCP  | Q91F25 cydia pomon |
| 104 | 20 | 100.0 | 77 | 2 |              |                    |

|  |   |   |      |        |              |                    |
|--|---|---|------|--------|--------------|--------------------|
| 105  | 20  | 100.0                                   | 78   | 1      | CY351_ECTHA  | P00122 ectothiorho |
| 106  | 20  | 100.0                                   | 78   | 2      | Q6PDB_HELAM  | Q6ppd8 helicoverpa |
| 107  | 20  | 100.0                                   | 78   | 2      | Q75H75_ORYSA | Q75h75 oryza sativ |
| 108  | 20  | 100.0                                   | 78   | 2      | Q8D105_SYNEL | Q8d105 synecococc  |
| 109  | 20  | 100.0                                   | 79   | 1      | DLTC_ABIDE   | Q8gr69 abiotrophia |
| 110  | 20  | 100.0                                   | 79   | 1      | DLTC_LACLA   | Q9c951 lactococcus |
| 111  | 20  | 100.0                                   | 79   | 2      | Q64CH6_9ARCH | Q64ch6 uncultured  |
| 112  | 20  | 100.0                                   | 79   | 2      | Q4T7Q6_TETNG | Q4t7q6 tetraodon n |
| 113  | 20  | 100.0                                   | 79   | 2      | Q9IF14_9HIV1 | Q9if14 human immun |
| 114  | 20  | 100.0                                   | 80   | 2      | Q8NKP1_SULAC | Q8nkp1 sulfolobus  |
| 115  | 20  | 100.0                                   | 80   | 2      | Q53QY5_HUMAN | Q53qy5 homo sapien |
| 116  | 20  | 100.0                                   | 80   | 2      | Q87T24_VIBPA | Q87t24 vibrio para |
| 117  | 20  | 100.0                                   | 81   | 2      | Q71J19_MACFA | Q71j19 macaca fasc |
| 118  | 20  | 100.0                                   | 81   | 2      | Q6ESF6_ORYSA | Q6esf6 oryza sativ |
| 119  | 20  | 100.0                                   | 81   | 2      | Q6HR28_BACAN | Q6hr28 bacillus an |
| 120  | 20  | 100.0                                   | 81   | 2      | Q92U02_RHIME | Q92u02 rhizobium m |
| 121  | 20  | 100.0                                   | 81   | 2      | Q7ZT96_CARAU | Q7zt96 carassius a |
| 122  | 20  | 100.0                                   | 82   | 2      | Q4VXZ3_HUMAN | Q4vxz3 homo sapien |
| 123  | 20  | 100.0                                   | 82   | 2      | Q4R805_MACFA | Q4r805 macaca fasc |
| 124  | 20  | 100.0                                   | 82   | 2      | Q775D9_9CAUD | Q775d9 bordetella  |
| 125  | 20  | 100.0                                   | 82   | 2      | Q5L1Y9_GEOXA | Q5l1y9 geobacillus |
| 126  | 20  | 100.0                                   | 82   | 2      | Q5WK37_BACSK | Q5wk37 bacillus cl |
| 127  | 20  | 100.0                                   | 82   | 2      | Q8PRN4_XANAC | Q8prn4 xanthomonas |
| 128  | 20  | 100.0                                   | 82   | 2      | Q4S2T2_TETNG | Q4s2t2 tetraodon n |
| 129  | 20  | 100.0                                   | 83   | 1      | Y46S_SYNY3   | P73882 synecocyst  |
| 130  | 20  | 100.0                                   | 83   | 2      | Q775E0_9CAUD | Q775e0 bordetella  |
| 131  | 20  | 100.0                                   | 83   | 2      | Q8NR16_CORGL | Q8nr16 corynebacte |
| 132  | 20  | 100.0                                   | 84   | 2      | Q857W9_9CAUD | Q857w9 mycobacteri |
| 133  | 20  | 100.0                                   | 84   | 2      | Q4JXF2_CORJK | Q4jxf2 corynebacte |
| 134  | 20  | 100.0                                   | 84   | 2      | Q9S1X4_STRCO | Q9s1x4 streptomyc  |
| 135  | 20  | 100.0                                   | 85   | 2      | Q42921_SCHPO | Q42921 schizosacch |
| 136  | 20  | 100.0                                   | 85   | 2      | Q7QSD1_GIALA | Q7qsd1 giardia lam |
| 137  | 20  | 100.0                                   | 85   | 2      | Q9XXH2_CABEL | Q9xxh2 caenorhabdi |
| 138  | 20  | 100.0                                   | 85   | 2      | Q7U6H4_SYNXP | Q7u6h4 synecococc  |
| 139  | 20  | 100.0                                   | 86   | 1      | GBG_NEUCR    | Q7rwt0 neurospora  |
| 140  | 20  | 100.0                                   | 87   | 2      | Q9MY39_HUMAN | Q9my39 homo sapien |
| 141  | 20  | 100.0                                   | 88   | 1      | Y2638_BACHD  | Q9k9k7 bacillus ha |
| 142  | 20  | 100.0                                   | 88   | 2      | Q5JG75_PYRKO | Q5jg75 pyrococcus  |
| 143  | 20  | 100.0                                   | 88   | 2      | Q58MT8_9CAUD | Q58mt8 cyanophage  |
| 144  | 20  | 100.0                                   | 88   | 2      | Q5SLG1_THET8 | Q5slg1 thermus the |
| 145  | 20  | 100.0                                   | 88   | 2      | Q72H44_THET2 | Q72h44 thermus the |
| 146  | 20  | 100.0                                   | 88   | 2      | Q8RA16_THETN | Q8ra16 thermoanaer |
| 147  | 20  | 100.0                                   | 88   | 2      | Q8END8_OCEIH | Q8end8 oceanobacil |
| 148  | 20  | 100.0                                   | 89   | 2      | Q9BCW5_HUMAN | Q9bcm5 homo sapien |
| 149  | 20  | 100.0                                   | 89   | 2      | Q9GIZ7_HUMAN | Q9giz7 homo sapien |
| 150  | 20  | 100.0                                   | 89   | 2      | Q9GJ10_HUMAN | Q9gj10 homo sapien |
| ALIGNMENTS   |   |   |      |        |              |                    |
| RESULT 1   |   |   |      |        |              |                    |
| ID   | Q89492_9BROM  | PRELIMINARY;                            | PRT; | 27 AA. |              |                    |
| AC   | Q89492_   |   |      |        |              |                    |
| DT   | 01-NOV-1996   | (TrEMBLrel. 01, Created)                |      |        |              |                    |
| DT   | 01-NOV-1996   | (TrEMBLrel. 01, Last sequence update)   |      |        |              |                    |
| DT   | 01-FEB-2005   | (TrEMBLrel. 29, Last annotation update) |      |        |              |                    |
| DE   | ORF 1.  |   |      |        |              |                    |
| OS   | Cucumber mosaic virus (cucumber mosaic cucumovirus).                  |   |      |        |              |                    |
| OC   | Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;   |   |      |        |              |                    |
| OC   | Cucumovirus.  |   |      |        |              |                    |
| OX   | NCBI_TaxID=12305;   |   |      |        |              |                    |
| RN   | [1]   |   |      |        |              |                    |
| RP   | NUCLEOTIDE SEQUENCE.  |   |      |        |              |                    |
| RX   | MEDLINE=88179532; PubMed=3354198;                                     |   |      |        |              |                    |
| RA   | Kaper J.M., Tousignant M.E., Streen M.T.;                             |   |      |        |              |                    |
| RT   | "Cucumber mosaic virus-associated RNA 5: XI. Comparison of 14 CARNA 5 |   |      |        |              |                    |
| RT   | variants relates ability to induce tomato necrosis to a conserved     |   |      |        |              |                    |
| RT   | nucleotide sequence."   |   |      |        |              |                    |
| RL   | Virology 163:284-292(1988).   |   |      |        |              |                    |
| DR   | EMBL; M20357; AAA46403.1; -; Genomic RNA.                             |   |      |        |              |                    |
| DR   | EMBL; M20350; AAA46385.1; -; Genomic_RNA.                             |   |      |        |              |                    |
| RESULT 2   |   |   |      |        |              |                    |
| ID   | Q86LN9_9METZ  | PRELIMINARY;                            | PRT; | 29 AA. |              |                    |
| AC   | Q86LN9_   |   |      |        |              |                    |
| DT   | 01-JUN-2003   | (TrEMBLrel. 24, Created)                |      |        |              |                    |
| DT   | 01-JUN-2003   | (TrEMBLrel. 24, Last sequence update)   |      |        |              |                    |
| DT   | 01-MAR-2004   | (TrEMBLrel. 26, Last annotation update) |      |        |              |                    |
| DE   | Paired-type homeodomain-containing protein (Fragment).                |   |      |        |              |                    |
| OS   | Spongilla sp. SL-2003.  |   |      |        |              |                    |
| OC   | Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;          |   |      |        |              |                    |
| OC   | Haploeclerida; Spongillidae; Spongilla.                               |   |      |        |              |                    |
| RN   | NCBI_TaxID=220381;  |   |      |        |              |                    |
| RP   | NUCLEOTIDE SEQUENCE.  |   |      |        |              |                    |
| RA   | Lee S.E., Gates R.D., Jacobs D.K.;                                    |   |      |        |              |                    |
| RT   | "Gene Fishing: the use of a simple protocol to isolate multiple       |   |      |        |              |                    |
| RT   | homeodomain classes from diverse invertebrate taxa."                  |   |      |        |              |                    |
| U  | J. Mol. Evol. 0:0-0(2003).  |   |      |        |              |                    |
| CC   | -1- SUBCELLULAR LOCATION: Nuclear (By similarity).                    |   |      |        |              |                    |
| DR   | EMBL; AY187697; AA045637.1; -; Genomic_DNA.                           |   |      |        |              |                    |
| DR   | GO; GO:0005634; C:nucleus; IEA.                                       |   |      |        |              |                    |
| DR   | GO; GO:0003700; F:transcription factor activity; IEA.                 |   |      |        |              |                    |
| DR   | GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.    |   |      |        |              |                    |
| DR   | InterPro; IPR001356; Homeobox.  |   |      |        |              |                    |
| DR   | Pfam; PF00046; Homeobox; 1.   |   |      |        |              |                    |
| DR   | PRINTS; PR00024; HOMEBOX.   |   |      |        |              |                    |
| DR   | ProDom; PD000010; Homeobox; 1.  |   |      |        |              |                    |
| KW   | DNA-binding; Homeobox; Nuclear protein.                               |   |      |        |              |                    |
| FT   | NON_TER 1 1   |   |      |        |              |                    |
| FT   | NON_TER 29 29   |   |      |        |              |                    |
| SQ   | SEQUENCE 29 AA; 3393 MW; 3B7DC4820DA3E4E9 CRC64;                      |   |      |        |              |                    |
| Query Match 100.0%; Score 20; DB 2; Length 29;             |   |   |      |        |              |                    |
| Best Local Similarity 100.0%; Pred. No. 7.1e+02;           |   |   |      |        |              |                    |
| Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |   |   |      |        |              |                    |
| Qy   | 1 REDL 4  |   |      |        |              |                    |
| Db   | 14 REDL 17  |   |      |        |              |                    |
| RESULT 3   |   |   |      |        |              |                    |
| ID   | Q4YFAB_PLABE  | PRELIMINARY;                            | PRT; | 30 AA. |              |                    |
| AC   | Q4YFAB_   |   |      |        |              |                    |
| DT   | 13-SEP-2005   | (TrEMBLrel. 31, Created)                |      |        |              |                    |
| DT   | 13-SEP-2005   | (TrEMBLrel. 31, Last sequence update)   |      |        |              |                    |
| DT   | 13-SEP-2005   | (TrEMBLrel. 31, Last annotation update) |      |        |              |                    |
| DE   | Hypothetical protein (Fragment).                                      |   |      |        |              |                    |
| GN   | ORFNames=PB404646.00.0;   |   |      |        |              |                    |
| OS   | Plasmodium berghei.   |   |      |        |              |                    |
| OC   | Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.         |   |      |        |              |                    |
| OX   | NCBI_TaxID=5821;  |   |      |        |              |                    |
| RN   | [1]   |   |      |        |              |                    |
| RP   | NUCLEOTIDE SEQUENCE.  |   |      |        |              |                    |

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RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rejandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RL transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CA01005700; CA103310.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 30 AA; 3559 MW; 3565280356933DA8 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 3 REDL 6

RESULT 4
Q4KA34_PSEFS
ID Q4KA34_PSEFS PRELIMINARY; PRT; 31 AA.
AC Q4KA34;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
DE Hypothetical protein.
GN ORFNames=PFL_3799;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PF-5;
RA PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L. III, Thomasow L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878(2005).
RL EMBL; CP000076; AAY93062.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 31 AA; 3593 MW; 45D45B4E6AE51501 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 13 REDL 16

RESULT 5
Q86LP0_9METZ
ID Q86LP0_9METZ PRELIMINARY; PRT; 32 AA.
AC Q86LP0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Paired-type homeodomain-containing protein (Fragment).
OS Acarnus sp. SL-2003.

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OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Poecilosclerida; Myxillina; Myxillidae; Acarnus.
OX NCBI_TaxID=220380;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee S.E., Gates R.D., Jacobs D.K.;
RT "Gene Fishing: the use of a simple protocol to isolate multiple
RT homeodomain classes from diverse invertebrate taxa."
RL J. Mol. Evol. 0:0-0(2003).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AY187696; AAC45636.1; -; Genomic_DNA.
DR HSSP; P06601; 1FJL.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON TER 1
FT NON TER 32
SQ SEQUENCE 32 AA; 3813 MW; 85872CAB6884930D CRC64;

Query Match 100.0%; Score 20; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 14 REDL 17

RESULT 6
Q95LA6_PIG
ID Q95LA6_PIG PRELIMINARY; PRT; 34 AA.
AC Q95LA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LIM homeodomain protein 3b (Fragment).
GN Name=Lhx3;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21453325; PubMed=11470784; DOI=10.1074/jbc.M103888200;
RA Sloop K.W., Dwyer C.J., Rhodes S.J.;
RT "An isoform-specific inhibitory domain regulates the LHX3 LIM
RT homeodomain factor holoprotein and the production of a functional
RT alternate translation form."
RL J. Biol. Chem. 276:36311-36319(2001).
RL EMBL; AF370445; AAL09570.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
KW Nuclear protein.
FT NON TER 34
SQ SEQUENCE 34 AA; 3748 MW; 7083C3258F8E414C CRC64;

Query Match 100.0%; Score 20; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 26 REDL 29

RESULT 7

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Mon Mar 20 08:51:25 2006

us-09-673-707-10.rup

Q9UQY7 TRAVE  
ID Q9UQY7 TRAVE PRELIMINARY; PRT; 35 AA.  
AC Q9UQY7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)  
DE Lignin peroxidase isoenzyme TVLP15 (Fragment).  
OS Trametes versicolor (White-rot fungus) (Coriolus versicolor).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Aphyllophorales; Trametes.  
OX NCBI\_TaxID=5325;  
RN [1]  
RP PROTEIN SEQUENCE. PubMed=8424691; DOI=10.1006/abbi.1993.1008;  
RX MEDLINE=9343365; Wellinder K.G., Nyman P.O.;  
RA Johansson T., Lindner K.G., Nyman P.O.;  
RT "Isozymes of lignin peroxidase and manganese(II) peroxidase from the  
white-rot basidiomycete Trametes versicolor. II. Partial sequences,  
peptide maps, and amino acid and carbohydrate compositions.";  
RL Arch. Biochem. Biophys. 300:57-62(1993).  
DR PIR; S29728; S29728.  
DR HSP; P11542; IQPA.  
SQ SEQUENCE 35 AA; 3680 MW; B497C9618EC1FDD7 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 22 REDL 25

RESULT 8  
Q570E3 ARATH  
ID Q570E3 ARATH PRELIMINARY; PRT; 35 AA.  
AC Q570E3;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Tubulin alpha-2/alpha-4 chain (Fragment).  
GN Name=At1g04820;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Toki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,  
RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,  
RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,  
RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,  
RA Havaehizaki Y., Shinozaki K.;  
RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK220765; BAD3966.1; -; mRNA.  
FT NON TER 1  
SQ SEQUENCE 35 AA; 3941 MW; BA65FC4A2584DA9C CRC64;

Query Match 100.0%; Score 20; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 7 REDL 10

RESULT 9  
Q5NQJ6 ZYMMO  
ID Q5NQJ6 ZYMMO PRELIMINARY; PRT; 35 AA.  
AC Q5NQJ6;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames=ZMO0384;  
OS Zymomonas mobilis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
OC Sphingomonadaceae; Zymomonas.  
OX NCBI\_TaxID=542;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX STRAIN=ATCC 31821 / ZM4 / CP4;  
PubMed=15592456; DOI=10.1038/nbt1045;  
RA Seo J.-S., Chong H., Park H.-S., Yoon K.-O., Jung C., Kim J.-J.,  
RA Hong J.-H., Kim J.-H., Kil J.-I., Park C.-J., Oh H.-M.,  
RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.-Y.,  
RA Kang H.-L., Lee S.-Y., Lee K.-J., Kang H.-S.;  
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis  
ZM4.";  
RL Nat. Biotechnol. 23:63-68(2005).  
DR EMBL; AE008692; AA89008.1; -; Genomic DNA.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 35 AA; 3855 MW; 51DC67425C928BBE CRC64;

Query Match 100.0%; Score 20; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 17 REDL 20

RESULT 10  
Q9QW57 9MURI  
ID Q9QW57 9MURI PRELIMINARY; PRT; 36 AA.  
AC Q9QW57;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE HES-1=HOMEODOMAIN protein.  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93087202; PubMed=1360650;  
RA Thomas P.O., Rathjen P.D.;  
RT "HES-1, a novel homeobox gene expressed by murine embryonic stem  
cells, identifies a new class of homeobox genes.";  
RL Nucleic Acids Res. 20:5840-5840(1992).  
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR012287; Homeodomain-rel.  
DR Pfam; PF00045; Homeobox; 1.  
DR ProDom; PD000010; Homeobox; 1.  
DR PROSITE; PS00071; HOMEBOX\_2; 1.  
KW DNA-binding; Homeobox; Nuclear protein; Transcription;  
KW Transcription regulation.  
SQ SEQUENCE 36 AA; 4262 MW; AEB316C35D10CC13 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
Db 23 REDL 26

RESULT 11  
 Q56Y22 ARATH PRELIMINARY; PRT; 38 AA.  
 AC Q56Y22;  
 DT 10-MAY-2005 (TRENBLrel. 30, Created)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)  
 DE Tubulin alpha-2/alpha-4 chain.  
 GN Name=Atlg04820;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Totski Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,  
 RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,  
 RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,  
 RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.;  
 RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK221178; BAD95252.1; -, mRNA.  
 SQ SEQUENCE 38 AA; 4258 MW; 2365FF71BC99EFF5 CRC64;  
 Query Match 100.0%; Score 20; DB 2; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 REDL 4  
 Db 10 REDL 13

RESULT 12  
 O19688 HUMAN PRELIMINARY; PRT; 39 AA.  
 AC O19688;  
 DT 01-JAN-1998 (TRENBLrel. 05, Created)  
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE HLA-B27 variant exon 2 (Alpha domain) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Blaszyk R., Weber M., Salama A.;  
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X83727; CAA58698.1; -, Genomic DNA.  
 DR GO; GO:0042612; C:MHC class I protein complex; IEA.  
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.  
 DR GO; GO:0019882; P:antigen presentation; IEA.  
 DR InterPro; IPR001039; MHC\_1\_alpha\_A1A2.  
 DR Pfam; PF00129; MHC\_1; 1.  
 DR ProDom; PD009050; MHC\_1; 1.  
 FT NON TER 1  
 FT NON TER 39  
 SQ SEQUENCE 39 AA; 4748 MW; F5E3FD2A53138508 CRC64;  
 Query Match 100.0%; Score 20; DB 2; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 REDL 4  
 Db 24 REDL 27

RESULT 13  
 O61645 APLCA PRELIMINARY; PRT; 39 AA.  
 AC O61645;  
 DT 01-AUG-1998 (TRENBLrel. 07, Created)  
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Alpha-tubulin (Fragment).  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspiidea;  
 OC Aplysioidea; Aplysiidae; Aplysia.  
 OX NCBI\_TaxID=6500;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sung Y.J., Zhu D.F., Ambron R.T.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF055329; AAC12647.1; -, mRNA.  
 DR GO; GO:0005874; C:microtubule; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0007018; P:microtubule-based movement; IEA.  
 DR InterPro; IPR002452; Alpha\_tubulin.  
 DR PANTHER; PTHR11588:SF1; Alpha\_tubulin; 1.  
 FT NON TER 1  
 SQ SEQUENCE 39 AA; 4393 MW; 0D3A0EB30DFC29AF CRC64;  
 Query Match 100.0%; Score 20; DB 2; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 REDL 4  
 Db 9 REDL 12

RESULT 14  
 Q8MTM6\_9DIPT PRELIMINARY; PRT; 39 AA.  
 AC Q8MTM6;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE EIF5A (Fragment).  
 OS Culicoides sonorensis.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;  
 OC Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.  
 OX NCBI\_TaxID=179676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=22309032; PubMed=12421417;  
 RA Campbell C.L., Wilson W.C.;  
 RT "Differentially expressed midgut transcripts in Culicoides sonorensis  
 (Diptera: ceratopogonidae) following Orbivirus (reoviridae) oral  
 feeding.";  
 RL Insect Mol. Biol. 11:595-604(2002).  
 DR EMBL; AY095267; AM28346.1; -, mRNA.  
 DR GO; GO:0003743; F:translation initiation factor activity; IEA.  
 DR GO; GO:0006413; P:translational initiation; IEA.  
 DR InterPro; IPR001884; EIF5A\_hypusine.  
 DR Pfam; PF01287; eIF-5a; 1.  
 FT NON TER 1  
 FT NON TER 39  
 SQ SEQUENCE 39 AA; 4461 MW; 0C68CB2813C539D3 CRC64;  
 Query Match 100.0%; Score 20; DB 2; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 REDL 4  
 Db 28 REDL 31

|   |  |                       |                    |                  |               |               |
|---|--|-----------------------|--------------------|------------------|---------------|---------------|
| RESULT 15   |  | Query Match           | 100.0%;            | Score 20;        | DB 2;         | Length 41;    |
| Q74264_9HIV1  |  | Best Local Similarity | 100.0%;            | Pred. No. 1e+03; | 0;            | Indels 0;     |
| ID Q74264_9HIV1 PRELIMINARY;  |  | Matches               | 4;                 | Conservative     | 0;            | Mismatches 0; |
| AC Q74264;  |  |                       |                    |                  |               | Gaps 0;       |
| DT 01-NOV-1996 (TrEMBLrel. 01, Created)                                   |  |                       |                    |                  |               |               |
| DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)                      |  |                       |                    |                  |               |               |
| DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)                    |  |                       |                    |                  |               |               |
| DE Reverse transcriptase (Fragment).                                      |  |                       |                    |                  |               |               |
| GN Name-pol;  |  |                       |                    |                  |               |               |
| OS Human immunodeficiency virus 1.  |  |                       |                    |                  |               |               |
| OC Viruses; Retroid viruses; Retroviridae; Lentivirus;                    |  |                       |                    |                  |               |               |
| OC Primate lentivirus group.  |  |                       |                    |                  |               |               |
| OC NCBI_TaxID=11676;  |  |                       |                    |                  |               |               |
| RN [1]  |  |                       |                    |                  |               |               |
| RP NUCLEOTIDE SEQUENCE.   |  |                       |                    |                  |               |               |
| RX MEDLINE=97000986; PubMed=8844016;                                      |  |                       |                    |                  |               |               |
| RA Quinones-Mateu M.E., Holguin A., Dopazo J., Najera I., Domingo E.;     |  |                       |                    |                  |               |               |
| RT "Point mutant frequencies in the pol gene of human immunodeficiency    |  |                       |                    |                  |               |               |
| RT virus type 1 are two- to threefold lower than those of env.";          |  |                       |                    |                  |               |               |
| RL AIDS Res. Hum. Retroviruses 12:1117-1128(1996).                        |  |                       |                    |                  |               |               |
| RN [2]  |  |                       |                    |                  |               |               |
| RP NUCLEOTIDE SEQUENCE.   |  |                       |                    |                  |               |               |
| RX MEDLINE=95074869; PubMed=7983713;                                      |  |                       |                    |                  |               |               |
| RA Najera I., Holguin A., Quinones-Mateu M.E., Munoz-Fernandez M.A.,      |  |                       |                    |                  |               |               |
| RA Najera R., Lopez-Galindez C., Domingo E.;                              |  |                       |                    |                  |               |               |
| RT "Pol gene quasiespecies of human immunodeficiency virus: mutations     |  |                       |                    |                  |               |               |
| RT associated with drug resistance in virus from patients undergoing no   |  |                       |                    |                  |               |               |
| RT drug therapy.";  |  |                       |                    |                  |               |               |
| RL J. Virol. 69:23-31(1995).  |  |                       |                    |                  |               |               |
| DR EMBL; U14893; AAC55799.1; -; Genomic_DNA.                              |  |                       |                    |                  |               |               |
| DR GO; GO:0003723; F:RNA binding; IEA.                                    |  |                       |                    |                  |               |               |
| DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.           |  |                       |                    |                  |               |               |
| DR GO; GO:0016740; F:transferase activity; IEA.                           |  |                       |                    |                  |               |               |
| DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.                  |  |                       |                    |                  |               |               |
| DR InterPro: IPR000477; RVTse.  |  |                       |                    |                  |               |               |
| KW RNA-directed DNA polymerase.   |  |                       |                    |                  |               |               |
| FT NON_TER 1  |  |                       |                    |                  |               |               |
| FT NON_TER 39   |  |                       |                    |                  |               |               |
| SQ SEQUENCE 39 AA; 4754 MW; 487862AD9B905DAF CRC64;                       |  |                       |                    |                  |               |               |
| Query Match   |  | 100.0%;               | Score 20;          | DB 2;            | Length 39;    |               |
| Best Local Similarity   |  | 100.0%;               | Pred. No. 9.8e+02; |                  |               |               |
| Matches   |  | 4;                    | Conservative       | 0;               | Mismatches 0; | Indels 0;     |
| Gaps  |  |                       |                    |                  |               |               |
| Qy  |  | 1 REDL 4              |                    |                  |               |               |
| Db  |  | 22 REDL 25            |                    |                  |               |               |
| RESULT 16   |  |                       |                    |                  |               |               |
| Q9UW29_9PEZI  |  | Query Match           | 100.0%;            | Score 20;        | DB 2;         | Length 41;    |
| ID Q9UW29_9PEZI PRELIMINARY;  |  | Best Local Similarity | 100.0%;            | Pred. No. 1e+03; |               |               |
| AC Q9UW29;  |  | Matches               | 4;                 | Conservative     | 0;            | Mismatches 0; |
| DT 01-MAY-2000 (TrEMBLrel. 13, Created)                                   |  |                       |                    |                  |               | Gaps 0;       |
| DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)                      |  |                       |                    |                  |               |               |
| DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)                    |  |                       |                    |                  |               |               |
| DE MAT-2 HMG box protein (Fragment).                                      |  |                       |                    |                  |               |               |
| OS Ceratocystis pinicola.   |  |                       |                    |                  |               |               |
| OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;         |  |                       |                    |                  |               |               |
| OC Hypocromycetidae; Microascales; Microascales incertae sedis;           |  |                       |                    |                  |               |               |
| OC Ceratocystis.  |  |                       |                    |                  |               |               |
| OX NCBI_TaxID=72031;  |  |                       |                    |                  |               |               |
| RN [1]  |  |                       |                    |                  |               |               |
| RP NUCLEOTIDE SEQUENCE.   |  |                       |                    |                  |               |               |
| RC STRAIN=C795;   |  |                       |                    |                  |               |               |
| RA Withuhn R., Harrington T., Steimel J., Wingfield B., Wingfield M.;     |  |                       |                    |                  |               |               |
| RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.                |  |                       |                    |                  |               |               |
| DR EMBL; AF164194; AAD48810.1; -; Genomic_DNA.                            |  |                       |                    |                  |               |               |
| FT NON_TER 1  |  |                       |                    |                  |               |               |
| FT NON_TER 41   |  |                       |                    |                  |               |               |
| SQ SEQUENCE 41 AA; 4848 MW; 6A29093D521ADC59 CRC64;                       |  |                       |                    |                  |               |               |
| Query Match   |  | 100.0%;               | Score 20;          | DB 2;            | Length 41;    |               |
| Best Local Similarity   |  | 100.0%;               | Pred. No. 1e+03;   |                  |               |               |
| Matches   |  | 4;                    | Conservative       | 0;               | Mismatches 0; | Indels 0;     |
| Gaps  |  |                       |                    |                  |               |               |
| Qy  |  | 1 REDL 4              |                    |                  |               |               |
| Db  |  | 22 REDL 25            |                    |                  |               |               |
| RESULT 17   |  |                       |                    |                  |               |               |
| Q8CH67_MOUSE  |  | Query Match           | 100.0%;            | Score 20;        | DB 2;         | Length 41;    |
| ID Q8CH67_MOUSE PRELIMINARY;  |  | Best Local Similarity | 100.0%;            | Pred. No. 1e+03; |               |               |
| AC Q8CH67;  |  | Matches               | 4;                 | Conservative     | 0;            | Mismatches 0; |
| DT 01-MAR-2003 (TrEMBLrel. 23, Created)                                   |  |                       |                    |                  |               | Gaps 0;       |
| DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)                      |  |                       |                    |                  |               |               |
| DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)                    |  |                       |                    |                  |               |               |
| DE Eukaryotic initiation factor 5A isoform II (Fragment).                 |  |                       |                    |                  |               |               |
| GN Name=Elf5a2;   |  |                       |                    |                  |               |               |
| OS Mus musculus (Mouse).  |  |                       |                    |                  |               |               |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |  |                       |                    |                  |               |               |
| OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  |  |                       |                    |                  |               |               |
| OC Muridae; Murinae; Mus.   |  |                       |                    |                  |               |               |
| OX NCBI_TaxID=10090;  |  |                       |                    |                  |               |               |
| RN [1]  |  |                       |                    |                  |               |               |
| RP NUCLEOTIDE SEQUENCE.   |  |                       |                    |                  |               |               |
| RC STRAIN=BALB/c;   |  |                       |                    |                  |               |               |
| RX MEDLINE=21100881; PubMed=11161802; DOI=10.1006/geno.2000.6418;         |  |                       |                    |                  |               |               |
| RA Jenkins Z.A., Haag P.G., Johansson H.E.;                               |  |                       |                    |                  |               |               |
| RT "human eIF5A2 on chromosome 3q25-q27 is a phylogenetically conserved   |  |                       |                    |                  |               |               |
| RT vertebrate variant of eukaryotic translation initiation factor 5A with |  |                       |                    |                  |               |               |
| RT tissue-specific expression.";  |  |                       |                    |                  |               |               |
| RL Genomics 71:101-109(2001).   |  |                       |                    |                  |               |               |
| RN [2]  |  |                       |                    |                  |               |               |
| RP NUCLEOTIDE SEQUENCE.   |  |                       |                    |                  |               |               |
| RC STRAIN=BALB/c;   |  |                       |                    |                  |               |               |
| RA Jenkins Z.A., Haag P.G., Johansson H.E.;                               |  |                       |                    |                  |               |               |
| RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.                |  |                       |                    |                  |               |               |
| DR EMBL; AF377869; AA017899.1; -; Genomic_DNA.                            |  |                       |                    |                  |               |               |
| DR GO; GO:0003743; F:translation initiation factor activity; IEA.         |  |                       |                    |                  |               |               |
| DR GO; GO:0006413; P:translational initiation; IEA.                       |  |                       |                    |                  |               |               |
| DR InterPro: IPR001884; EIF5A_hypusine.                                   |  |                       |                    |                  |               |               |
| DR Pfam; PF01287; eIF-5a; 1.  |  |                       |                    |                  |               |               |
| KW Initiation factor.   |  |                       |                    |                  |               |               |
| FT NON_TER 1  |  |                       |                    |                  |               |               |
| FT NON_TER 41   |  |                       |                    |                  |               |               |
| SQ SEQUENCE 41 AA; 4438 MW; E27B44C07A1C9622 CRC64;                       |  |                       |                    |                  |               |               |
| Query Match   |  | 100.0%;               | Score 20;          | DB 2;            | Length 41;    |               |
| Best Local Similarity   |  | 100.0%;               | Pred. No. 1e+03;   |                  |               |               |
| Matches   |  | 4;                    | Conservative       | 0;               | Mismatches 0; | Indels 0;     |
| Gaps  |  |                       |                    |                  |               |               |
| Qy  |  | 1 REDL 4              |                    |                  |               |               |
| Db  |  | 10 REDL 13            |                    |                  |               |               |
| RESULT 18   |  |                       |                    |                  |               |               |
| Q8NWC5_PONPY  |  | Query Match           | 100.0%;            | Score 20;        | DB 2;         | Length 41;    |
| ID Q8NWC5_PONPY PRELIMINARY;  |  | Best Local Similarity | 100.0%;            | Pred. No. 1e+03; |               |               |
| AC Q8NWC5;  |  | Matches               | 4;                 | Conservative     | 0;            | Mismatches 0; |
| DT 01-MAR-2002 (TrEMBLrel. 20, Created)                                   |  |                       |                    |                  |               | Gaps 0;       |
| DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)                      |  |                       |                    |                  |               |               |
| DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)                    |  |                       |                    |                  |               |               |
| DE NPIP-like protein (Fragment).  |  |                       |                    |                  |               |               |
| OS Pongo pygmaeus (Orangutan).  |  |                       |                    |                  |               |               |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |  |                       |                    |                  |               |               |
| OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; |  |                       |                    |                  |               |               |
| OC Pongo.   |  |                       |                    |                  |               |               |
| OX NCBI_TaxID=9600;   |  |                       |                    |                  |               |               |
| RN [1]  |  |                       |                    |                  |               |               |
| RP NUCLEOTIDE SEQUENCE.   |  |                       |                    |                  |               |               |
| RX MEDLINE=21470411; PubMed=11586358; DOI=10.1038/35097067;               |  |                       |                    |                  |               |               |
| RA Johnson M.E., Viggiano L., Bailey J.A., Abdul-Rauf M., Goodwin G.,     |  |                       |                    |                  |               |               |

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RA Rocchi M., Eichler E.E.;
RT "Positive selection of a gene family during the emergence of humans
RL Nature 413:514-519(2001).
DR EMBL; AF364210; AAL50437.1; -; Genomic_DNA.
DR EMBL; AF364215; AAL50447.1; -; Genomic_DNA.
DR InterPro; IPR009443; NPIP.
DR Pfam; PF06409; NPIP; 1.
DR NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5332 MW; EEB122D84370E988 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 5 REDL 8

RESULT 19
Q8WN16_HYLKL PRELIMINARY; PRT; 45 AA.
AC Q8WN16;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE NPIP-like protein (Fragment).
OS Hylobates klossii (Kloss's gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Hylobatidae; Hylobates.
OC NCBI_TaxID=9587;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21470411; PubMed=11586358; DOI=10.1038/35097067;
RA Johnson M.E., Viggiano L., Bailey J.A., Abdul-Rauf M., Goodwin G.,
RA Rocchi M., Eichler E.E.;
RT "Positive selection of a gene family during the emergence of humans
RL Nature 413:514-519(2001).
DR EMBL; AF364217; AAL50451.1; -; Genomic_DNA.
DR InterPro; IPR009443; NPIP.
DR Pfam; PF06409; NPIP; 1.
DR NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5404 MW; EEB294384370E988 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 5 REDL 8

RESULT 20
Q84U35_9ASPA PRELIMINARY; PRT; 45 AA.
AC Q84U35;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE MYB19 (Fragment).
GN Name=MYB19;
OS Dendrobium sp. XWV-2002-19.
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Dendrobieae; Dendrobiinae;
OC Dendrobium.
OC NCBI_TaxID=217465;

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RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22661209; PubMed=12777054; DOI=10.1023/A:1023050110077;
RA Wu X.-M., Lim S.-H., Yang W.-C.;
RT "Characterization, expression and phylogenetic study of R2R3-MYB genes
RL in orchid.";
RL Plant Mol. Biol. 51:959-972(2003).
DR EMBL; AF485910; AAO49428.1; -; mRNA.
DR HSSP; P06876; 1GV2.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; MYB_DNA_bd.
DR PROSITE; PS50090; MYB_3; 1.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5286 MW; E7348A72534C36C9 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 8 REDL 11

RESULT 21
Q9GT46_ANOGA PRELIMINARY; PRT; 46 AA.
AC Q9GT46;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Ribosomal protein S18 (Fragment).
GN Name=IrpS18;
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OC NCBI_TaxID=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=G3;
RC MEDLINE=20481919; PubMed=11005829; DOI=10.1073/pnas.180060997;
RA Oduol F., Xu J., Niare O., Natarajan R., Vernick K.D.;
RT "Genes identified by an expression screen of the vector mosquito
RT Anopheles gambiae display differential molecular immune response to
RT malaria parasites and bacteria.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:11397-11402(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G3;
RA Oduol F.O., Xu J., Niare O., Natarajan R., Vernick K.D.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribosomal protein S13p family.
DR EMBL; AF283268; AAC15373.1; -; mRNA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001892; Ribosomal_S13.
DR Pfam; PF00416; Ribosomal_S13; 1.
DR PROSITE; PS00646; RIBOSOMAL_S13_1; 1.
DR PROSITE; PS0159; RIBOSOMAL_S13_2; 1.
KW Ribonucleoprotein; Ribosomal protein.
FT NON_TER 1
SQ SEQUENCE 46 AA; 5519 MW; 0B91AEB7D54EFA85 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DR TIGR; PSPT03546; -;  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 47 AA; 5258 MW; 935E23600334F315 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 47;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
|||  
Db 2 REDL 5

RESULT 22  
Q8WNH3 CERAE  
ID Q8WNH3\_CERAE PRELIMINARY; PRT; 46 AA.  
AC Q8WNH3;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE NPIP-like protein (Fragment).  
OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopitheciidae; Cercopithecinae; Cercopithecus.  
NCBI\_TaxID=9534;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21470411; PubMed=11586358; DOI=10.1038/35097067;  
RA Johnson M.E., Viggiano L., Bailey J.A., Abdul-Rauf M., Goodwin G.,  
RA Rocchi M., Eichler E.E.;  
RT "Positive selection of a gene family during the emergence of humans  
RT and African apes";  
RL Nature 413:514-519(2001).  
DR EMBL; AF364227; AAL50471.1; -; Genomic\_DNA.  
DR InterPro; IPR009443; NPIP.  
DR Pfam; PF06409; NPIP; 1.  
FT NON\_TER 1  
FT TER 46  
SQ SEQUENCE 46 AA; 5429 MW; E552A244F6B0A333 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4  
|||  
Db 5 REDL 8

RESULT 23  
Q87284\_PSESM  
ID Q87284\_PSESM PRELIMINARY; PRT; 47 AA.  
AC Q87284;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocuNames=PSPT03546;  
OS Pseudomonas syringae (pv. tomato).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
NCBI\_TaxID=323;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=DC3000;  
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;  
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,  
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,  
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,  
RA Nelson W.C., Davidse T.M., Zafar N., Zhou L., Liu J., Yuan Q.,  
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,  
RA Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,  
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,  
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,  
RA Bender C.L., White O., Fraser C.M., Collier A.;  
RT "The complete genome sequence of the Arabidopsis and tomato pathogen  
RT Pseudomonas syringae pv. tomato DC3000";  
Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).  
DR EMBL; AE016853; AA057021.1; -; Genomic DNA.



DR GO; GO:0042612; C:MHC class I protein complex; IEA.  
 DR GO; GO:0030106; P:MHC class I receptor activity; IEA.  
 DR GO; GO:0019882; P:antigen presentation; IEA.  
 DR InterPro; IPR001039; MHC\_I\_alpha\_A1A2.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR ProDom; PD000050; MHC\_I; 1.  
 FT NON\_TER 1  
 FT NON\_TER 49  
 SQ SEQUENCE 49 AA; 5983 MW; BDFE863415FF2B5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 42 REDL 45

## RESULT 26

ID Q7YQ55 PHOSS PRELIMINARY; PRT; 49 AA.  
 AC Q7YQ55  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MHC class I antigen alpha 1 subunit (Fragment).  
 GN Name=Phsi;  
 OS Phocoena sinus (Vaquita).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;  
 OC Odontoceti; Phocoenidae; Phocoena.  
 OX NCBI\_TaxID=42100;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Munguia-Vega A.; Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,  
 RA Rojas-Bracho L.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY170895; AAO17683.1; -; Genomic\_DNA.  
 DR SMR; Q7YQ55; 1-49.  
 DR GO; GO:0042612; C:MHC class I protein complex; IEA.  
 DR GO; GO:0030106; P:MHC class I receptor activity; IEA.  
 DR InterPro; IPR001039; MHC\_I\_alpha\_A1A2.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR ProDom; PD000050; MHC\_I; 1.  
 FT NON\_TER 1  
 FT NON\_TER 49  
 SQ SEQUENCE 49 AA; 6010 MW; BDFE94A415FF2B5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 42 REDL 45

## RESULT 27

ID Q7YQ56 PHOSS PRELIMINARY; PRT; 49 AA.  
 AC Q7YQ56  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MHC class I antigen alpha 1 subunit (Fragment).

GN Name=Phsi;  
 OS Phocoena sinus (Vaquita).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;  
 OC Odontoceti; Phocoenidae; Phocoena.  
 OX NCBI\_TaxID=42100;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Munguia-Vega A.; Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,  
 RA Rojas-Bracho L.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY170894; AAO17682.1; -; Genomic\_DNA.  
 DR SMR; Q7YQ56; 1-49.  
 DR GO; GO:0042612; C:MHC class I protein complex; IEA.  
 DR GO; GO:0030106; P:MHC class I receptor activity; IEA.  
 DR InterPro; IPR001039; MHC\_I\_alpha\_A1A2.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR ProDom; PD000050; MHC\_I; 1.  
 FT NON\_TER 1  
 FT NON\_TER 49  
 SQ SEQUENCE 49 AA; 5953 MW; AFCEA53415FF2B5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 42 REDL 45

## RESULT 28

ID Q7YQ57 PHOSS PRELIMINARY; PRT; 49 AA.  
 AC Q7YQ57  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MHC class I antigen alpha 1 subunit (Fragment).  
 GN Name=Phsi;  
 OS Phocoena sinus (Vaquita).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;  
 OC Odontoceti; Phocoenidae; Phocoena.  
 OX NCBI\_TaxID=42100;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Munguia-Vega A.; Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,  
 RA Rojas-Bracho L.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY170893; AAO17681.1; -; Genomic\_DNA.  
 DR SMR; Q7YQ57; 1-49.  
 DR GO; GO:0042612; C:MHC class I protein complex; IEA.  
 DR GO; GO:0030106; P:MHC class I receptor activity; IEA.  
 DR InterPro; IPR001039; MHC\_I\_alpha\_A1A2.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR ProDom; PD000050; MHC\_I; 1.  
 FT NON\_TER 1  
 FT NON\_TER 49

Query Match 100.0%; Score 20; DB 2; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
 Db 42 REDL 45

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SQ SEQUENCE 49 AA; 5983 MW; BDFE863415FF2B5B CRC64;
Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 42 REDL 45

RESULT 29
Q7YQ58 PHOSS
ID Q7YQ58 PHOSS PRELIMINARY; PRT; 49 AA.
AC Q7YQ58;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MHC class I antigen alpha 1 subunit (Fragment).
DE Name=Phsi;
GN Phocoena sinus (Vaquita).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Phocoenidae; Phocoena.
OX NCBI_TaxID=42100;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Munguia-Vega A.;
RT "Study of the major histocompatibility complex in the evolutionary and
demographic history of the porpoise (Phocoena sinus).";
Thesis (2003), CIBNOR, La Paz, BCS, Mexico, In press.
[2]
RA Munguia-Vega A., Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,
Rojas-Bracho L.;
RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY170891; AA017679.1; -; Genomic_DNA.
DR SMR; Q7YQ58; 1-49.
DR GO; GO:0042612; C:MHC class I protein complex; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019882; P:antigen presentation; IEA.
DR InterPro; IPR001039; MHC_I_alpha_A1A2.
DR Pfam; PF00129; MHC_I; 1.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5848 MW; BDF6243419093F5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 42 REDL 45

RESULT 30
Q7YQ59 PHOSS
ID Q7YQ59 PHOSS PRELIMINARY; PRT; 49 AA.
AC Q7YQ59;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MHC class I antigen alpha 1 subunit (Fragment).
DE Name=Phsi;
GN Phocoena sinus (Vaquita).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Phocoenidae; Phocoena.
OX NCBI_TaxID=42100;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Munguia-Vega A.;
RT "Study of the major histocompatibility complex in the evolutionary and
demographic history of the porpoise (Phocoena sinus).";
Thesis (2003), CIBNOR, La Paz, BCS, Mexico, In press.
[2]
RA Munguia-Vega A., Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,
Rojas-Bracho L.;
RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY170892; AA017680.1; -; Genomic_DNA.
DR SMR; Q7YQ58; 1-49.
DR GO; GO:0042612; C:MHC class I protein complex; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019882; P:antigen presentation; IEA.
DR InterPro; IPR001039; MHC_I_alpha_A1A2.
DR Pfam; PF00129; MHC_I; 1.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5848 MW; BDF6243419093F5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 42 REDL 45

RESULT 31
Q7YQ60 PHOSS
ID Q7YQ60 PHOSS PRELIMINARY; PRT; 49 AA.
AC Q7YQ60;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MHC class I antigen alpha 1 subunit (Fragment).
DE Name=Phsi;
GN Phocoena sinus (Vaquita).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Phocoenidae; Phocoena.
OX NCBI_TaxID=42100;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Munguia-Vega A.;
RT "Study of the major histocompatibility complex in the evolutionary and
demographic history of the porpoise (Phocoena sinus).";
Thesis (2003), CIBNOR, La Paz, BCS, Mexico, In press.
[2]
RA Munguia-Vega A., Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,
Rojas-Bracho L.;
RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY170890; AA017678.1; -; Genomic_DNA.
DR SMR; Q7YQ60; 1-49.
DR GO; GO:0042612; C:MHC class I protein complex; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019882; P:antigen presentation; IEA.
DR InterPro; IPR001039; MHC_I_alpha_A1A2.
DR Pfam; PF00129; MHC_I; 1.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5983 MW; BDFE863415FF2B5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 42 REDL 45

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RA Munguia-Vega A.;
RT "Study of the major histocompatibility complex in the evolutionary and
demographic history of the porpoise (Phocoena sinus).";
Thesis (2003), CIBNOR, La Paz, BCS, Mexico, In press.
[2]
RA Munguia-Vega A., Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,
Rojas-Bracho L.;
RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY170891; AA017679.1; -; Genomic_DNA.
DR SMR; Q7YQ59; 1-49.
DR GO; GO:0042612; C:MHC class I protein complex; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019882; P:antigen presentation; IEA.
DR InterPro; IPR001039; MHC_I_alpha_A1A2.
DR Pfam; PF00129; MHC_I; 1.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5954 MW; BDFE8634128F5C5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 42 REDL 45

RESULT 31
Q7YQ60 PHOSS
ID Q7YQ60 PHOSS PRELIMINARY; PRT; 49 AA.
AC Q7YQ60;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MHC class I antigen alpha 1 subunit (Fragment).
DE Name=Phsi;
GN Phocoena sinus (Vaquita).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Phocoenidae; Phocoena.
OX NCBI_TaxID=42100;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Munguia-Vega A.;
RT "Study of the major histocompatibility complex in the evolutionary and
demographic history of the porpoise (Phocoena sinus).";
Thesis (2003), CIBNOR, La Paz, BCS, Mexico, In press.
[2]
RA Munguia-Vega A., Flores-Ramirez S.F., Vazquez-Juarez R., Miller R.D.,
Rojas-Bracho L.;
RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY170890; AA017678.1; -; Genomic_DNA.
DR SMR; Q7YQ60; 1-49.
DR GO; GO:0042612; C:MHC class I protein complex; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019882; P:antigen presentation; IEA.
DR InterPro; IPR001039; MHC_I_alpha_A1A2.
DR Pfam; PF00129; MHC_I; 1.
DR ProDom; PD000050; MHC_I; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5983 MW; BDFE863415FF2B5B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDL 4
DB 42 REDL 45

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Db          42 REDL 45

RESULT 32
Q4ZR70_PSESY PRELIMINARY; PRT; 49 AA.
AC Q4ZR70;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Psyr_3320;
OS Pseudomonas syringae pv. syringae B728a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RG DOE Joint Genome Institute;
RA Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S.,
RA Nolan M., Goltzman E., Thiel J., Malfatti S., Lapidus A., Detter J.C.,
RA Land M., Richardson P.M., Kyripides N.C., Ivanova N.;
RT "Comparison of two complete genome sequences of Pseudomonas syringae
RT pv. syringae B728a and pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Loper J.;
RN Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Feil H., Feil W.S., Lindow S.E.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000075; AAY38352.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 49 AA; 5403 MW; 2989483E23600334 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 REDL 4
Db 7 REDL 10

RESULT 33
TBA_BLEJA STANDARD; PRT; 50 AA.
AC Q08628;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tubulin alpha chain (Fragment).
OS Blepharisma japonicum.
OC Eukaryota; Alveolata; Ciliophora; Heterotriches; Heterotrichida;
OC Blepharismidae; Blepharisma.
OX NCBI_TaxID=5961;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9328144; PubMed=7685500;
RA Liang A., Heckmann K.;
RT "Blepharisma uses UAA as a termination codon.";
RL Naturwissenschaften 80:225-226(1993).
CC -!- FUNCTION: Tubulin is the major constituent of microtubules. It
CC binds two moles of GTP, one at an exchangeable site on the beta
CC chain and one at a nonexchangeable site on the alpha-chain.
CC -!- SUBUNIT: Dimer of alpha and beta chains.
CC -!- SIMILARITY: Belongs to the tubulin family.

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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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DR EMBL; S62518; AAB27144.1; -; mRNA.
DR PIR; S36687; S36687.
DR InterPro; IPR002452; Alpha tubulin.
DR InterPro; IPR000217; Tubulin.
DR PANTHER; PTHR11588:SF1; Alpha tubulin; 1.
DR PANTHER; PTHR11588; Tubulin; 1.
DR PROSITE; PS00227; TUBULIN; PARTIAL.
KW GTP-binding; Microtubule; Nucleotide-binding.
FT NON TER 1
SQ SEQUENCE 50 AA; 5659 MW; 3749548FCEA9E3F9 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 REDL 4
Db 19 REDL 22

RESULT 34
Q4X611_PLACH PRELIMINARY; PRT; 50 AA.
ID Q4X611;
AC Q4X611;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC302493.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the ribosomal protein S13P family.
DR EMBL; CAJ01009502; CAH87495.1; -; Genomic_DNA.
DR InterPro; IPR001892; Ribosomal S13.
DR ProDom; PD001363; Ribosomal S13.
DR PROSITE; PS00646; RIBOSOMAL_S13_1; 1.
DR PROSITE; PS00159; RIBOSOMAL_S13_2; 1.
KW Hypothetical protein; Ribonucleoprotein; Ribosomal protein.
FT NON TER 1
SQ SEQUENCE 50 AA; 5889 MW; DE05635A6A3419ED CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 REDL 4
Db 4 REDL 7

RESULT 35
Q7ZT89_CARAU

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Db 23 REDL 26

RESULT 37

Q8NFF0 HUMAN

ID Q8NFF0 HUMAN PRELIMINARY; PRT; 51 AA.

AC Q8NFF0;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Small testis-specific peroxisomal protein.

GN Name=PX11; Synonyms=Stiepp;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Testis;

RA Burfeind P., Burfeind C., Preuss T., Mannan A., Voigt S., Neesen J.R.,

RL Dixkens C., Engel W.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF466827; AAN03789.1; -; mRNA.

DR Ensembl; ENSG00000179165; Homo sapiens.

DR HGNC; HGNC:18312; PX11.

SQ SEQUENCE 51 AA; 6394 MW; 094DCA6D5E27473 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 51;

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

QY 1 REDL 4

DB 16 REDL 19

RESULT 38

Q7LZL4 XENLA

ID Q7LZL4 XENLA PRELIMINARY; PRT; 51 AA.

AC Q7LZL4;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Ribosomal protein S18, cytosolic (Fragment).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.

OX NCBI\_TaxID=8355;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Grossberger D., Flajnik M., Marcus A.;

RT "Ribosomal and chromosomal protein cDNA clones of Xenopus laevis

RT thymus isolated with differential screening.";

RL Comp. Biochem. Physiol. 98:127-133(1991).

CC -1- SIMILARITY: Belongs to the ribosomal protein S13P family.

DR PIR; C61510; C61510.

DR GO; GO:0005840; C:ribosome; IEA.

DR GO; GO:0003723; F:RNA binding; IEA.

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

DR GO; GO:0006412; P:protein biosynthesis; IEA.

DR InterPro; IPR001892; Ribosomal\_S13.

DR Pfam; PF00416; Ribosomal\_S13; I.

DR ProDom; PD001363; Ribosomal\_S13; 1.

DR PROSITE; PS00159; RIBOSOMAL\_S13\_2; 1.

KW Ribonucleoprotein; Ribosomal protein.

FT NON\_TER 1

FT NON\_TER 51

SQ SEQUENCE 51 AA; 5967 MW; 4A1A828762D92B03 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 51;

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

QY 1 REDL 4

DB 31 REDL 34

RESULT 36

Q64BT2 9ARCH

ID Q64BT2 9ARCH PRELIMINARY; PRT; 51 AA.

AC Q64BT2;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Hypothetical protein.

GN ORFNames=G226G2\_14;

OS uncultured archaeon G226G2\_14;

OC Archaea; environmental samples.

OX NCBI\_TaxID=285389;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;

RX PubMed=15353801; DOI=10.1126/science.1100025;

RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.;

RA Richardson P.M., DeLong E.F.;

RT "Reverse methanogenesis: testing the hypothesis with environmental

RT genomics.";

RL Science 305:1457-1462(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;

RX Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AV714843; AAU83145.1; -; Genomic\_DNA.

KW Hypothetical protein.

SQ SEQUENCE 51 AA; 5992 MW; 855C222E5E6F4BF9 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 51;

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

QY 1 REDL 4

DB 31 REDL 34

Db 23 REDL 26

Q72T89 CARAU PRELIMINARY; PRT; 50 AA.

Q72T89;

AC Q72T89;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Preprogalanin 2A (Fragment).

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Carassius.

NCBI\_TaxID=7957;

RN [1]

RP NUCLEOTIDE SEQUENCE.

MEDELIN=22531610; PubMed=12644310; DOI=10.1016/S0303-7207(02)00301-5;

Uniappan S., Lin X., Peter R.E.;

RT "Characterization of complementary deoxyribonucleic acids encoding

RT preprogalanin and its alternative splice variants in the goldfish.";

RL Mol. Cell. Endocrinol. 200:177-187(2003).

DR EMBL; AF416931; AAO65780.1; -; Genomic\_DNA.

DR GO; GO:0005576; C:extracellular region; IEA.

DR GO; GO:0005179; F:hormone activity; IEA.

DR InterPro; IPR008174; Galanin.

DR PANTHER; PTHR16839; Galanin; 2.

DR Pfam; PF01296; Galanin; 1.

DR ProDom; PD005562; Galanin; 1.

DR PROSITE; PS00861; GALANIN; 1.

FT NON\_TER 1

FT NON\_TER 50

SQ SEQUENCE 50 AA; 5550 MW; BE938050D6A47F40 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

QY 1 REDL 4

DB 31 REDL 34

Db 23 REDL 26

Q72T89 CARAU PRELIMINARY; PRT; 50 AA.

Q72T89;

AC Q72T89;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Preprogalanin 2A (Fragment).

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Carassius.

NCBI\_TaxID=7957;

RN [1]

RP NUCLEOTIDE SEQUENCE.

MEDELIN=22531610; PubMed=12644310; DOI=10.1016/S0303-7207(02)00301-5;

Uniappan S., Lin X., Peter R.E.;

RT "Characterization of complementary deoxyribonucleic acids encoding

RT preprogalanin and its alternative splice variants in the goldfish.";

RL Mol. Cell. Endocrinol. 200:177-187(2003).

DR EMBL; AF416931; AAO65780.1; -; Genomic\_DNA.

DR GO; GO:0005576; C:extracellular region; IEA.

DR GO; GO:0005179; F:hormone activity; IEA.

DR InterPro; IPR008174; Galanin.

DR PANTHER; PTHR16839; Galanin; 2.

DR Pfam; PF01296; Galanin; 1.

DR ProDom; PD005562; Galanin; 1.

DR PROSITE; PS00861; GALANIN; 1.

FT NON\_TER 1

FT NON\_TER 50

SQ SEQUENCE 50 AA; 5550 MW; BE938050D6A47F40 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

QY 1 REDL 4

DB 31 REDL 34

Db 23 REDL 26

Q72T89 CARAU PRELIMINARY; PRT; 50 AA.

Q72T89;

AC Q72T89;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Preprogalanin 2A (Fragment).

OS Carassius auratus (Goldfish).

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||||  
Db 7 REDL 10

## RESULT 39

Q8MZQ7\_9DIPT PRELIMINARY; PRT; 52 AA.  
AC Q8MZQ7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome P450 (Fragment).  
GN Name=Cyp4C3;  
OS Drosophila pachea.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=103846;  
RN [1]  
RP NUCLEOTIDE SEQUENCE  
RA Azadan R.J., Danielson P.B., Fogleman J.C.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF506532; AAM27400.1; -; mRNA.  
DR FlyBase; FBgn0062760; DpacCyp4C3.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR001128; Cytochrome\_P450.  
FT NON\_TER 1  
SQ SEQUENCE 52 AA; 6072 MW; 9EDE3D761CEFF7DD6 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||||  
Db 27 REDL 30

## RESULT 40

Q58LK4\_9CAUD PRELIMINARY; PRT; 52 AA.  
AC Q58LK4;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=PSSM4\_094;  
OS Cyanophage P-SSM4.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.  
OX NCBI\_TaxID=268747;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Lindell D., Sullivan M.B., Johnson Z.I., Tolonen A., Rohwer F.,  
RA Chisholm S.W.;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY940168; AAX46895.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 52 AA; 6163 MW; 7AF8852AF1933EB0 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||||  
Db 33 REDL 36

## RESULT 41

Q5XYZ2\_BORGA PRELIMINARY; PRT; 52 AA.  
AC Q5XYZ2;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=EGP139;  
OS Borrelia garinii PBI.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
OC Borrelia burgdorferi group.  
OX NCBI\_TaxID=290434;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Gloeckner G., Lehmann R., Romualdi A., Pradella S.,  
RA Schulte-Spechtel U., Schilhabel M., Wilske B., Sühnel J., Platzner M.;  
RL "Comparative analysis of the Borrelia garinii genome."; [2]  
RN Nucleic Acids Res. 32:6038-6046(2004).  
RP NUCLEOTIDE SEQUENCE.  
RA Gloeckner G., Schilhabel M., Lehmann R., Platzner M.;  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY722922; AAU85990.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 52 AA; 6617 MW; D1BB39EACADBB3D CRC64;

Query Match 100.0%; Score 20; DB 2; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4  
|||||  
Db 13 REDL 16

## RESULT 42

Q96XL7\_SULTO PRELIMINARY; PRT; 54 AA.  
AC Q96XL7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE 54aa long hypothetical transcription factor.  
GN OrderedLocNames=ST2500.1; ORFNames=STS247;  
OS Sulfolobus tokodaii.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OX NCBI\_TaxID=111955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA STRAIN=JCM 10545 / 7;  
RX MEDLINE=21456156; PubMed=11572479;  
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,  
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,  
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,  
RA Aoki K.-I., Masuda S., Yanagishi M., Nishimura M., Yanagishi A.,  
RA Oshima T., Kikuchi H.;  
RT "Complete genome sequence of an aerobic thermoacidophilic  
RT Crenarchaeon, Sulfolobus tokodaii strain7.";  
RL DNA Res. 8:123-140(2001).  
DR EMBL; BA000023; BAB67610.1; -; Genomic\_DNA.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 54 AA; 6380 MW; E9D0637C4204B5F4 CRC64;

|                       |   |   |                    |            |                      |  |
|-----------------------|---|---|--------------------|------------|----------------------|--|
| Query Match           |   | 100.0%;                                 | Score 20;          | DB 2;      | Length 54;           |  |
| Best Local Similarity |   | 100.0%;                                 | Pred. No. 1.4e+03; |            |                      |  |
| Matches               | 4;  | Conservative                            | 0;                 | Mismatches | 0; Indels 0; Gaps 0; |  |
|                       |   |   |                    |            |                      |  |
| Qy                    | 1 REDL 4  |   |                    |            |                      |  |
|                       |   |   |                    |            |                      |  |
| Db                    | 25 REDL 28  |   |                    |            |                      |  |
| RESULT 45             |   |   |                    |            |                      |  |
| ID                    | O69433_9BACI  | PRELIMINARY;                            | PRT;               | 54 AA.     |                      |  |
| AC                    | O69433;   |   |                    |            |                      |  |
| DT                    | 01-AUG-1998   | (TRENBLrel. 07, Created)                |                    |            |                      |  |
| DT                    | 01-AUG-1998   | (TRENBLrel. 07, Last sequence update)   |                    |            |                      |  |
| DT                    | 01-MAR-2004   | (TRENBLrel. 26, Last annotation update) |                    |            |                      |  |
| DE                    | TnpA protein (Fragment).  |   |                    |            |                      |  |
| GN                    | Name=tnpA;  |   |                    |            |                      |  |
| OS                    | Exiguobacterium sp.   |   |                    |            |                      |  |
| OC                    | Bacteria; Firmicutes; Bacillales; Bacillaceae; Exiguobacterium.       |   |                    |            |                      |  |
| OC                    | NCBI_TaxID=44751;   |   |                    |            |                      |  |
| RN                    | [1]   |   |                    |            |                      |  |
| RP                    | NUCLEOTIDE SEQUENCE.  |   |                    |            |                      |  |
| RC                    | STRAIN=TC38-2b;   |   |                    |            |                      |  |
| RX                    | MEDLINE=98195721; PubMed=9534232;                                     |   |                    |            |                      |  |
| RA                    | Bogdanova E.S., Bass I.A., Minakhin L.S., Petrova M.A., Mindlin S.Z., |   |                    |            |                      |  |
| RA                    | Volodin A.A., Kalyaeva E.S., Tiedge G.M., Hobman J.L., Brown N.L.,    |   |                    |            |                      |  |
| RA                    | Nikifirov V.G.;   |   |                    |            |                      |  |
| RT                    | "Horizontal spread of mer operons among Gram-positive bacteria in     |   |                    |            |                      |  |
| RT                    | natural environments.";   |   |                    |            |                      |  |
| RL                    | Microbiology 144:609-620(1998).                                       |   |                    |            |                      |  |
| RN                    | [2]   |   |                    |            |                      |  |
| RP                    | NUCLEOTIDE SEQUENCE.  |   |                    |            |                      |  |
| RC                    | STRAIN=TC38-2b;   |   |                    |            |                      |  |
| RA                    | Minakhin L.;  |   |                    |            |                      |  |
| RL                    | Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.               |   |                    |            |                      |  |
| DR                    | EMBL; Y08064; CAA69303.1; -; Genomic_DNA.                             |   |                    |            |                      |  |
| DR                    | GO; GO:0003677; F:DNA binding; IEA.                                   |   |                    |            |                      |  |
| DR                    | GO; GO:0004803; F:transposase activity; IEA.                          |   |                    |            |                      |  |
| DR                    | GO; GO:0006313; P:DNA transposition; IEA.                             |   |                    |            |                      |  |
| DR                    | InterPro; IPR002513; Transposase_7.                                   |   |                    |            |                      |  |
| DR                    | Pfam; PF01526; Transposase_7; 1.                                      |   |                    |            |                      |  |
| FT                    | NON TER 1   |   |                    |            |                      |  |
| FT                    | NON TER 1   |   |                    |            |                      |  |
| SQ                    | SEQUENCE 54 AA; 6229 MW; 8939739E0F0D4803 CRC64;                      |   |                    |            |                      |  |
| Query Match           |   | 100.0%;                                 | Score 20;          | DB 2;      | Length 54;           |  |
| Best Local Similarity |   | 100.0%;                                 | Pred. No. 1.4e+03; |            |                      |  |
| Matches               | 4;  | Conservative                            | 0;                 | Mismatches | 0; Indels 0; Gaps 0; |  |
|                       |   |   |                    |            |                      |  |
| Qy                    | 1 REDL 4  |   |                    |            |                      |  |
|                       |   |   |                    |            |                      |  |
| Db                    | 15 REDL 18  |   |                    |            |                      |  |
| RESULT 46             |   |   |                    |            |                      |  |
| ID                    | O69233_BACCE  | PRELIMINARY;                            | PRT;               | 54 AA.     |                      |  |
| AC                    | O69233;   |   |                    |            |                      |  |
| DT                    | 01-AUG-1998   | (TRENBLrel. 07, Created)                |                    |            |                      |  |
| DT                    | 01-AUG-1998   | (TRENBLrel. 07, Last sequence update)   |                    |            |                      |  |
| DT                    | 01-FEB-2005   | (TRENBLrel. 29, Last annotation update) |                    |            |                      |  |
| DE                    | TnpA protein (Transposase) (Fragment).                                |   |                    |            |                      |  |
| GN                    | Name=tnpA;  |   |                    |            |                      |  |
| OS                    | Bacillus cereus.  |   |                    |            |                      |  |
| OC                    | Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;              |   |                    |            |                      |  |
| OC                    | Bacillus cereus group.  |   |                    |            |                      |  |
| OX                    | NCBI_TaxID=1396;  |   |                    |            |                      |  |
| RN                    | [1]   |   |                    |            |                      |  |
| RP                    | NUCLEOTIDE SEQUENCE.  |   |                    |            |                      |  |
| RC                    | STRAIN=RC607;   |   |                    |            |                      |  |
| RX                    | MEDLINE=98195721; PubMed=9534232;                                     |   |                    |            |                      |  |
| RA                    | Bogdanova E.S., Bass I.A., Minakhin L.S., Petrova M.A., Mindlin S.Z., |   |                    |            |                      |  |

|                       |   |   |                    |            |                      |           |
|-----------------------|---|---|--------------------|------------|----------------------|-----------|
| Query Match           |   | 100.0%;                                 | Score 20;          | DB 2;      | Length 54;           |           |
| Best Local Similarity |   | 100.0%;                                 | Pred. No. 1.4e+03; |            |                      |           |
| Matches               | 4;  | Conservative                            | 0;                 | Mismatches | 0; Indels 0; Gaps 0; |           |
|                       |   |   |                    |            |                      |           |
| Qy                    | 1 REDL 4  |   |                    |            |                      |           |
|                       |   |   |                    |            |                      |           |
| Db                    | 17 REDL 20  |   |                    |            |                      |           |
| RESULT 43             |   |   |                    |            |                      |           |
| ID                    | O9GLJ2_PIG  | PRELIMINARY;                            | PRT;               | 54 AA.     |                      |           |
| AC                    | O9GLJ2;   |   |                    |            |                      |           |
| DT                    | 01-MAR-2001   | (TRENBLrel. 16, Created)                |                    |            |                      |           |
| DT                    | 01-MAR-2001   | (TRENBLrel. 16, Last sequence update)   |                    |            |                      |           |
| DT                    | 01-MAR-2004   | (TRENBLrel. 26, Last annotation update) |                    |            |                      |           |
| DE                    | DNA-PK interaction-like protein (Fragment).                           |   |                    |            |                      |           |
| OS                    | Sus scrofa (Pig).   |   |                    |            |                      |           |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |   |                    |            |                      |           |
| OC                    | Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;   |   |                    |            |                      |           |
| OC                    | Sub.  |   |                    |            |                      |           |
| NCBI_TaxID=9823;      |   |   |                    |            |                      |           |
| RP                    | NUCLEOTIDE SEQUENCE.  |   |                    |            |                      |           |
| RA                    | Smith T.P.L., Fahrrenkrug S.C., Rohrer G.A., Simmen F.A.,             |   |                    |            |                      |           |
| RA                    | Rexroad C.E. III, Keefe J.W.;   |   |                    |            |                      |           |
| RL                    | Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.               |   |                    |            |                      |           |
| DR                    | EMBL; AF267715; AAG25931.1; -; Genomic_DNA.                           |   |                    |            |                      |           |
| DR                    | HSSP; Q99828; 1DGU.   |   |                    |            |                      |           |
| DR                    | SMR; Q9GLJ2; 1-54.  |   |                    |            |                      |           |
| DR                    | GO; GO:0005509; F:calcium ion binding; IEA.                           |   |                    |            |                      |           |
| DR                    | InterPro; IPR002048; EF-hand.   |   |                    |            |                      |           |
| DR                    | InterPro; IPR011992; EF-Hand_type.                                    |   |                    |            |                      |           |
| DR                    | Pfam; PF00036; ehand; 1.  |   |                    |            |                      |           |
| DR                    | ProDom; PD000012; EF-hand; 1.   |   |                    |            |                      |           |
| DR                    | PROSITE; PS00018; EF_HAND; UNKNOWN_1.                                 |   |                    |            |                      |           |
| FT                    | NON TER 1   |   |                    |            |                      |           |
| FT                    | NON TER 54  |   |                    |            |                      |           |
| FT                    | NON TER 54  |   |                    |            |                      |           |
| SQ                    | SEQUENCE 54 AA; 6107 MW; 1A8057DE68A57A4A CRC64;                      |   |                    |            |                      |           |
| Query Match           |   | 100.0%;                                 |                    |            |                      | Score 20; |
| Best Local Similarity |   | 100.0%;                                 | Pred. No. 1.4e+03; |            |                      |           |
| Matches               | 4;  | Conservative                            | 0;                 | Mismatches | 0; Indels 0; Gaps 0; |           |
|                       |   |   |                    |            |                      |           |
| Qy                    | 1 REDL 4  |   |                    |            |                      |           |
|                       |   |   |                    |            |                      |           |
| Db                    | 24 REDL 27  |   |                    |            |                      |           |
| RESULT 44             |   |   |                    |            |                      |           |
| ID                    | Q94KJ8_PINTA  | PRELIMINARY;                            | PRT;               | 54 AA.     |                      |           |
| AC                    | Q94KJ8;   |   |                    |            |                      |           |
| DT                    | 01-DEC-2001   | (TRENBLrel. 19, Created)                |                    |            |                      |           |
| DT                    | 01-DEC-2001   | (TRENBLrel. 19, Last sequence update)   |                    |            |                      |           |
| DT                    | 01-OCT-2003   | (TRENBLrel. 25, Last annotation update) |                    |            |                      |           |
| DE                    | Alpha-tubulin (Fragment).   |   |                    |            |                      |           |
| OS                    | Pinus taeda (loblolly pine).  |   |                    |            |                      |           |
| OC                    | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;    |   |                    |            |                      |           |
| OC                    | Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.    |   |                    |            |                      |           |
| OC                    | NCBI_TaxID=3352;  |   |                    |            |                      |           |
| RN                    | [1]   |   |                    |            |                      |           |
| RP                    | NUCLEOTIDE SEQUENCE.  |   |                    |            |                      |           |
| RA                    | Lorenz W.W., Dean J.F.D.;   |   |                    |            |                      |           |
| RL                    | Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.               |   |                    |            |                      |           |
| DR                    | EMBL; AF357237; AAK49527.1; -; mRNA.                                  |   |                    |            |                      |           |
| DR                    | GO; GO:0005874; C:microtubule; IEA.                                   |   |                    |            |                      |           |
| DR                    | GO; GO:0005198; F:structural molecule activity; IEA.                  |   |                    |            |                      |           |
| DR                    | GO; GO:0007018; P:microtubule-based movement; IEA.                    |   |                    |            |                      |           |
| DR                    | InterPro; IPR002452; Alpha_tubulin.                                   |   |                    |            |                      |           |
| DR                    | PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.                             |   |                    |            |                      |           |
| FT                    | NON TER 1   |   |                    |            |                      |           |
| FT                    | NON TER 1   |   |                    |            |                      |           |
| SQ                    | SEQUENCE 54 AA; 6111 MW; 2A980A49B95A84A5 CRC64;                      |   |                    |            |                      |           |
| Query Match           |   | 100.0%;                                 | Score 20;          | DB 2;      | Length 54;           |           |
| Best Local Similarity |   | 100.0%;                                 | Pred. No. 1.4e+03; |            |                      |           |
| Matches               | 4;  | Conservative                            | 0;                 | Mismatches | 0; Indels 0; Gaps 0; |           |
|                       |   |   |                    |            |                      |           |
| Qy                    | 1 REDL 4  |   |                    |            |                      |           |
|                       |   |   |                    |            |                      |           |
| Db                    | 24 REDL 27  |   |                    |            |                      |           |
| RESULT 45             |   |   |                    |            |                      |           |
| ID                    | O69433_9BACI  | PRELIMINARY;                            | PRT;               | 54 AA.     |                      |           |
| AC                    | O69433;   |   |                    |            |                      |           |
| DT                    | 01-AUG-1998   | (TRENBLrel. 07, Created)                |                    |            |                      |           |
| DT                    | 01-AUG-1998   | (TRENBLrel. 07, Last sequence update)   |                    |            |                      |           |
| DT                    | 01-MAR-2004   | (TRENBLrel. 26, Last annotation update) |                    |            |                      |           |
| DE                    | TnpA protein (Fragment).  |   |                    |            |                      |           |
| GN                    | Name=tnpA;  |   |                    |            |                      |           |
| OS                    | Exiguobacterium sp.   |   |                    |            |                      |           |
| OC                    | Bacteria; Firmicutes; Bacillales; Bacillaceae; Exiguobacterium.       |   |                    |            |                      |           |
| OC                    | NCBI_TaxID=44751;   |   |                    |            |                      |           |
| RN                    | [1]   |   |                    |            |                      |           |
| RP                    | NUCLEOTIDE SEQUENCE.  |   |                    |            |                      |           |
| RC                    | STRAIN=TC38-2b;   |   |                    |            |                      |           |
| RX                    | MEDLINE=98195721; PubMed=9534232;                                     |   |                    |            |                      |           |
| RA                    | Bogdanova E.S., Bass I.A., Minakhin L.S., Petrova M.A., Mindlin S.Z., |   |                    |            |                      |           |
| RA                    | Volodin A.A., Kalyaeva E.S., Tiedge G.M., Hobman J.L., Brown N.L.,    |   |                    |            |                      |           |
| RA                    | Nikifirov V.G.;   |   |                    |            |                      |           |
| RT                    | "Horizontal spread of mer operons among Gram-positive bacteria in     |   |                    |            |                      |           |
| RT                    | natural environments.";   |   |                    |            |                      |           |
| RL                    | Microbiology 144:609-620(1998).                                       |   |                    |            |                      |           |
| RN                    | [2]   |   |                    |            |                      |           |
| RP                    | NUCLEOTIDE SEQUENCE.  |   |                    |            |                      |           |
| RC                    | STRAIN=TC38-2b;   |   |                    |            |                      |           |
| RA                    | Minakhin L.;  |   |                    |            |                      |           |
| RL                    | Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.               |   |                    |            |                      |           |
| DR                    | EMBL; Y08064; CAA69303.1; -; Genomic_DNA.                             |   |                    |            |                      |           |
| DR                    | GO; GO:0003677; F:DNA binding; IEA.                                   |   |                    |            |                      |           |
| DR                    | GO; GO:0004803; F:transposase activity; IEA.                          |   |                    |            |                      |           |
| DR                    | GO; GO:0006313; P:DNA transposition; IEA.                             |   |                    |            |                      |           |
| DR                    | InterPro; IPR002513; Transposase_7.                                   |   |                    |            |                      |           |
| DR                    | Pfam; PF01526; Transposase_7; 1.                                      |   |                    |            |                      |           |
| FT                    | NON TER 1   |   |                    |            |                      |           |
| FT                    | NON TER 1   |   |                    |            |                      |           |
| SQ                    | SEQUENCE 54 AA; 6229 MW; 8939739E0F0D4803 CRC64;                      |   |                    |            |                      |           |
| Query Match           |   | 100.0%;                                 | Score 20;          | DB 2;      | Length 54;           |           |
| Best Local Similarity |   | 100.0%;                                 | Pred. No. 1.4e+03; |            |                      |           |
| Matches               | 4;  | Conservative                            | 0;                 | Mismatches | 0; Indels 0; Gaps 0; |           |
|                       |   |   |                    |            |                      |           |
| Qy                    | 1 REDL 4  |   |                    |            |                      |           |
|                       |   |   |                    |            |                      |           |
| Db                    | 15 REDL 18  |   |                    |            |                      |           |
| RESULT 46             |   |   |                    |            |                      |           |
| ID                    | O69233_BACCE  | PRELIMINARY;                            | PRT;               | 54 AA.     |                      |           |
| AC                    | O69233;   |   |                    |            |                      |           |
| DT                    | 01-AUG-1998   | (TRENBLrel. 07, Created)                |                    |            |                      |           |
| DT                    | 01-AUG-1998   | (TRENBLrel. 07, Last sequence update)   |                    |            |                      |           |
| DT                    | 01-FEB-2005   | (TRENBLrel. 29, Last annotation update) |                    |            |                      |           |
| DE                    | TnpA protein (Transposase) (Fragment).                                |   |                    |            |                      |           |
| GN                    | Name=tnpA;  |   |                    |            |                      |           |
| OS                    | Bacillus cereus.  |   |                    |            |                      |           |
| OC                    | Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;              |   |                    |            |                      |           |
| OC                    | Bacillus cereus group.  |   |                    |            |                      |           |
| OX                    | NCBI_TaxID=1396;  |   |                    |            |                      |           |
| RN                    | [1]   |   |                    |            |                      |           |
| RP                    | NUCLEOTIDE SEQUENCE.  |   |                    |            |                      |           |
| RC                    | STRAIN=RC607;   |   |                    |            |                      |           |
| RX                    | MEDLINE=98195721; PubMed=9534232;                                     |   |                    |            |                      |           |
| RA                    | Bogdanova E.S., Bass I.A., Minakhin L.S., Petrova M.A., Mindlin S.Z., |   |                    |            |                      |           |

RA Volodin A.A., Kalyaeva E.S., Tiedge G.M., Hobman J.L., Brown N.L.,  
RA Nikifirov V.G.;  
RT "Horizontal spread of mer operons among Gram-positive bacteria in  
RT natural environments.";  
RL Microbiology 144:609-620(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=RC607;  
RA Minakhin L.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=RC607;  
RX MEDLINE=89123092; PubMed=2536669;  
RA Wang Y., Moore M., Levinson H.S., Silver S., Walsh C.T., Mahler I.;  
RT "Nucleotide sequence of a chromosomal mercury resistance determinant  
RT from a *Bacillus* sp. with broad-spectrum mercury resistance.";  
RL J. Bacteriol. 171:83-92(1989).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=RC607;  
RX MEDLINE=20026822; PubMed=10559175;  
RA Gupta A., Phung L.T., Chakravarty L., Silver S.;  
RT "Mercury resistance in *Bacillus cereus* RC607: transcriptional  
RT organization and two new open reading frames.";  
RL J. Bacteriol. 181:7080-7086(1999).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=RC607;  
RA Endo G., Silver S., Huang C., Narita M.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y08065; CAA69304.1; -; Genomic DNA.  
DR EMBL; AB066362; BAB62437.1; -; Genomic DNA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0004803; F:transposase activity; IEA.  
DR GO; GO:0006333; P:DNA transposition; IEA.  
DR InterPro; IPR002513; Transposase\_7.  
DR Pfam; PF01526; Transposase\_7; 1.  
FT NON TER 1  
FT SEQUENCE 54 AA; 6229 MW; 8939739E0F0D4803 CRC64;  
  
Query Match 100.0%; Score 20; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 REDL 4  
Db 15 REDL 18  
  
RESULT 47  
Q5QLQ2\_ORYSA PRELIMINARY; PRT; 55 AA.  
AC Q5QLQ2;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Hypothetical protein OS:JNB0063G05.16.  
GN Name=OSJNB0063G05.16;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
RA Hujishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
RA Ikono M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,

RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
RA Naniki N., Negishi M., Ohka I., Ono N., Saji S., Sakai K., Shibata M.,  
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,  
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,  
RA Yano M., Jiang J., Gojobori T.;  
RT "The genome sequence and structure of rice chromosome 1.";  
RL Nature 420:312-316(2002).  
DR EMBL; AP003760; BAD73646.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 55 AA; 6600 MW; C1E151A6B294F958 CRC64;  
  
Query Match 100.0%; Score 20; DB 2; Length 55;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 REDL 4  
Db 15 REDL 18  
  
RESULT 48  
Q8F9J9\_LEPIN PRELIMINARY; PRT; 55 AA.  
AC Q8F9J9;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames=LA0196;  
OS Leptospira interrogans.  
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.  
OX NCBI\_TaxID=173;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;  
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;  
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,  
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,  
RA Zhang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,  
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,  
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,  
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,  
RA Xu J.-G., Zhao G.-P.;  
RT "Unique physiological and pathogenic features of *Leptospira*  
RT interrogans revealed by whole-genome sequencing.";  
RL Nature 422:888-893(2003).  
DR EMBL; AE011209; AAN47395.1; -; Genomic\_DNA.  
KW Complete proteome.  
SQ SEQUENCE 55 AA; 6864 MW; 9D252ABA799938DA CRC64;  
  
Query Match 100.0%; Score 20; DB 2; Length 55;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 REDL 4  
Db 4 REDL 7  
  
RESULT 49  
Q5E042\_VIBF1 PRELIMINARY; PRT; 56 AA.  
AC Q5E042;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames=VFA0534;  
OS *Vibrio fischeri* (strain ATCC 700601 / ES114).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; *Vibrio*.

```

OX NCBI_TaxID=312309;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15703294; DOI=10.1073/pnas.0409900102;
RA Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M., Gunsalus R.,
RA Lestrich P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E.,
RA Stevens A., Visick K., Whistler C., Greenberg E.P.;
RT "Complete genome sequence of Vibrio fischeri: a symbiotic bacterium
RT with pathogenic congeners."
RL Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005).
DR EMBL; CP000021; AAW87604.1; -; Genomic_DNA.
DR InterPro; IPR010093; Xis.
DR TIGRFAMs; TIGR01764; excise; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 56 AA; 6520 MW; 6D58134FB659D9DA CRC64;

Query Match 100.0%; Score 20; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 44 REDL 47

RESULT 50
Q4HAV9_9DEIO
ID Q4HAV9_9DEIO PRELIMINARY; PRT; 57 AA.
AC Q4HAV9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
DE ORFNames=DgeODRAFT_1362;
OS Deinococcus geothermalis DSM 11300.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=319795;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 11300;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Deinococcus geothermalis
RT DSM 11300."
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 11300;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Deinococcus geothermalis
RT DSM 11300."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHE01000003; EAL83256.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 57 AA; 6328 MW; A47FA5372B973436 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDL 4
Db 15 REDL 18

Search completed: March 20, 2006, 07:57:28
Job time : 154.5 secs

```



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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:36 ; Search time 75.5 Seconds  
(without alignments)  
23.278 Million cell updates/sec

Title: US-09-673-707-9  
Perfect score: 20  
Sequence: 1 KDEL 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : A\_Geneseq\_21:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*  
9: geneseqp2005s:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 20    | 100.0       | 4      | 2  | AAR41971 Mammalian |
| 2          | 20    | 100.0       | 4      | 2  | AAR48246 Endoplasm |
| 3          | 20    | 100.0       | 4      | 2  | AAR49442 Immunomod |
| 4          | 20    | 100.0       | 4      | 2  | AAR49584 Sequence  |
| 5          | 20    | 100.0       | 4      | 2  | AAR95063 Mammalian |
| 6          | 20    | 100.0       | 4      | 2  | AAR94944 Microsoma |
| 7          | 20    | 100.0       | 4      | 2  | AAR95219 Pseudomon |
| 8          | 20    | 100.0       | 4      | 2  | AAR21969 Linker #3 |
| 9          | 20    | 100.0       | 4      | 2  | AAR31861 Endoplasm |
| 10         | 20    | 100.0       | 4      | 2  | AAR56513 Endoplasm |
| 11         | 20    | 100.0       | 4      | 2  | AAR76396 Endoplasm |
| 12         | 20    | 100.0       | 4      | 2  | AAR52264 C-termina |
| 13         | 20    | 100.0       | 4      | 2  | AAR64614 Endomembr |
| 14         | 20    | 100.0       | 4      | 2  | AAR51437 C-termina |
| 15         | 20    | 100.0       | 4      | 2  | AAR61591 Endomembr |
| 16         | 20    | 100.0       | 4      | 2  | AAR51434 C-termina |
| 17         | 20    | 100.0       | 4      | 2  | ABB76201 Peptide u |
| 18         | 20    | 100.0       | 4      | 2  | AAR92911 Pseudomon |
| 19         | 20    | 100.0       | 4      | 2  | AAR85767 Endomembr |
| 20         | 20    | 100.0       | 4      | 2  | AAY30052 Organelle |
| 21         | 20    | 100.0       | 4      | 2  | AAY27177 Organelle |
| 22         | 20    | 100.0       | 4      | 2  | AAY49700 Pseudomon |
| 23         | 20    | 100.0       | 4      | 2  | AAR96345 Endoplasm |
| 24         | 20    | 100.0       | 4      | 2  | AAR92925 Pseudomon |

|    |    |       |   |   |           |           |
|----|----|-------|---|---|-----------|-----------|
| 25 | 20 | 100.0 | 4 | 2 | AAV29637  | KDEL pept |
| 26 | 20 | 100.0 | 4 | 2 | AAV25688  | Membrane  |
| 27 | 20 | 100.0 | 4 | 3 | AAV98152  | Protein 1 |
| 28 | 20 | 100.0 | 4 | 3 | ABO09912  | Targeting |
| 29 | 20 | 100.0 | 4 | 3 | AAV70697  | Rat endop |
| 30 | 20 | 100.0 | 4 | 3 | AAV56883  | Endoplasm |
| 31 | 20 | 100.0 | 4 | 3 | AAV32395  | Endoplasm |
| 32 | 20 | 100.0 | 4 | 3 | AAAB03195 | Endoplasm |
| 33 | 20 | 100.0 | 4 | 3 | AAV90442  | Mammalian |
| 34 | 20 | 100.0 | 4 | 3 | AAV69694  | Mammalian |
| 35 | 20 | 100.0 | 4 | 3 | AAV92046  | Endoplasm |
| 36 | 20 | 100.0 | 4 | 3 | AAV93738  | Amino aci |
| 37 | 20 | 100.0 | 4 | 3 | AAAB30285 | CD4+ T-ce |
| 38 | 20 | 100.0 | 4 | 4 | AAAB35117 | Adenoviru |
| 39 | 20 | 100.0 | 4 | 4 | AAAG67291 | Amino aci |
| 40 | 20 | 100.0 | 4 | 4 | AAAG78315 | ER lumen  |
| 41 | 20 | 100.0 | 4 | 4 | AAAB45947 | Transdomi |
| 42 | 20 | 100.0 | 4 | 4 | AAAB96038 | Endoplasm |
| 43 | 20 | 100.0 | 4 | 4 | AAAB70755 | Endoplasm |
| 44 | 20 | 100.0 | 4 | 4 | AAAB20214 | Endoplasm |
| 45 | 20 | 100.0 | 4 | 4 | AAAB31370 | Amino aci |
| 46 | 20 | 100.0 | 4 | 4 | AAU03564  | Peptide r |
| 47 | 20 | 100.0 | 4 | 4 | AAAB84355 | Amino aci |
| 48 | 20 | 100.0 | 4 | 4 | AAAB48315 | Calreticu |
| 49 | 20 | 100.0 | 4 | 4 | AAAB50814 | Human end |
| 50 | 20 | 100.0 | 4 | 4 | AAAE05817 | Protein 1 |
| 51 | 20 | 100.0 | 4 | 4 | AAU07199  | Human ICA |
| 52 | 20 | 100.0 | 4 | 4 | AAAB98995 | C-termina |
| 53 | 20 | 100.0 | 4 | 4 | AAAB82330 | Endoplasm |
| 54 | 20 | 100.0 | 4 | 4 | AAAB68569 | Endoplasm |
| 55 | 20 | 100.0 | 4 | 4 | AAU76352  | Synthetic |
| 56 | 20 | 100.0 | 4 | 5 | AAU76352  | Synthetic |
| 57 | 20 | 100.0 | 4 | 5 | AAAE20413 | KDEL, ER  |
| 58 | 20 | 100.0 | 4 | 5 | AAAS1010  | Leader pe |
| 59 | 20 | 100.0 | 4 | 5 | ABB07544  | Amino aci |
| 60 | 20 | 100.0 | 4 | 5 | AAU99125  | KDEL memb |
| 61 | 20 | 100.0 | 4 | 5 | AAO22202  | Peptide r |
| 62 | 20 | 100.0 | 4 | 5 | AAE18835  | Human cal |
| 63 | 20 | 100.0 | 4 | 5 | AAO14396  | Endoplasm |
| 64 | 20 | 100.0 | 4 | 5 | AAE13432  | Human KDE |
| 65 | 20 | 100.0 | 4 | 5 | AAU76185  | Calreticu |
| 66 | 20 | 100.0 | 4 | 5 | AAU96731  | Human XAG |
| 67 | 20 | 100.0 | 4 | 5 | ABG68877  | Endoplasm |
| 68 | 20 | 100.0 | 4 | 5 | AAE28525  | Endoplasm |
| 69 | 20 | 100.0 | 4 | 5 | AAE19017  | Peptide # |
| 70 | 20 | 100.0 | 4 | 5 | AAE28690  | Human cal |
| 71 | 20 | 100.0 | 4 | 5 | ABG94836  | Endomembr |
| 72 | 20 | 100.0 | 4 | 5 | ABB09909  | Radiolabe |
| 73 | 20 | 100.0 | 4 | 5 | ABG92980  | Endoplasm |
| 74 | 20 | 100.0 | 4 | 5 | ABG92970  | Calreticu |
| 75 | 20 | 100.0 | 4 | 5 | AAE13263  | KDEL pept |
| 76 | 20 | 100.0 | 4 | 5 | AAE17969  | ER-retent |
| 77 | 20 | 100.0 | 4 | 5 | ABB75930  | Endoplasm |
| 78 | 20 | 100.0 | 4 | 5 | ABB08104  | Endoplasm |
| 79 | 20 | 100.0 | 4 | 5 | ADG68265  | Polyimmun |
| 80 | 20 | 100.0 | 4 | 5 | ADG68265  | Aspergill |
| 81 | 20 | 100.0 | 4 | 6 | ABG98468  | Signal pe |
| 82 | 20 | 100.0 | 4 | 6 | ABU64905  | Human cal |
| 83 | 20 | 100.0 | 4 | 6 | AAE33358  | Endoplasm |
| 84 | 20 | 100.0 | 4 | 6 | ABU08976  | Rat endop |
| 85 | 20 | 100.0 | 4 | 6 | AAO16771  | Cytoplasm |
| 86 | 20 | 100.0 | 4 | 6 | AAE35569  | ER-retent |
| 87 | 20 | 100.0 | 4 | 6 | AAE14821  | Endoplasm |
| 88 | 20 | 100.0 | 4 | 6 | ABJ19274  | Anti-huma |
| 89 | 20 | 100.0 | 4 | 6 | ABU64800  | Human cal |
| 90 | 20 | 100.0 | 4 | 6 | ABP56565  | Calreticu |
| 91 | 20 | 100.0 | 4 | 6 | ABP56575  | Signal pe |
| 92 | 20 | 100.0 | 4 | 6 | ABP56611  | Calreticu |
| 93 | 20 | 100.0 | 4 | 6 | ABR39556  | Calreticu |
| 94 | 20 | 100.0 | 4 | 6 | ABU09487  | Endoplasm |
| 95 | 20 | 100.0 | 4 | 6 | ABR39588  | Amino aci |
| 96 | 20 | 100.0 | 4 | 6 | ABR39418  | Endoplasm |
| 97 | 20 | 100.0 | 4 | 6 | ABU14033  | Calreticu |

|     |    |       |   |   |           |           |
|-----|----|-------|---|---|-----------|-----------|
| 98  | 20 | 100.0 | 4 | 6 | ABP71099  | Peptide 1 |
| 99  | 20 | 100.0 | 4 | 6 | Aae36304  | Endoplasm |
| 100 | 20 | 100.0 | 4 | 6 | Abp72886  | Human cal |
| 101 | 20 | 100.0 | 4 | 6 | Abu09657  | Calreticu |
| 102 | 20 | 100.0 | 4 | 6 | Aae32718  | Calreticu |
| 103 | 20 | 100.0 | 4 | 6 | Abg72269  | Peptide u |
| 104 | 20 | 100.0 | 4 | 6 | Aae34842  | Endoplasm |
| 105 | 20 | 100.0 | 4 | 6 | Abu96669  | ER retent |
| 106 | 20 | 100.0 | 4 | 6 | Aae37781  | Localisat |
| 107 | 20 | 100.0 | 4 | 6 | Aao31116  | Endoplasm |
| 108 | 20 | 100.0 | 4 | 6 | Aao32272  | ER retent |
| 109 | 20 | 100.0 | 4 | 6 | Ada50227  | KDEL pept |
| 110 | 20 | 100.0 | 4 | 6 | Abri61855 | Pseudomon |
| 111 | 20 | 100.0 | 4 | 6 | Abu63380  | Rat ER re |
| 112 | 20 | 100.0 | 4 | 6 | Ada26346  | Canine GR |
| 113 | 20 | 100.0 | 4 | 6 | Abc32836  | Cytoplasm |
| 114 | 20 | 100.0 | 4 | 7 | Ada07010  | Calreticu |
| 115 | 20 | 100.0 | 4 | 7 | Ada08301  | Calreticu |
| 116 | 20 | 100.0 | 4 | 7 | Adb66860  | Fusion nu |
| 117 | 20 | 100.0 | 4 | 7 | Ada44808  | Endoplasm |
| 118 | 20 | 100.0 | 4 | 7 | Adc34608  | Mammalian |
| 119 | 20 | 100.0 | 4 | 7 | Aae38954  | Calreticu |
| 120 | 20 | 100.0 | 4 | 7 | Adc28554  | Golgi ret |
| 121 | 20 | 100.0 | 4 | 7 | Aae39838  | Human end |
| 122 | 20 | 100.0 | 4 | 7 | Adc84560  | Carboxyl  |
| 123 | 20 | 100.0 | 4 | 7 | Adt28914  | Calreticu |
| 124 | 20 | 100.0 | 4 | 7 | Adel10750 | Structura |
| 125 | 20 | 100.0 | 4 | 7 | Adf3276   | KDEL loca |
| 126 | 20 | 100.0 | 4 | 7 | Adf32312  | Calreticu |
| 127 | 20 | 100.0 | 4 | 7 | Adf28981  | ER reteti |
| 128 | 20 | 100.0 | 4 | 7 | Adf57572  | Rat endop |
| 129 | 20 | 100.0 | 4 | 7 | Adf90408  | Calreticu |
| 130 | 20 | 100.0 | 4 | 7 | Adh92032  | Cytoplasm |
| 131 | 20 | 100.0 | 4 | 7 | Adj53825  | Calreticu |
| 132 | 20 | 100.0 | 4 | 8 | Adf93265  | Plant alb |
| 133 | 20 | 100.0 | 4 | 8 | Adg25840  | Pseudomon |
| 134 | 20 | 100.0 | 4 | 8 | Adf94964  | Endoplasm |
| 135 | 20 | 100.0 | 4 | 8 | Adh11621  | Human KDE |
| 136 | 20 | 100.0 | 4 | 8 | Adh61900  | Human tar |
| 137 | 20 | 100.0 | 4 | 8 | Adh51589  | Human pep |
| 138 | 20 | 100.0 | 4 | 8 | Adi36229  | Human cal |
| 139 | 20 | 100.0 | 4 | 8 | Adi30564  | ER-retain |
| 140 | 20 | 100.0 | 4 | 8 | Adk15769  | Fusion pr |
| 141 | 20 | 100.0 | 4 | 8 | Adm13763  | Endoplasm |
| 142 | 20 | 100.0 | 4 | 8 | Adm35872  | Endoplasm |
| 143 | 20 | 100.0 | 4 | 8 | Adl23799  | Calreticu |
| 144 | 20 | 100.0 | 4 | 8 | Adm68937  | Endoplasm |
| 145 | 20 | 100.0 | 4 | 8 | Adl91589  | Endoplasm |
| 146 | 20 | 100.0 | 4 | 8 | Adl14837  | Yeast end |
| 147 | 20 | 100.0 | 4 | 8 | Adn49849  | C-termina |
| 148 | 20 | 100.0 | 4 | 8 | Adn07009  | Pseudomon |
| 149 | 20 | 100.0 | 4 | 8 | Adn49386  | Delta 6-d |
| 150 | 20 | 100.0 | 4 | 8 | Adn37764  | Endoplasm |

RESULT 1

AAR41971 standard; peptide; 4 AA.

XX AAR41971;

AC AAR41971;

XX

DT 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 22-OCT-1993 (first entry)

XX

DE Mammalian endoplasmic reticulum retention signal.

XX

KW yeast expression cassette; yeast alpha-factor leader; KEX2p;

KW heterologous protein production; mating pheromone; YAP3;

KW dibasic processing endoprotease.

ALIGNMENTS

Query Match 100.0%; Score 20; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4

DB 1 KDEL 4

RESULT 2

AAR48246

ID AAR48246 standard; peptide; 4 AA.

XX AAR48246;

AC AAR48246;

XX

DT 25-MAR-2003 (revised)

DT 29-JUL-1994 (first entry)

XX

DE Endoplasmic reticulum retention signal KDEL.

XX

KW Single chain antibody; sFv; heavy chain; light chain; kappa;

KW variable domain; hydrophilic linker; antibodies;

KW endoplasmic reticulum retention.

XX

OS Synthetic.

XX

XX WO9402610-A1.

XX

PD 03-FEB-1994.

XX

PF 16-JUL-1993; 93WO-US006735.

XX

XX 17-JUL-1992; 92US-00916939.

PR 17-MAR-1993; 93US-00045274.

XX

XX (DAND ) DANA FARBER CANCER INST INC.

XX

XX Marasco WA, Haseltine WA;

XX

DR WPI; 1994-048868/06.

XX Intracellular binding of antigens - by using antibody targetting with  
PT vector system, for e.g. tumour suppression.  
XX  
XX  
PS Claim 32; Page 99; 155pp; English.  
XX  
CC New vector systems comprise a sequence adapted for intracellular delivery  
and expression contg. a promoter operably linked to an antibody gene  
CC encoding an antibody which binds to a specific target antigen. The  
CC antibody is esp. a single chain antibody in which the heavy and light  
CC chain variable regions are joined via a hydrophilic linker peptide.  
CC Localisation sequences are pref. included in the constructs. See AAR48246  
CC -9 and AAR48252-3 for pref. (known) endoplasmic reticulum retention  
CC signals. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
| | | |  
Db 1 KDEL 4

RESULT 3  
AAR49442  
ID AAR49442 standard; protein; 4 AA.  
XX  
AC AAR49442;  
XX  
XX 25-MAR-2003 (revised)  
DT 16-SEP-1994 (first entry)  
XX  
XX Immunomodulatory trafficking sequence #1.  
DE  
XX Naturally-occurring; immunomodulatory protein; human; therapy; class I;  
KW major histocompatibility complex; class II; allotype; type I diabetes;  
KW autoimmune disease; rheumatoid arthritis; T-cell-mediated response;  
KW multiple sclerosis; transplant rejection; vaccine; MHC.  
XX  
OS Homo sapiens.  
XX  
XX WO9404171-A1.  
PN  
XX 03-MAR-1994.  
PD  
XX 11-AUG-1993; 93WO-US007545.  
XX  
XX 11-AUG-1992; 92US-00925460.  
PR 15-JUN-1993; 93US-00077255.  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX Urban RG, Chicx RM, Vignali DA, Hedley ML, Stern LJ;  
PI Strominger JL;  
PI  
XX WPI; 1994-082825/10.  
DR  
XX Novel immunomodulatory peptide(s) and nucleic acids - useful for  
PT treatment of auto:immune diseases, transplant rejection and for  
PT vaccination.  
XX  
XX Claim 13; Page 94; 139pp; English.

The sequences given in AAR49291-505 and AAR46981-7038 represent peptide  
CC fragments of naturally-occurring immunomodulatory proteins. These  
CC fragments are between 10-30 residues in length and bind to a human major  
CC histocompatibility complex (MHC) class II allotype. These peptides may be  
CC used for therapy of autoimmune diseases, such as type I diabetes,  
CC rheumatoid arthritis and multiple sclerosis, and to reduce transplant  
CC rejection. They may also be used for vaccination providing an exclusively

CC T-cell-mediated response, which can be class I or class-II based, or  
CC both, depending on the length and character of the immunogenic peptides.  
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to  
CC correct PR field.)  
XX  
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
| | | |  
Db 1 KDEL 4

RESULT 4  
AAR49584  
ID AAR49584 standard; peptide; 4 AA.  
XX  
AC AAR49584;  
XX  
XX 25-MAR-2003 (revised)  
DT 15-SEP-1994 (first entry)  
XX  
XX Sequence of endoplasmic reticulum (ER) retention peptide.  
DE  
XX Endoplasmic reticulum; ER; trafficking sequence.  
KW  
XX Synthetic.  
OS  
XX WO9404557-A1.  
PN  
XX 03-MAR-1994.  
PD  
XX 11-AUG-1992; 92WO-US006692.  
XX  
XX 11-AUG-1992; 92WO-US006692.  
PR  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX Urban RG, Chicx RM, Vignali DAA, Hedley ML, Stern LJ;  
PI Strominger JL;  
PI  
XX WPI; 1994-083102/10.  
DR  
XX New peptide binding to MHC class II allotype - useful for treating auto-  
PT immune diseases, transplant rejection and for immunisation.  
PT  
XX Claim 20; Page 49; 60pp; English.  
XX  
XX A trafficking sequence is an AA sequence which functions to control  
CC intracellular trafficking (directed movement from organelle to organelle  
CC or to the cell surface) of a polypeptide to which it is attached. Such  
CC trafficking sequences might traffic the polypeptide to ER, a lysosome, or  
CC an endosome, and include signal peptides, ER retention peptides such as  
CC AAR49584; and lysosome-targeting peptides such as AAR49585 and AAR49586.  
CC An example of a signal peptide with such a function is the signal peptide  
CC of MHC class II alpha (AAR49587). (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
| | | |  
Db 1 KDEL 4

RESULT 5

AAR95063  
ID AAR95063 standard; peptide; 4 AA.  
XX  
AC AAR95063;  
XX  
DT 22-AUG-1996 (first entry)  
XX  
DE Mammalian endoplasmic reticulum retention signal.  
XX  
KW Nucleic acid transfer system; gene transfer; gene therapy;  
KW cell targeting; multidomain protein; vector; cancer;  
KW endoplasmic reticulum.  
XX  
OS Synthetic.  
XX  
FN WO9613599-A1.  
XX  
PD 09-MAY-1996.  
XX  
PF 31-OCT-1995; 95WO-EP004270.  
XX  
PR 01-NOV-1994; 94EP-00810627.  
XX  
PA (WELLS/) WELLS W.  
XX  
PI Wells W, Fominaya J;  
XX  
XX WPI; 1996-239505/24.  
XX  
XX Nucleic acid transfer system for gene therapy, e.g. against cancer -  
PT includes toxin translocation domain to target nucleic acid to specific  
PT cell.  
XX  
PS Disclosure; Page 11; 106pp; English.  
XX  
CC Endoplasmic reticulum retention signals include a mammalian signal  
CC (AAR95063), a bacterial signal (AAT05064) from Pseudomonas exotoxin, and  
CC a yeast signal (AAR95065). The signal may form part of a multidomain  
CC protein (see also AAR95053-58) that is used with an effector nucleic acid  
CC for the transfer of nucleic acids to targeted cells as a means of gene  
CC therapy. The endoplasmic reticulum retention signal functions to affect  
CC intracellular routing of the internalized protein/nucleic acid complex  
XX  
SQ Sequence 4 AA;  
  
Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KDEL 4  
Db ||||  
1 KDEL 4  
  
RESULT 6  
AAR94944  
ID AAR94944 standard; protein; 4 AA.  
XX  
AC AAR94944;  
XX  
DT 31-OCT-1996 (first entry)  
XX  
DE Microsomal retention signal.  
XX  
KW Toxin; subunit; vaccine; transgenic plant; immunogen; antigen; adjuvant;  
KW immunisation.  
XX  
OS Synthetic.  
XX  
FN WO9612801-A1.  
XX  
PD 02-MAY-1996.  
XX

PF 24-OCT-1995; 95WO-US013376.  
XX  
PR 24-OCT-1994; 94US-00328716.  
XX  
PA (TEXA ) UNIV TEXAS A & M SYSTEM.  
PA (TULA ) TULANE EDUCATIONAL FUND.  
XX  
PI Arntzen CJ, Mason HS, Haq TA, Clements JD;  
XX  
XX WPI; 1996-230602/23.  
XX  
XX Transgenic plants contg. E. coli heat labile enterotoxin subunits - used  
PT as oral vaccines for animals which consume the plant.  
XX  
XX Example 13; Page 95; 130pp; English.  
XX  
CC A transgenic plant comprising or expressing a DNA sequence encoding an  
CC immunogenic agent can be used as an oral vaccine for animals. The  
CC vaccine is administered by the oral consumption of the plant and provides  
CC the first known functional method for immunising animals using transgenic  
CC plants, where the plants express bacterial antigens that act as both  
CC immunogens and adjuvants. The method provides an inexpensive production  
CC and delivery system for such antigens to animals. This sequence acts as a  
CC microsomal retention signal and was used to modify the LT-B Escherichia  
CC coli toxin subunit C-terminal sequence. The sequence coding for the whole  
CC LT-B gene was used in the construction of such a transgenic plant. The  
CC immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B  
CC subunit) or optionally LT-A or CT-A  
XX  
SQ Sequence 4 AA;  
  
Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KDEL 4  
Db ||||  
1 KDEL 4  
  
RESULT 7  
AAR95219  
ID AAR95219 standard; protein; 4 AA.  
XX  
AC AAR95219;  
XX  
DT 16-DEC-1996 (first entry)  
XX  
DE Pseudomonas exotoxin modified C-terminal sequence.  
XX  
KW Antibody; fusion protein; single chain; inhibition; tumour; diagnosis;  
KW detection; imaging; immunotoxin; targeting; assay; immunoassay;  
KW Lewis(Y) carbohydrate antigen.  
XX  
OS Pseudomonas sp.  
XX  
FN WO9613594-A1.  
XX  
PD 09-MAY-1996.  
XX  
PF 26-OCT-1995; 95WO-US013811.  
XX  
PR 28-OCT-1994; 94US-00331396.  
PR 28-OCT-1994; 94US-00331397.  
PR 28-OCT-1994; 94US-00331398.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Pastan I, Benhar I, Padlan EA, Jung S, Lee B, Willingham M;  
PI Fitzgerald D, Brinkmann U, Pai L;  
XX  
XX WPI; 1996-251462/25.  
XX

PT Single chain fusion proteins and antibodies - useful to diagnose and  
 PT treat cancer, specifically bind Lewis(Y) related carbohydrate antigen.  
 PS Disclosure; Page 14; 116pp; English.  
 XX  
 CC A novel recombinant DNA molecule which encodes a single chain fusion  
 CC protein or antibody comprising the Fv region of both the light and heavy  
 CC chains of an antibody (Ab) fused together, and an effector molecule,  
 CC where the fusion protein or Ab has the binding specificity of monoclonal  
 CC Ab (MAb) B1, B3 or B5, can be used for the production of such fusion  
 CC proteins or antibodies. The fusion proteins can be used in compositions  
 CC as an immunotoxin to inhibit tumour cell growth. The single chain  
 CC antibody can be used to detect the presence or absence of cells bearing a  
 CC Lewis(Y) carbohydrate antigen in a patient. The antibodies are also  
 CC useful as multiple targeting moieties, providing at least 2 kinds of  
 CC biological activity. They can also be used in diagnostic assays and for  
 CC the imaging of tumours when attached to a radiolabel and for the  
 CC pathological diagnosis of tumours. Humanised antibodies are less  
 CC immunogenic than the mouse MAbs B1, B3 and B5, making them more suitable  
 CC for long term treatment. The effector molecule used is preferably a drug  
 CC or cytotoxin which then produces an immunotoxin capable of selectively  
 CC killing particular cells. Preferred toxins are the Pseudomonas exotoxin  
 CC or Diphtheria toxin. These are both highly toxic compounds and so are  
 CC modified to eliminate domain Ia of the Pseudomonas toxin, various amino  
 CC acid deletions in domains II and III, single amino acid substitutions and  
 CC addition of one or more sequences at the C-terminal end. The wild type C-  
 CC terminal sequence of the Pseudomonas exotoxin is given in AAR95221  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KDEL 4  
 Db | | | |  
 1 KDEL 4  
 RESULT 8  
 AAW21969  
 ID AAW21969 standard; peptide; 4 AA.  
 AC  
 AC AAW21969;  
 XX  
 DT 03-DEC-1997 (first entry)  
 XX  
 DE Linker #3 for immunotoxin containing Pseudomonas exotoxin.  
 XX  
 KW PCR; primer; amplify; polymerase chain reaction; antibody; immunotoxin;  
 KW variable heavy chain; VH; murine monoclonal antibody; Lewisy; carcinoma;  
 KW carbohydrate antigen; Pseudomonas exotoxin; proteolytic activation;  
 KW cytotoxic activity; tumour; autoimmune condition; rheumatoid arthritis;  
 KW graft versus host disease; organ transplant rejection; type I diabetes;  
 KW multiple sclerosis; systemic lupus erythematosus; myasthenia gravis;  
 KW T cell; B cell; cytosol; bone marrow; transplant; therapy.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9713529-A1.  
 FN  
 XX 17-APR-1997.  
 PD  
 XX 11-OCT-1996; 96WO-US016327.  
 PF  
 XX 13-OCT-1995; 95US-0005388P.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Pastan I, Kuan C;  
 PI  
 XX WPI; 1997-235666/21.  
 DR  
 XX

PT Immuno:toxin(s) comprising Pseudomonas exotoxin linked to di:sulphide  
 PT stabilised variable heavy and light chain regions of an antibody - useful  
 PT for killing target cells bearing characteristic marker.  
 XX  
 PS Claim 9; Page 50; 64pp; English.  
 XX  
 CC AAW21967-W21969 represent linkers used in the immunotoxins of the  
 CC invention. The immunotoxins bind to target cells, and comprise, a  
 CC Pseudomonas exotoxin (PE) that does not need proteolytic activation for  
 CC cytotoxic activity fused to a VH framework region of an Fv antibody (Ab)  
 CC fragment. The VH chain region is bound through at least one disulphide  
 CC bond to a variable light (VL) chain framework region. The PE is lacking  
 CC residues 1-279 and is at least 10-fold more cytotoxic to the target cells  
 CC than an immunotoxin comprising PE attached to a VH chain framework region  
 CC of an Fv Ab fragment lacking a disulphide bond to a VL chain framework  
 CC region. These sequences are used to join the VH chain region to the PE.  
 CC The immunotoxins can be used for killing target cells in the treatment of  
 CC tumours, autoimmune conditions, graft versus host disease, organ  
 CC transplant rejection, type I diabetes, multiple sclerosis, rheumatoid  
 CC arthritis, systemic lupus erythematosus, myasthenia gravis, etc, all  
 CC caused by T and B cells. They can also be used to deliver an antibody to  
 CC the cytosol of a cell, and in vitro in the elimination of harmful cells  
 CC from bone marrow before transplant. The immunotoxins have high  
 CC cytotoxicity to target cells and a small size to provide greater  
 CC penetration to target cells  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KDEL 4  
 Db | | | |  
 1 KDEL 4  
 RESULT 9  
 AAW31861  
 ID AAW31861 standard; peptide; 4 AA.  
 XX  
 AC AAW31861;  
 XX  
 DT 06-MAY-1998 (first entry)  
 XX  
 DE Endoplasmic reticulum retention peptide.  
 XX  
 KW RNA-loaded antigen presenting cell; trafficking sequence; APC production;  
 KW tumour formation; pathogen infection; antigenic epitope; immune response;  
 KW T cell proliferation; cytotoxic T lymphocyte; adoptive immunotherapy;  
 KW therapy; TAE; CTL; PAE; endoplasmic reticulum retention peptide.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9741210-A1.  
 FN  
 XX 06-NOV-1997.  
 PD  
 XX 30-APR-1997; 97WO-US007317.  
 PF  
 XX 30-APR-1996; 96US-00640444.  
 PR  
 XX (UYDU-) UNIV DUKE.  
 PA  
 XX Nair SK, Boczkowski DJ, Gilboa E;  
 PI  
 XX WPI; 1997-549715/50.  
 DR  
 XX Use of RNA-loaded antigen presenting cells - to induce T-cell  
 PT proliferation for the treatment or prevention of tumour formation or  
 PT pathogen infection.  
 XX  
 PS Claim 49; Page 38; 47pp; English.

XX This sequence represents a endoplasmic reticulum retention peptide, and  
 CC can be used in the method of the invention. The method is for producing  
 CC an RNA-loaded antigen presenting cell (APC) that presents on its surface  
 CC a tumour or pathogen antigenic epitope (TAE or PAE respectively) that  
 CC induces T cell proliferation and an immune response against the tumour or  
 CC pathogen, and comprises introducing into an APC in vitro, RNA that  
 CC encodes the antigen. The RNA-loaded APCs can be used to stimulate  
 CC cytotoxic T lymphocyte (CTL) proliferation ex vivo or in vivo. The ex  
 CC vivo expanded CTL can be administered to a patient in a method of  
 CC adoptive immunotherapy. The methods can be used for treating or  
 CC preventing tumour formation or pathogen infection caused by e.g. HIV,  
 CC hepatitis, influenza, poliomyelitis, measles, herpes, mumps or rubella  
 CC viruses, Salmonella, Shigella or Enterobacter. The method circumvents the  
 CC need to purify RNA or isolate and identify a TAE or PAE  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
 ||||  
 DB 1 KDEL 4

RESULT 10  
 AAW56513  
 ID AAW56513 standard; peptide; 4 AA.

AC AAW56513;

DT 28-SEP-1998 (first entry)

XX Endoplasmic reticulum recycling peptide.

XX Intracellular targeting sequence; endoplasmic reticulum; DNA vaccine;  
 KW Genetic immunisation; allergy; autoimmune disease; cancer; infection;  
 KW psoriasis.

XX Synthetic.

XX WO9817323-A1.

XX 30-APR-1998.

XX 23-OCT-1997; 97WO-US019545.

XX 23-OCT-1996; 96US-0029592P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Williams WV, Madaio M, Weiner DB;

XX WPI; 1998-261198/23.

XX Plasmid encoding immunogenic target protein - used in, e.g. protective or  
 PT therapeutic vaccines against allergy, cancer, microbial infection or auto  
 PT -immune disease.

XX Claim 7; Page 62; 84pp; English.

XX This peptide, when joined to the C-terminus of a protein, acts as an  
 CC endoplasmic reticulum (ER) recycling signal that localises the protein  
 CC from the Golgi body back to the ER when expressed in a cell. A claimed  
 CC novel plasmid comprises a sequence, linked to regulatory elements, that  
 CC encodes an immunogenic target protein that includes, or is linked to, an  
 CC intracellular targeting sequence (ITS) such as this peptide. Other ITS  
 CC peptides (see AAW56512 and AAW56514) are provided that direct  
 CC localisation in the lysosome or the ER. The novel plasmid is used as a  
 CC protective or therapeutic DNA vaccine to immunise against the immunogenic  
 CC target protein (claimed), particularly in cases of allergy, cancer (or

CC other proliferative diseases such as psoriasis), microbial infection or  
 CC autoimmune disease, e.g. rheumatoid arthritis, insulin-dependent diabetes  
 CC mellitus, Crohn's disease, asthma, pernicious anaemia and many others. A  
 CC particular use is against pathogens that, at least for part of their life  
 CC cycle, are intracellular, e.g. hepatitis C, HIV, Neisseria gonorrhoeae,  
 CC Listeria and Shigella. The cytotoxic T cell response is enhanced by  
 CC delivering the immunogenic target protein to the ER  
 XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
 ||||  
 DB 1 KDEL 4

RESULT 11  
 AAW76396  
 ID AAW76396 standard; peptide; 4 AA.

XX AAW76396;

XX 11-JAN-1999 (first entry)

XX Endoplasmic reticulum transport signal consensus.

XX Exotoxin A; ETA; drug delivery; membrane transport;  
 KW endoplasmic reticulum.

XX Synthetic.

XX WO9842876-A1.

XX 01-OCT-1998.

XX 24-MAR-1998; 98WO-US005710.

XX 26-MAR-1997; 97US-0042056P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Draper RK;

XX WPI; 1998-532023/45.

XX Delivering compounds to cells as new conjugate with detoxified exotoxin A  
 PT - able to cross membranes and deliver to the cytoplasm, e.g. nucleic  
 PT acids, antibodies, tumour suppressors etc.

XX Disclosure; Page 8; 76pp; English.

XX This peptide is the consensus intracellular transport signal used for  
 CC returning back to the endoplasmic reticulum (ER) proteins that have the  
 CC escaped the ER and entered to Golgi complex. The mechanism involves the  
 CC KDEL receptor. The KDEL motif can replace a REDL motif (see AAW76395)  
 CC present at the C-terminal end of Pseudomonas aeruginosa exotoxin A (ETA,  
 CC see AAW76391). This motif is important in the intracellular transport and  
 CC cytotoxicity of ETA. This suggests that ETA interacts with the KDEL  
 CC receptor and that ETA may reach the interior of the ER before penetrating  
 CC the cytosol. The invention provides a means of delivering compounds to  
 CC cells as conjugates with modified ETA. The modified ETA is able to cross  
 CC membranes and deliver e.g. therapeutic agents to the cytoplasm, such as  
 CC nucleic acids, peptides, peptide nucleic acids, single chain antibodies  
 CC and tumour suppressors

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



PR 10-MAR-1994; 94US-00209604.  
XX (REGC ) UNIV CALIFORNIA.  
PA  
XX Paulson JG, Colley KJ, Browne JK, Adler B, Weinstein J;  
PI Ujita-Lee E;  
XX WPI; 1998-398046/34.  
DR  
XX Expression cassette for producing glycosyltransferase in secretable form  
PT - lacking membrane anchor and Golgi retention signal, used for synthesis  
PT of oligosaccharide(s).  
XX Disclosure; Col 3; 16pp; English.  
PS  
XX The invention relates to expression cassettes which contain a promoter  
CC and a DNA sequence encoding a secreted glycosyltransferase that lacks the  
CC membrane anchor and the Golgi retention signal. The glycosyl-  
CC transferases are used in enzymatic oligosaccharide synthesis. They are  
CC produced in a soluble form that is secreted into the culture medium  
CC without loss of enzymatic activity, resulting in increased production and  
CC simpler recovery (free of any membrane-bound glycosyl- transferase),  
CC compared with extraction from mammalian tissue. The present sequence  
CC represents a carboxy-terminal sequence sufficient for retention of a  
CC protein in the endoplasmic reticulum  
XX  
XX Sequence 4 AA;  
SQ  
Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KDEL 4  
Db ||||  
1 KDEL 4  
RESULT 15  
AAW61591  
ID AAW61591 standard; peptide; 4 AA.  
XX  
AC AAW61591;  
XX  
XX 27-OCT-1998 (first entry)  
DT  
XX Endomembrane retention signal.  
DE  
XX J chain; targeting molecule; epithelial; beta-sheet; asthma; cancer;  
KW inflammatory disorder; autoimmune disorder; celiac disease; colitis;  
KW pneumonia; cystic fibrosis.  
XX  
XX Synthetic.  
OS  
XX WO9830592-A1.  
PN  
XX 16-JUL-1998.  
PD  
XX 09-JAN-1998; 98WO-US000542.  
PF  
XX 10-JAN-1997; 97US-00782481.  
PR  
XX (EPIC-) EPICYTE PHARM INC.  
PA  
XX Hein MB, Hiatt AC, Fitchen JH;  
PI WPI; 1998-399067/34.  
DR  
XX New epithelial tissue targeting agent - used to deliver biologically  
PT active compounds to an epithelial surface for internalisation.  
PT  
XX Example 1; Page 48; 142pp; English.  
PS  
XX The endomembrane retention signal is used in the synthesis of a targeting  
CC

CC molecule (TM). The TMs are used to target biological agents to epithelial  
CC surfaces at which they can be internalised. The TMs comprise a  
CC polypeptide that: (a) forms a closed covalent loop; (b) contains at least  
CC 3, preferably 4, peptide domains having beta-sheet character separated by  
CC domains lacking beta-sheet character; and (c) is not full length dimeric  
CC IgA. The TMs are useful to prevent and/or treat diseases associated with  
CC epithelial surfaces, e.g. asthma, cancer, (myco)bacterial, viral or  
CC fungal infection, inflammatory disorders, autoimmune disorders, celiac  
CC disease, colitis, pneumonia and cystic fibrosis  
XX  
XX Sequence 4 AA;  
SQ  
Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KDEL 4  
Db ||||  
1 KDEL 4  
RESULT 16  
AAW51434  
ID AAW51434 standard; peptide; 4 AA.  
XX  
AC AAW51434;  
XX  
XX 02-SEP-1998 (first entry)  
DT  
XX C-terminal sequence of localisation peptides for the ER.  
DE  
XX Bifunctional chelating polysaccharide; targeting peptide; heparin;  
KW nuclear localisation; fluorescent indicator; dextran; ficol; glycogen;  
KW amylopectin; mannan; inulin; starch; agarose; cellulose; ER;  
KW endoplasmic reticulum.  
XX  
XX Synthetic.  
OS  
XX US5773227-A.  
PN  
XX 30-JUN-1998.  
PD  
XX 23-JUN-1993; 93US-00082269.  
PF  
XX 23-JUN-1993; 93US-00082269.  
PR  
XX (MOLE-) MOLECULAR PROBES INC.  
PA  
XX Meyer T, Kuhn MA, Allbritton NL;  
PI WPI; 1998-386995/33.  
XX  
XX Bifunctional chelating polysaccharides used for analysing intracellular  
PT ion levels - have chelating moieties attached which act as a fluorescent  
PT indicator in the presence of selected metal ions.  
XX  
XX Disclosure; Col 9; 29pp; English.  
PS  
XX The invention relates to a water soluble polysaccharide with a molecular  
CC weight greater than 1000 Daltons covalently attached to (a) at least one  
CC chelating moiety selective for a monovalent or divalent metal ion (to act  
CC as a fluorescent indicator for the metal ion) and (b) at least one  
CC targeting peptide (to localise the compound to the inside of a cellular  
CC organelle). Preferably the polysaccharide is dextran, ficol, heparin,  
CC glycogen, amylopectin, mannan, inulin, starch, agarose or cellulose with  
CC a molecular weight less than 3,000,000. The metal ion is preferably Na+,  
CC K+, Li+, Ca2+ or Mg2+. The compounds are useful for analysing intra-  
CC cellular ion levels, especially Ca2+. The present sequence represents a  
CC carboxyl terminal sequence commonly shared by localisation peptides for  
CC the endoplasmic reticulum (ER)  
XX  
XX Sequence 4 AA;  
SQ



Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
 ||||  
 Db 1 KDEL 4

## RESULT 17

ABB76201  
 ID ABB76201 standard; peptide; 4 AA.

XX  
 AC ABB76201;

XX 05-AUG-2002 (first entry)

XX Peptide used to modify Pseudomonas exotoxin.

XX Exotoxin; Pseudomonas; immunotoxin; mesothelin; scFv; mesothelioma;  
 KW ovarian cancer; stomach cancer; squamous cell cancer; antitumour;  
 KW therapy; diagnosis.

XX Synthetic.

XX WO9928471-A2.

XX 10-JUN-1999.

XX 25-NOV-1998; 98WO-US025270.

XX 01-DEC-1997; 97US-0067175P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Pastan IH, Chowdhury PS;

XX WPI; 1999-371123/31.

XX New anti-mesothelin antibodies.

XX Disclosure; Page 29; 63pp; English.

XX The present sequence is a peptide that can be added to the C-terminal end  
 CC of a Pseudomonas exotoxin (PE) to produce a modified PE. Claimed  
 CC immunocjugates comprise a therapeutic agent, such as PE or a cytotoxic  
 CC fragment of PE, and an anti-mesothelin antibody, such as scFv SS (see  
 CC ABB76197), and are obtained by recombinant methods. The recombinant  
 CC immunocjugates are used in a claimed method for inhibiting the growth  
 CC of a malignant cell that expresses mesothelin on its cell surface,  
 CC especially in mesothelioma, ovarian cancer, stomach cancer or squamous  
 CC cell cancer

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
 ||||  
 Db 1 KDEL 4

## RESULT 18

AAW92911  
 ID AAW92911 standard; protein; 4 AA.

XX  
 AC AAW92911;

XX 17-MAY-1999 (first entry)

XX Pseudomonas sp. exotoxin A PE ER retention peptide motif #3.

XX Exotoxin A; chimeric immunogen; non-toxic; PE-like; vaccine; pathogen;  
 KW antibody production; non-native epitope; immune response; antigen;  
 KW cancer; parasite; cell binding domain; domain Ia; humoral; cell-mediated;  
 KW secretory; IgA-mediated; mucosal surface; IgA antibody; retention domain;  
 KW endoplasmic reticulum.

XX Pseudomonas sp.

XX WO9902712-A1.

XX 21-JAN-1999.

XX 10-JUL-1998; 98WO-US014336.

XX 11-JUL-1997; 97US-0056924P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (GETH ) GENENTECH INC.

XX Fitzgerald DJ, Mresny RJ;

XX WPI; 1999-120913/10.

XX New Pseudomonas exotoxin chimeric immunogens - comprise a foreign epitope  
 PT for producing an immune response to pathogens, e.g. virus, bacteria or  
 PT protozoa or to cancer antigens.

XX Disclosure; Page 33; 85pp; English.

XX This invention describes a method in which a secretory IgA-mediated  
 CC immune response is elicited in a subject. The method involves  
 CC administering to at least 1 mucosal surface of the subject a non-toxic  
 CC Pseudomonas exotoxin A-like (PE-like) chimeric immunogen comprising a  
 CC cell recognition domain of that binds to a cell surface receptor on the  
 CC mucosal surface, a translocation domain comprising an amino acid sequence  
 CC of PE domain II to effect translocation to a cell cytosol, a foreign  
 CC epitope domain comprising an amino acid sequence of that encodes a  
 CC foreign epitope, and a sequence encoding an endoplasmic reticulum (ER)  
 CC retention domain that comprises an ER retention sequence. Also described  
 CC is a composition comprising secretory IgA antibodies that specifically  
 CC recognise an epitope of HIV-1. The method can be used for eliciting an  
 CC immune response to pathogens, e.g. virus, bacteria or parasitic protozoa  
 CC or to a cancer antigen. The antibodies produced can also be isolated and  
 CC used, e.g. for affinity chromatography. The PE immunogens can be made by  
 CC wholly recombinant techniques which allows insertion of existing variants  
 CC of an epitope, or new variants of rapidly evolving epitopes. The PE can  
 CC be engineered to alter the function of its domains, thereby providing a  
 CC variety of activities, e.g. by replacing the native cell binding domain  
 CC of PE A (domain Ia) with a ligand for a particular cell receptor, the  
 CC chimera can be targeted to bind to the particular cell type. By providing  
 CC a cell recognition domain that binds to a mucosal surface a secretory  
 CC immune response involving IgA can be elicited. This sequence represents a  
 CC PE protein endoplasmic reticulum (ER) retention domain motif

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
 ||||  
 Db 1 KDEL 4

## RESULT 19

AAW85767  
 ID AAW85767 standard; peptide; 4 AA.

XX AAW85767;

XX 27-SEP-1999 (first entry)

transcription; cell growth; cell proliferation; cell differentiation; apoptosis.

Unidentified.

WO9936553-A2.

22-JUL-1999.

15-JAN-1999; 99WO-US000178.

15-JAN-1998; 98US-0071591P.

21-JAN-1998; 98US-0072016P.

22-JAN-1998; 98US-00012097.

22-JAN-1998; 98US-0072219P.

(ARIA-) ARIAD GENE THERAPEUTICS INC.

Clackson TP, Gilman MZ, Holt DA, Keenan TP, Rozamus L, Yang W; WPI; 1999-468986/39.

Multimerizing chimeric proteins in cells useful in gene therapy, for e.g. target gene transcription and growth of engineered cells.

Disclosure; Page 56; 155pp; English.

The specification describes a process for multimerising chimeric proteins in cells. The method comprises forming a complex between a rapamycin compound and cells containing at least one recombinant nucleic acid (rNA) construct encoding specialised chimeric proteins (CPs). The method is used for multimerising chimeric proteins in cells, which is useful for gene therapy, activating the transcription of a desired gene, actuating cell growth, proliferation, differentiation or apoptosis, or triggering other biological events in engineered cells in a rapalog-dependent manner. The present sequence can be included in the chimeric proteins of the invention

Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4

DB 1 KDEL 4

RESULT 21

AAV27177

ID AAV27177 standard; peptide; 4 AA.

XX

AC AAY27177;

XX

DT 15-SEP-1999 (first entry)

XX

DE Organelle-targeting domain peptide fragment.

XX

KW Drug-induced growth; cell proliferation; cell differentiation; leukemia; signalling domain; drug-binding domain; hemopoietic disease; leukopenia; neurodegenerative disease; thrombocytopenia; beta-thalassemia; sickle cell anemia; Fanconi anemia; myelodysplastic syndrome; chronic granulomatous disease; leukocyte adhesion deficiency.

XX

OS Unidentified.

XX

PN WO9934836-A1.

XX

PD 15-JUL-1999.

XX

XX 07-JAN-1999; 99WO-US000348.

XX

Endomembrane retention signal.

Targeting molecule; J chain; immunoglobulin; IgM; IgA; substrate; epithelial cell; cancer; treatment; therapy;

non-small cell lung carcinoma; breast carcinoma; colon carcinoma; ovarian carcinoma; prostate carcinoma; endometriosis; viral infection; inflammation.

Synthetic.

WO9920310-A1.

29-APR-1999.

20-OCT-1998; 98WO-US022304.

20-OCT-1997; 97US-00954211.

(EPIC-) EPICYTE PHARM INC.

Hein MB, Hiatt AC, Fitch JH; WPI; 1999-288174/24.

Targeting molecule useful in drug delivery for treating cancer, viral infection or inflammatory disorders.

Example 1; Page 47; 102pp; English.

A targeting agent for improving the delivery of drugs to target cells, particularly for delivery of enzymes, binding agents, inhibitors, nucleic acids, carbohydrates and lipids, is new. The targeting agent comprises a polypeptide which forms a closed covalent loop and contains at least three peptide domains having beta-sheet character, each of the domains being separated by domains lacking beta-sheet character. The targeting molecule preferably comprises all or a portion of a native J chain sequence. J chain is a 15 kD protein that, in vivo, links IgM or IgA monomers to form pentameric IgM or dimeric IgA. The polypeptide is linked to at least one biological agent which is capable of entering and killing a non-polarised epithelial cell. The targeting molecule may be linked to the biological agent by a substrate for an intracellular or extracellular enzyme which is associated with or secreted by the non-polarised target cell. The targeting molecule can be used in a pharmaceutical composition for treating a patient afflicted with a disease associated with non-polarised epithelial cells, especially cancer e.g. non-small cell lung carcinoma, breast carcinoma, colon carcinoma, ovarian carcinoma, prostate carcinoma and endometriosis, viral infection or inflammatory disorders. This peptide is an endomembrane retention signal which can be attached to the carboxy terminal end of the targeting molecules described

Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4

DB 1 KDEL 4

RESULT 20

AAV30052

ID AAV30052 standard; peptide; 4 AA.

XX

AC AAY30052;

XX

DT 06-OCT-1999 (first entry)

XX

DE Organelle targeting domain peptide sequence.

XX

KW Multimerisation; chimeric protein; rapamycin compound; gene therapy;

PR 08-JAN-1998; 98US-0070754P.  
 PR 09-JAN-1998; 98US-0070893P.  
 PR 02-OCT-1998; 98US-0102888P.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Blau CA;  
 XX  
 DR WPI; 1999-430335/36.  
 XX  
 PT A method to positively select engineered cells and controlling cell  
 PT differentiation and growth, useful for expanding subpopulations of cells.  
 XX  
 PS Disclosure; Page 6; 77pp; English.  
 XX  
 CC The invention relates to a method for rendering a subpopulation of  
 CC mammalian cells susceptible to drug-induced growth, proliferation or  
 CC differentiation. The method comprises transducing one or more cells of a  
 CC population of primary mammalian cells with at least one recombinant DNA  
 CC construct encoding a fusion protein. The fusion protein comprises at  
 CC least one signalling domain and at least one drug-binding domain which is  
 CC heterologous with respect to the signaling domain and binds to a selected  
 CC drug. Exposure of the transduced cells to the drug induces growth,  
 CC proliferation or differentiation of the cells. The methods can be used to  
 CC expand a subpopulation of primary mammalian (especially human) cells.  
 CC This is useful for obtaining populations of megakaryocytes, neutrophils  
 CC or erythroid cells. The methods are useful for treating a hemopoietic  
 CC disease or pathological condition, or neurodegenerative disease in a  
 CC mammal. In particular, the methods can be used for rendering a  
 CC subpopulation of human embryonic stem cells susceptible to drug-induced  
 CC growth, proliferation or differentiation. The methods are also useful for  
 CC administering hemopoietic stem cell therapy to a mammal. Hemopoietic  
 CC diseases suitable for treatment include thrombocytopenia, leukopenia,  
 CC leukemia, beta-thalassemia, sickle cell anemia, Fanconi anemia, aplastic  
 CC anemia, myelodysplastic syndrome, chronic granulomatous disease and  
 CC leukocyte adhesion deficiency  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KDEL 4  
 ||||  
 Db 1 KDEL 4  
 RESULT 22  
 ID AAY49700  
 AC AAY49700 standard; peptide; 4 AA.  
 XX  
 AC AAY49700;  
 XX  
 DT 18-JAN-2000 (first entry)  
 XX  
 DE Pseudomonas exotoxin peptide #4.  
 XX  
 KW Pseudomonas exotoxin; PE; mutagenised; IL-13; chimeric; interleukin;  
 KW cytotoxin; fusion protein; cancer; glioma; neoplasia.  
 XX  
 OS Synthetic.  
 OS Pseudomonas sp.  
 XX  
 PN WO9951643-A1.  
 XX  
 PD 14-OCT-1999.  
 XX  
 PF 31-MAR-1999; 99WO-US007188.  
 XX  
 PF 03-APR-1998; 98US-00054711.  
 XX  
 PA (PENN-) PENN STATE RES FOUND.

XX Debinski W;  
 XX  
 DR WPI; 1999-633731/54.  
 XX  
 PT New mutagenized interleukin 13 molecules for delivery of cytotoxins to  
 PT cells over expressing IL13 receptors.  
 XX  
 PS Disclosure; Page 17; 57pp; English.  
 XX  
 CC The present invention describes targeting ligands which are mutagenized  
 CC IL13 (interleukin 13) molecules having one or more mutations in the  
 CC domain that interacts with the hIL14 receptor subunit designated the 140  
 CC kDa hIL14Rbeta subunit. A cytotoxic molecule covalently attached to a  
 CC mutagenized hIL13 can be used for delivering an effector molecule to a  
 CC cell bearing an IL13 receptor. Where the effector molecule is a  
 CC cytotoxin, neoplastic cells (e.g. a glioma) can be killed or inhibited.  
 CC The methods are used to target effector molecules to kidney cancers, to  
 CC skin cancers (Kaposi's sarcoma) and to brain cancers (gliomas and  
 CC medulloblastomas). When the mutagenized cell is attached to a detectable  
 CC label the chimeric label can be used to detect the presence or absence of  
 CC tumour cells, or localize and/or quantify a cell or cells expressing an  
 CC IL13 receptor. The label localizes at the site of overexpression and  
 CC indicates the presence, absence, quantity or location of such cells. If  
 CC the effector molecule is an antibody the chimeric molecule may act to  
 CC enhance and direct an immune response toward target cancer cells. The  
 CC mutagenized IL13s may be conjugated to a drug such as vinblastine,  
 CC doxorubicin, gemtistein, an antisense molecule, ribozymes or any other  
 CC pharmacological agent to specifically target target cells over expressing  
 CC IL13 receptors. The targeting ligands have increased specificity for  
 CC cancer cells as compared to normal cells and are therefore very effective  
 CC for specifically delivering effector molecules to various neoplasias. The  
 CC present sequence is used in the exemplification of the present invention  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KDEL 4  
 ||||  
 Db 1 KDEL 4  
 RESULT 23  
 ID AAW96345  
 AC AAW96345 standard; peptide; 4 AA.  
 XX  
 AC AAW96345;  
 XX  
 DT 19-JUL-1999 (first entry)  
 XX  
 DE Endoplasmic reticulum localisation signal peptide.  
 XX  
 KW Antibody; immune response; modulation; MHC; IRM; receptor; intrabody;  
 KW major histocompatibility complex; graft rejection;  
 KW immunomodulatory response molecule; regulation; transplantation;  
 KW retention signal; localisation signal; golgi apparatus; ER;  
 KW endoplasmic reticulum.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9914353-A2.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 18-SEP-1998; 98WO-US019563.  
 XX  
 PF 19-SEP-1997; 97US-0059339P.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 XX

|           |   |
|-----------|---|
| XX        | bacteria, or protozoa or to cancer antigens.                                  |
| PS        | Claim 13; Page 64; 92pp; English.   |
| XX        | This invention describes a non-toxic Pseudomonas exotoxin A-like (PE-         |
| CC        | like), chimeric immunogen. This PE-like immunogen can be used in vaccines     |
| CC        | and for producing antibodies against the non-native epitope. It can be        |
| CC        | used for producing an immune response to a pathogen, e.g. a virus,            |
| CC        | bacteria or parasitic protozoa or a cancer antigen. The antibodies can        |
| CC        | also be isolated and used for e.g. affinity chromatography. The PE            |
| CC        | immunogens can be made by wholly recombinant techniques which allows          |
| CC        | insertion of existing variants of an epitope, or new variants of rapidly      |
| CC        | evolving epitopes. The PE can be engineered to alter the function of its      |
| CC        | domains, thereby providing a variety of activities, e.g. by replacing the     |
| CC        | native cell binding domain of PE A (domain Ia) with a ligand for a            |
| CC        | particular cell receptor, the chimera can be targeted to bind to the          |
| CC        | particular cell type. The immunogens can elicit humoral, cell-mediated        |
| CC        | and secretory immune responses against the non-native epitope. This           |
| CC        | sequence represents a PE protein endoplasmic reticulum (ER) retention         |
| CC        | domain motif  |
| XX        |   |
| XX        |   |
| SQ        | Sequence 4 AA;  |
|           | Query Match            100.0%; Score 20; DB 2; Length 4;                      |
|           | Best Local Similarity 100.0%; Pred. No. 2e+06;                                |
|           | Matches     4; Conservative     0; Mismatches     0; Indels     0; Gaps     0 |
| Oy        | 1 KDEL 4  |
| Dd        |   |
|           | 1 KDEL 4  |
| RESULT 25 |   |
| AAY29637  |   |
| ID        | AAY29637 standard; peptide; 4 AA.   |
| AC        | AAY29637;   |
| XX        |   |
| DT        | 20-OCT-1999 (first entry)   |
| DE        | KDEL peptide for targeting proteins and bearing them to ER.                   |
| XX        |   |
| KW        | Dimerizing agent; regulation; gene transcription; growth; rapamycin;          |
| KW        | proliferation; differentiation; chimeric protein; FKBP; FKB domain;           |
| KW        | FKS06-binding protein; human FRAP protein; biological response;               |
| KW        | apoptosis; gene therapy.  |
| OS        | Unidentified.   |
| PN        | WO9941258-A1.   |
| PD        | 19-AUG-1999.  |
| XX        |   |
| Pf        | 12-FEB-1999;        99WO-US003095.  |
| XX        |   |
| PR        | 13-FEB-1998;        98US-0074584P.  |
| XX        | (HARD ) HARVARD COLLEGE.  |
| PI        | Schreiber SL, Crabtree GR, Liberles SD;                                       |
| XX        |   |
| DR        | WPI; 1999-508621/42.  |
| XX        | New C3 substituted rapamycin derivatives acting as dimerization agents        |
| PT        | for chimeric proteins, used to trigger biological responses, e.g. growth      |
| PT        | or proliferation, in transformed cells - have minimal immunosuppressant       |
| PT        | activity.   |
| XX        |   |
| PS        | Disclosure; Page 49; 148pp; English.  |
| XX        | The present invention describes rapamycin derivatives (I) containing the      |
| CC        | basic substructure and optionally having one or more substituents and         |
| CC        | unsaturations (between carbons 1 and 8), as pure stereoisomers or their       |

CC mixtures and derivatives. (I) are used to dimerise/multimerise chimeric  
 CC proteins that contain domains of the FK506-binding protein, FKBP, and an  
 CC FRB domain (from human FRAP protein), so can be used as switches to  
 CC trigger selected biological responses, e.g. growth, proliferation,  
 CC differentiation, apoptosis and gene transcription, particularly in  
 CC conjunction with gene therapy, but also for controlling production or  
 CC recombinant proteins and viruses and generally in biological research.  
 CC (I) have much lower immunosuppressive activity than known rapamycins,  
 CC e.g. 200 times lower, so are safer to use. The present sequence  
 CC represents an amino acid sequence which targets proteins bearing them to  
 CC the endoplasmic reticulum (ER), given in the present invention

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
 ||||  
 Db 1 KDEL 4

#### RESULT 26

AAAY25688  
 ID AAY25688 standard; protein; 4 AA.

AC AAY25688;

DT 01-OCT-1999 (first entry)

DE Membrane retaining protein leader sequence motif 1.

KW SYNVG protein; aggregate; lipid bilayer; beta-glucuronidase; GUS;  
 KW transmembrane; therapeutic; sequestration; adhesive; membrane retention.

OS Unidentified.

PN US5935822-A.

PD 10-AUG-1999.

PF 21-MAR-1995; 95US-00407900.

PR 21-MAR-1995; 95US-00407900.

PA (COLS ) UNIV COLORADO.

PI Staehelin A, Giddings T, Galbraith D;

DR WPI; 1999-468145/39.

PT Aggregating a desired molecule in a lipid bilayer, useful for protective  
 PT production, directed secretion and in therapy, diagnosis and the  
 PT biosynthetic production of molecules.

PS Disclosure; Col 35-36; 27pp; English.

CC This invention describes novel aggregate molecules (AgM) comprising an  
 CC adhesive molecule attached to a desired product molecule. The products of  
 CC the invention are used in a method to aggregate a desired product  
 CC molecule in a lipid bilayer and comprises forming oligomers between two  
 CC or more aggregate molecules that are physically associate with a lipid  
 CC bilayer such that the aggregate molecules are accumulated in association  
 CC with the lipid bilayer, where the aggregate molecules comprise a beta-  
 CC glucuronidase (GUS) adhesive molecule and the desired product molecule is  
 CC linked to the adhesive molecule by a transmembrane molecule. The method  
 CC can be applied to production of a therapeutic composition. The  
 CC sequestration acts to protect the integrity of a product molecule, as  
 CC well as to facilitate recovery of the molecule. AAY25688-Y25694 represent  
 CC leader sequence motifs which allow the retention of proteins in the  
 CC membranes of cells

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
 ||||  
 Db 1 KDEL 4

#### RESULT 27

AAAY98152  
 ID AAY98152 standard; peptide; 4 AA.

AC AAY98152;

DT 22-AUG-2000 (first entry)

DE Protein localisation signal sequence.

KW Localisation signal; transgenic plant; hydrogen peroxidase production;  
 KW colorimetric test; oxalate oxidase; pathogen resistance; endo-chitinase.

OS Unidentified.

PN WO200022148-A1.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-FR002412.

PR 09-OCT-1998; 98FR-00012704.

PA (BIOG-) BIOGEMMA.

PI Pagniez M, Grison R, Toppin A;

DR WPI; 2000-317998/27.

PT Producing transgenic plants expressing a hydrogen peroxide-producing  
 PT protein, useful for imparting pathogen resistance or as marker for  
 PT transformation with second gene.

PS Disclosure; Page 7; 41pp; French.

CC The present sequence represents a protein localisation signal sequence.  
 CC The peptide can be used in the method of the invention. The invention  
 CC relates to the production of transgenic plants that express a protein  
 CC able to produce hydrogen peroxide. The production method comprises  
 CC transforming a plant cell with Agrobacterium rhizogenes containing a  
 CC vector that carries a gene encoding the protein to be expressed in the  
 CC transgenic plant, selection is made for the expression of the gene in a  
 CC colorimetric test using peroxidase. Plants are transformed to produce a  
 CC protein of interest, specifically oxalate oxidase (OO): (i) to impart  
 CC resistance to pathogens (OO degrades oxalic acid, a phytotoxin produced  
 CC by many phytopathogens); or (ii) as a selection system for plants  
 CC transformed with a second gene, encoding another protein of interest,  
 CC introduced in the same vector as the gene encoding the first protein of  
 CC interest. Particularly the second protein confers resistance to pathogens  
 CC (fungi, bacteria, insects, nematodes etc.) and is specifically endo-  
 CC chitinase. The method uses a simple and rapid method, based on a  
 CC colorimetric test, to select for transformation, particularly using as  
 CC test sample roots induced by Agrobacterium rhizogenes. It is not  
 CC necessary that the cells being treated should survive the test, so high  
 CC (toxic) concentrations of substrate can be used

SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 29  
 AAY70697  
 ID AAY70697 standard; peptide; 4 AA.  
 XX  
 AC AAY70697;

PD 14-OCT-1999.  
 XX  
 PF 14-APR-1998; 98CA-02228822.  
 XX  
 PR 14-APR-1998; 98CA-02228822.  
 XX  
 PA (SALE/) SALEH M T.  
 XX  
 PI Saleh MT;  
 XX  
 DR WPI; 2000-127150/12.  
 XX  
 PT Polypeptide vectors comprising an endoplasmic reticulum retrieval signal  
 PT for delivery of drugs and epitopes to the immune system.  
 XX  
 PS Claim 1; Page 7; 8pp; English.  
 XX  
 CC The invention provides a polypeptide vector, no longer than 69 amino  
 CC acids in length that comprises a helix-loop-helix motif, an endoplasmic  
 CC reticulum (ER) retention signal (either KDEL and/or RDEL) a protease  
 CC recognition sequence subtended by a disulfide bond and glycosylation  
 CC site(s). The vector may be used for delivery of drugs and epitopes to the  
 CC immune system. The vector is small in size, rigid in structure and can be  
 CC modified to optimize it's efficacy of delivery. There is no need for  
 CC adjuvants or the need to recruit circulating cells from the immune system  
 CC to any specific site as the construct will target cells of the immune  
 CC system through the carbohydrate structure in the glycosylation motif. The  
 CC vector does not have any specific cytotoxic effects as it has no  
 CC cytotoxic enzyme activity. The present sequence represents a ER retrieval  
 CC signal used in the vector of the invention  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
 ||||  
 Db 1 KDEL 4

RESULT 31  
 AAY32395  
 ID AAY32395 standard; peptide; 4 AA.  
 XX  
 AC AAY32395;

XX 13-MAR-2000 (first entry)  
 XX  
 DE Endoplasmic reticulum retention signal.

XX Endoplasmic reticulum; retention signal; monocotyledonous plant; monocot;  
 KW rice; wheat; transgenic plant; mammalian polypeptide; antibody;  
 KW expression cassette.

OS Synthetic.

XX WO9966026-A2.

XX 23-DEC-1999.

XX 15-JUN-1999; 99WO-US013584.

XX 15-JUN-1998; 98US-0089322P.

XX (INNE-) INNES CENT JOHN.

PA (CHRI/) CHRISTOU P.

XX Christou P, Stroger E, Fischer R, Martin-Vaquero C, Schillberg S;

PI Ma JK;

XX WPI; 2000-097739/08.

XX Production of mammalian polypeptides, especially antibodies, by  
 PT monocotyledonous plants.  
 XX

PS Claim 2; Page 57; 76pp; English.

XX This sequence represents an endoplasmic reticulum (ER) retention signal.  
 CC Levels of mammalian polypeptide expression in transgenic monocotyledonous  
 CC plants can be enhanced by use of this signal. The invention provides  
 CC rice, wheat and other monocot plants that have been transformed with  
 CC expression cassettes for production of mammalian polypeptides, such as  
 CC antibodies. ER retention signals (see also AAY32396), 5' untranslated  
 CC regions and leader peptides are employed in various combinations to  
 CC provide high expression yield. Plant cell or seed containing polypeptides  
 CC selected from Fv, Fab, F(ab)2, diabody, dimeric scFv, whole antibody and  
 CC four-chain secretory antibody are claimed. Multi-chain complexes such as  
 CC four-chain secretory antibodies are produced by expression of component  
 CC polypeptides from separate vectors, all introduced into the same cell by  
 CC transformation

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
 ||||  
 Db 1 KDEL 4

RESULT 32

AAB03195

ID AAB03195 standard; peptide; 4 AA.

XX

AC AAB03195;

XX 23-OCT-2000 (first entry)

XX Endoplasmic reticulum (ER) localisation signal peptide.

XX ER localisation signal; endoplasmic reticulum; subcellular targeting;  
 KW murine; porcine VCAW-specific single chain antibody; scFv; human;  
 KW vascular cell adhesion molecule; transgenic animal;  
 KW organ transplantation; xenotransplantation;  
 KW xenograft rejection suppression.

XX Mus sp.

XX WO200031126-A2.

XX 02-JUN-2000.

XX 22-NOV-1999; 99WO-GB003888.

XX 20-NOV-1998; 98GB-00025555.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Ramrakha PS, George AJT, Haskard D, Lechler RI;

XX WPI; 2000-400039/34.

XX Biological tissue for combating cellular phase of rejection process  
 PT resulting from xenotransplantation comprises endothelial cells which may  
 PT be induced to generate compound which down-regulates expression of cell  
 PT adhesion molecule.

XX Example 2; Page 15; 36pp; English.

XX The invention relates to a biological tissue comprising endothelial cells  
 CC which can be induced to generate a compound which downregulates the  
 CC expression of a cell adhesion molecule. The invention also encompasses a

DR WPI; 2000-292008/25.



PA (SELE-) SELECTIVE GENETICS INC.  
 XX Baird A, Berry M, Logan A, Gonzalez AM;  
 PI WPI; 2000-160565/14.  
 DR  
 XX A gene-activated matrix device comprising a neuronal therapeutic encoding  
 PT agent is capable of inducing neuronal axonal generation.  
 XX  
 PS Disclosure; Page 65; 125pp; English.  
 XX  
 CC The invention relates to a novel device for promoting neuronal  
 CC regeneration or altering neuronal growth, comprising a gene-activated  
 CC matrix (GAM). The GAM comprises a biocompatible matrix, and at least one  
 CC DNA encoding a neuronal therapeutic product operably linked to a  
 CC promoter. The DNA is non-covalently associated with the matrix. The  
 CC device may further comprise a targeting agent, which is complexed with or  
 CC conjugated to DNA encoding a neuronal therapeutic agent, and which is  
 CC capable of binding to a surface receptor of a neuronal or a repair cell.  
 CC This targeting agent may also comprise a linker providing a nuclear or  
 CC cytoplasmic translocation signal sequence. The invention also encompasses  
 CC methods of preparing a GAM for promoting neuronal regeneration and  
 CC survival. The neuronal therapeutic agent encoded by the GAM DNA is  
 CC capable of inducing neuronal axonal generation or regeneration, and may  
 CC include neurotrophic factors which are members of the neurotrophin  
 CC or FGF (fibroblast growth factor) families; inhibitors of antagonists of  
 CC axonal generation (e.g., transforming growth factor (TGF)-beta  
 CC inhibitors); or a guidance factor which promotes defined nerve growth.  
 CC The device can be used to transfer the neuronal therapeutic-encoding DNA  
 CC into a neuronal cell or repair cell. The device promotes axonal  
 CC generation or regeneration without axonal entrapment. The device allows a  
 CC neuronal connection to be established or re-established. The methods and  
 CC devices of the invention are useful for treatment of neurodegenerative  
 CC diseases such as Alzheimer's disease, Parkinson's disease or Huntington's  
 CC disease. Direct plasmid DNA transfer from a matrix to a mammalian repair  
 CC cell through stimulation of the wound healing process offers a number of  
 CC advantages. Firstly, the ease of producing and purifying DNA constructs  
 CC compares favourably with traditional protein production method costs.  
 CC Secondly, matrices can act as structural scaffolds that promote cell  
 CC ingrowth and proliferation. Thirdly, direct gene transfer may be an  
 CC advantageous method of delivery for molecules that normally undergo  
 CC complex biosynthetic processing or for receptors, which must be properly  
 CC positioned in the cell membrane. Sequences AAY69694-Y69696 represent  
 CC cytoplasmic translocation signal sequences  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
 Db ||||  
 1 KDEL 4

RESULT 35  
 AAY92046  
 ID AAY92046 standard; peptide; 4 AA.  
 AC  
 XX AAY92046;

01-AUG-2000 (first entry)

Endoplasmic reticulum retention signal sequence.

XX Cyclophilin-like peptidyl prolyl cis-trans isomerase; food processing;  
 KW Endoplasmic retention signal; cis-trans isomerization; protein secretion;  
 KW toxin; ADP-glucose pyrophosphorylase; glucanase; beta-1,4-endoglucanase.  
 XX  
 OS Aspergillus niger.  
 XX  
 PN WO200018934-A1.

XX 06-APR-2000.  
 PD  
 XX 30-SEP-1999; 99WO-IB001669.  
 PF  
 XX 30-SEP-1998; 98GB-00021198.  
 PR  
 XX (DANI-) DANISCO AS.  
 PA  
 XX Derkx PMF, Madrid SM;  
 PI  
 XX WPI; 2000-293167/25.  
 DR  
 XX New peptidyl prolyl cis-trans isomerase, designated CYPB, from  
 PT Aspergillus niger, useful in methods for increasing the yield of secreted  
 PT polypeptides, such as enzymes used in food processing, from cells.  
 XX  
 PS Claim 8; Page 34; 52pp; English.  
 XX  
 CC AAY92045-46 are endoplasmic retention (ER) signal sequences found at the  
 CC carboxy terminal of polypeptides targeted to the ER in Aspergillus niger.  
 CC AAY92047 is a novel ER signal sequence found at the C-terminal end of  
 CC CYPB, a cyclophilin-like peptidyl prolyl cis-trans isomerase, also from  
 CC A. niger. CYPB is capable of catalyzing the cis-trans isomerization of a  
 CC peptide bond on the N-terminal side of proline residues in polypeptides.  
 CC CYPB are useful in methods for increasing the yield of secreted  
 CC polypeptides from cells. The secreted polypeptides may be enzymes (such  
 CC as chymosin, thaumatin or alpha-galactosidase) that can be used in food  
 CC processing, a pest toxin, adenosine diphosphate (ADP)-glucose  
 CC pyrophosphorylase, a glucanase or beta-1,4-endoglucanase  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
 Db ||||  
 1 KDEL 4

RESULT 36  
 AAY93738  
 ID AAY93738 standard; peptide; 4 AA.  
 XX  
 AC AAY93738;

03-OCT-2000 (first entry)

Amino acid sequence of a microsomal retention signal.

XX Plant expression vector; antigen; hepatitis B surface antigen; HBsAg;  
 KW vaccine.  
 XX

Unidentified.

WO200037610-A2.

29-JUN-2000.

23-DEC-1999; 99WO-US031020.

23-DEC-1998; 98US-0113827P.

(BOYC-) BOYCE THOMPSON INST PLANT RES.  
 (HEAL-) HEALTH RES INST.

Mason HS, Thanavala Y, Arntzen CJ, Richter E;

WPI; 2000-452181/39.

New expression vector for transforming plants comprising two expression

PT cassettes useful for producing plant material comprising anti-hepatitis B  
PT antibodies.

XX Disclosure; Page 31; 144pp; English.

XX The specification describes a plant expression vector which comprises two  
XX expression cassettes, the first comprising a polynucleotide encoding an  
CC antigen and the second comprising a non-identical polynucleotide encoding  
CC the same antigen. The antigen is especially a hepatitis B surface antigen  
CC (HBsAg). The expression vector is used to transform bacterial and plant  
CC cells to elicit the production of anti-hepatitis B antibodies and are  
CC useful as vaccines. The present sequence represents a microsomal  
CC retention signal, which is used in the course of the invention

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|  
|  
|  
|  
Db 1 KDEL 4

RESULT 37  
AAB30285  
ID AAB30285 standard; peptide; 4 AA.

XX AAB30285;

AC 12-FEB-2001 (first entry)

XX CD4+ T-cell activation methods peptide ligand #47.

XX CD4+ T-cell activation; peptide epitope; autoimmune disease;  
KW infectious disease; cancer; immunological mass fingerprinting.

XX Synthetic.

XX WO200063702-A1.

XX 26-OCT-2000.

XX 20-APR-2000; 2000WO-US010888.

XX 21-APR-1999; 99US-00295868.

XX 21-APR-1999; 99US-0130355P.

XX (ZYCO-) ZYCOs INC.

PA (UNLO ) KINGS COLLEGE LONDON.

PI Peakman M, Chicx RM;

XX WPI; 2000-665270/64.

XX Identifying a class II major histocompatibility complex-binding fragment  
PT of a polypeptide useful for diagnosing and protecting against diabetes  
PT comprises contacting a ligand, a polypeptide and a mammalian antigen  
PT presenting cell.

XX Disclosure; Page 63; 118pp; English.

XX The present invention is concerned with a method, designated  
CC immunological mass fingerprinting, which enables the identification of  
CC peptide epitopes that activate CD4+ T-cells. Peptides of this kind are  
CC also given. CD4+ cells are involved in the pathogenesis of disease, and  
CC the peptides can be used in the prevention and treatment of autoimmune  
CC diseases such as diabetes, multiple sclerosis, rheumatoid arthritis,  
CC myasthenia gravis, systemic lupus erythematosus, autoimmune premature  
CC ovarian failure, Graves' thyroiditis, Hashimoto's thyroiditis, primary  
CC hypothyroidism, coeliac disease, primary biliary cirrhosis, autoimmune  
CC hepatitis, Addison's disease, vitiligo, systemic sclerosis and anti-

CC glomerular basement membrane disease, infectious diseases including  
CC leprosy, measles, hepatitis C, HIV and parasitic diseases, and cancer  
XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 1 KDEL 4  
|  
|  
|  
|  
Db 1 KDEL 4

RESULT 38  
AAB35117  
ID AAB35117 standard; peptide; 4 AA.

XX AAB35117;

XX 11-SEP-2003 (revised)

DT 27-MAR-2001 (first entry)

XX Adenovirus E3/19K protein.

XX Drug resistance mechanism; multi-drug resistance; MDR; cancer;  
KW chemotherapeutic drug.

XX unidentified adenovirus.

XX WO200072008-A2.

XX 30-NOV-2000.

XX 25-MAY-2000; 2000WO-US014812.

XX 25-MAY-1999; 99US-0136018P.

XX (RIGE-) RIGEL PHARM INC.

XX Xu X;

XX WPI; 2001-025195/03.

XX Screening multi-drug resistance conferring polypeptides involves  
PT expressing library of retroviral vectors encoding randomized candidate  
PT peptides and selecting cells expressing MDR phenotype conferred by  
PT peptide.

XX Disclosure; Page 19; 73pp; English.

XX The present invention provides a method for screening for a peptide which  
CC confers multi-drug resistance (MDR) on a cell. This involves expressing a  
CC library of retroviral vectors encoding randomized candidate peptides in  
CC cells and screening for those peptides which cause a multi drug resistant  
CC phenotype. This method is particularly useful in identifying treatments  
CC for multi-drug resistant cancer. (Updated on 11-SEP-2003 to standardise  
CC OS field)

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|  
|  
|  
|  
Db 1 KDEL 4

RESULT 39  
AAG67291  
ID AAG67291 standard; peptide; 4 AA.

XX AC AAG67291;  
 XX  
 DT 13-NOV-2001 (first entry)  
 XX  
 DE Amino acid sequence of an endoplasmic reticulum retention signal.  
 XX  
 KW hB7-H2; T cell stimulator; immunosuppression; cancer; AIDS;  
 KW congenital immune deficiency; cellular immune response;  
 KW inflammatory condition; autoimmune disease; rheumatoid arthritis;  
 KW multiple sclerosis; insulin-dependent diabetes mellitus.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200164704-A1.  
 XX  
 XX 07-SEP-2001.  
 PD  
 XX  
 XX 02-MAR-2001; 2001WO-US006769.  
 PF  
 XX  
 XX 02-MAR-2000; 2000US-0186519P.  
 PR  
 XX  
 XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
 PA  
 XX  
 XX Chen L;  
 PI  
 XX  
 XX WPI; 2001-514837/56.  
 DR  
 XX  
 XX An isolated DNA encoding a hB7-H2 polypeptide, useful for treating  
 PT cancer, AIDS, or autoimmune diseases (e.g. rheumatoid arthritis, multiple  
 PT sclerosis or insulin-dependent diabetes mellitus).  
 PT  
 XX  
 PS Disclosure; Page 21; 50pp; English.  
 XX  
 CC The specification describes polypeptide, designated hB7-H2. The hB7-H2  
 CC polypeptide co-stimulates T cells. The hB7-H2 proteins and its variants  
 CC are generally useful as immune response-stimulating therapeutics. For  
 CC example, the polypeptides can be used for treatment of disease conditions  
 CC characterized by immunosuppression, e.g., cancer, AIDS or AIDS-related  
 CC complex, other virally or environmentally-induced conditions, and certain  
 CC congenital immune deficiencies. They may also be employed to increase  
 CC immune function that has been impaired by the use of radiotherapy or  
 CC immunosuppressive drugs such as certain chemotherapeutic agents, and  
 CC therefore are particularly useful when given in conjunction with such  
 CC drugs or radiotherapy. The hB7-H2 nucleic acid and polypeptide can be  
 CC used to treat conditions involving cellular immune responses, e.g.,  
 CC inflammatory conditions (such as, for example, those induced by  
 CC infectious agents including Mycobacterium tuberculosis or M. leprae), or  
 CC other pathologic cell-mediated responses such as those involved in  
 CC autoimmune diseases (e.g. rheumatoid arthritis), multiple sclerosis, or  
 CC insulin-dependent diabetes mellitus). AAG67288-91 can be used to direct  
 CC hB7-H2 to specific intracellular compartments  
 XX  
 XX Sequence 4 AA;  
 Query Match 100.0%; Score 20; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KDEL 4  
 Db 1 KDEL 4  
 RESULT 40  
 AAG78315  
 ID AAG78315 standard; protein; 4 AA.  
 XX  
 AC AAG78315;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 15-NOV-2001 (first entry)  
 XX

DE ER lumen retention signal.  
 XX  
 KW Proridin; ricin; A chain; B chain; L domain; ER lumen retention signal;  
 KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;  
 KW retroviral infection; anti-HIV; virucide activity; viral protease.  
 XX  
 OS unidentified.  
 XX  
 XX WO200160393-A1.  
 XX  
 XX 23-AUG-2001.  
 PD  
 XX  
 XX 15-FEB-2001; 2001WO-US005282.  
 PF  
 XX  
 XX 16-FEB-2000; 2000US-0182759P.  
 PR  
 XX  
 XX (BECH-) BECHTEL BWXT IDAHO LLC.  
 PA  
 XX  
 XX Keener WK, Ward TE;  
 PI  
 XX  
 XX WPI; 2001-581908/65.  
 DR  
 XX  
 XX Novel composition comprising toxin e.g., ricin based antiviral compound  
 PT useful for treating viral infections such as human immunodeficiency virus  
 PT infection.  
 PT  
 XX  
 XX Example 6; Page 64; 66pp; English.  
 PS  
 XX  
 CC The sequence relates to the amino acid sequence of an ER lumen retention  
 CC signal fused to ricin A chain in order to enhance its toxicity. The  
 CC invention relates to a novel toxin (e.g., ricin) based antiviral agent  
 CC which is toxic to virus-infected cells, but non-toxic to uninfected  
 CC cells. The invention has anti-HIV and virucide activities. Its mechanism  
 CC of action is through inactivation of cellular ribosomes and enhancement  
 CC of binding of the antiviral agent to galactose residues on cell surfaces,  
 CC and its cellular internalisation. The invention is useful for treating  
 CC human immunodeficiency virus infection and other viral infections,  
 CC especially retroviral infections. The antiviral agent is activated in  
 CC viral particles or early-stage infected cells, killing the cells upon  
 CC infection and effectively preventing the integration of the viral genome  
 CC into the host genome thereby preventing the latency/rebound problem. The  
 CC agent enters all HIV susceptible cells, and not just cells known to act  
 CC as host cells for the virus. The antiviral agent remains inert in a cell  
 CC until degraded in it, unless the cell is infected with the virus, where  
 CC the viral protease activates it. (Updated on 11-SEP-2003 to standardise  
 CC OS field)  
 XX  
 XX Sequence 4 AA;  
 Query Match 100.0%; Score 20; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KDEL 4  
 Db 1 KDEL 4  
 RESULT 41  
 AAB45947  
 ID AAB45947 standard; peptide; 4 AA.  
 XX  
 XX AAB45947;  
 AC  
 XX  
 XX 02-APR-2001 (first entry)  
 DT  
 XX  
 XX Transdominant effector peptide associated screening peptide #27.  
 DE  
 XX  
 XX Intracellular transdominant bioactive agent; screening; cell phenotype;  
 KW effector peptide.  
 XX  
 XX Unidentified.  
 OS  
 XX

PR 09-DEC-1999; 99US-0169846P.  
XX (ZYCO-) ZYCOS INC.  
XX Hedley ML, Urban RC, Chicz RM;  
XX WPI; 2001-265996/27.  
XX Novel nucleic acids encoding polypeptide polypeptides containing multiple  
XX epitopes from one or more proteins, useful for treating tumors and as  
XX vaccines against pathogenic agents.  
XX Disclosure; Page 25; 64pp; English.  
XX This invention relates to polynucleotides encoding a hybrid polypeptide  
XX comprising a signal sequence and three segments that are either  
XX contiguous or separated by a spacer amino acid or spacer peptide. The  
XX invention specifically details polynucleotides encoding a polypeptide  
XX peptide where the peptide segments are tumor antigens or a naturally  
XX occurring protein of a pathogenic agent. The polypeptide peptides exhibit  
XX antiviral and immunostimulatory activity. The polynucleotide and  
XX polypeptide peptides are useful for eliciting an immune response in a  
XX mammal. The polynucleotide and protein are useful as vaccines for  
XX treating tumors and pathogenic infections. The polynucleotide is also  
XX useful for preventing or treating human papillomavirus (HPV)-associated  
XX diseases, particularly exophytic condyloma, flat condyloma, cervical  
XX cancer, respiratory papilloma, conjunctival papilloma, genital-tract HPV  
XX infection, cervical dysplasia, high grade squamous intraepithelial  
XX lesions, and anal HPV infection. The polynucleotide and polypeptide are  
XX useful for generating or enhancing prophylactic or therapeutic immune  
XX response against pathogens, tumors or autoimmune diseases in a  
XX population of individuals having diverse MHC allotypes, as positive  
XX controls in T cell stimulation assays in vitro, and as tools to  
XX understand processing of epitopes within cells. Peptides AAB95994 -  
XX AAB96037 and AAB96044 - AAB96048 represent major histocompatibility  
XX complex I (MHC I) associated tumor and pathogen antigens. The peptides  
XX can be used as part of the polypeptide proteins of the invention. Also  
XX included are examples of the polypeptide proteins represented by AAB96050  
XX - AAB96052, and localisation signal peptides AAB96038 - AAB96043 and  
XX AAB96049 which can be used in the construction of the polypeptide  
XX peptides  
XX SQ Sequence 4 AA;  
Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KDEL 4  
Db 1 KDEL 4  
RESULT 42  
AAB96038  
ID AAB96038 standard; peptide; 4 AA.  
XX AAB96038;  
AC AAB96038;  
XX 25-JUN-2001 (first entry)  
XX Endoplasmic reticulum retention signal peptide SEQ ID 111.  
DE  
DE Epitope; tumor antigen; antiviral; immunostimulatory; cervical cancer;  
KW human papillomavirus-associated disease; condyloma; cervical dysplasia;  
KW cervical dysplasia; major histocompatibility complex; MHC I.  
XX Unidentified.  
OS WO200119408-A1.  
PN 22-MAR-2001.  
XX 18-SEP-2000; 2000WO-US025559.  
PF 16-SEP-1999; 99US-00398534.  
PR 16-SEP-1999; 99US-0154665P.  
PR 09-DEC-1999; 99US-00458173.  
PR

PR 09-DEC-1999; 99US-0169846P.  
XX (ZYCO-) ZYCOS INC.  
XX Hedley ML, Urban RC, Chicz RM;  
XX WPI; 2001-265996/27.  
XX Novel nucleic acids encoding polypeptide polypeptides containing multiple  
XX epitopes from one or more proteins, useful for treating tumors and as  
XX vaccines against pathogenic agents.  
XX Disclosure; Page 25; 64pp; English.  
XX This invention relates to polynucleotides encoding a hybrid polypeptide  
XX comprising a signal sequence and three segments that are either  
XX contiguous or separated by a spacer amino acid or spacer peptide. The  
XX invention specifically details polynucleotides encoding a polypeptide  
XX peptide where the peptide segments are tumor antigens or a naturally  
XX occurring protein of a pathogenic agent. The polypeptide peptides exhibit  
XX antiviral and immunostimulatory activity. The polynucleotide and  
XX polypeptide peptides are useful for eliciting an immune response in a  
XX mammal. The polynucleotide and protein are useful as vaccines for  
XX treating tumors and pathogenic infections. The polynucleotide is also  
XX useful for preventing or treating human papillomavirus (HPV)-associated  
XX diseases, particularly exophytic condyloma, flat condyloma, cervical  
XX cancer, respiratory papilloma, conjunctival papilloma, genital-tract HPV  
XX infection, cervical dysplasia, high grade squamous intraepithelial  
XX lesions, and anal HPV infection. The polynucleotide and polypeptide are  
XX useful for generating or enhancing prophylactic or therapeutic immune  
XX response against pathogens, tumors or autoimmune diseases in a  
XX population of individuals having diverse MHC allotypes, as positive  
XX controls in T cell stimulation assays in vitro, and as tools to  
XX understand processing of epitopes within cells. Peptides AAB95994 -  
XX AAB96037 and AAB96044 - AAB96048 represent major histocompatibility  
XX complex I (MHC I) associated tumor and pathogen antigens. The peptides  
XX can be used as part of the polypeptide proteins of the invention. Also  
XX included are examples of the polypeptide proteins represented by AAB96050  
XX - AAB96052, and localisation signal peptides AAB96038 - AAB96043 and  
XX AAB96049 which can be used in the construction of the polypeptide  
XX peptides  
XX SQ Sequence 4 AA;  
Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KDEL 4  
Db 1 KDEL 4  
RESULT 43  
AAB96038  
ID AAB96038 standard; peptide; 4 AA.  
XX AAB96038;  
AC AAB96038;  
XX 17-MAY-2001 (first entry)  
XX Endoplasmic reticulum re-import transport protein motif.  
DE  
DE Cell membrane transport; compartment transport; transport protein;  
KW membrane-specific transport; gene therapy.  
XX Unidentified.  
OS DE19933492-A1.  
PN 18-JAN-2001.  
XX 16-JUL-1999; 99DE-01033492.  
PF

PN US6153380-A.  
XX 28-NOV-2000.  
XX 23-JAN-1997; 97US-00789333.  
XX 23-JAN-1996; 96US-00589108.  
XX 23-JAN-1996; 96US-00589911.  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX (RIGE-) RIGEL PHARM INC.  
XX Rothenberg SM, Nolan GP;  
XX WPI; 2001-060084/07.  
XX Methods for screening intracellular transdominant effector peptides and  
XX RNA molecules comprise delivering random oligonucleotides to cells, which  
XX are then screened for an altered phenotype.  
XX Disclosure; Col 67-68; 57pp; English.  
XX This invention describes novel in vitro screening methods (I) for a  
XX transdominant intracellular bioactive agent capable of altering the  
XX phenotype of a cell. (I) comprises: (a) introducing a molecular library  
XX of randomized candidate nucleic acids into several cells; and (b)  
XX screening the cells for a cell exhibiting an altered phenotype, where the  
XX altered phenotype is due to the presence of a transdominant bioactive  
XX agent. The methods are particularly useful for screening intracellular  
XX transdominant effector peptides and RNA molecules selected inside living  
XX cells from randomized pools. (I) is also useful for introducing random  
XX libraries into cells to screen for bioactive compounds. The methods allow  
XX rapid and highly efficient screening of large numbers of random  
XX oligonucleotides and their corresponding expression products in a single  
XX step. In addition, the methods allow screening in the absence of  
XX significant prior characterization of the cellular defect  
XX SQ Sequence 4 AA;  
Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KDEL 4  
Db 1 KDEL 4  
RESULT 42  
AAB96038  
ID AAB96038 standard; peptide; 4 AA.  
XX AAB96038;  
AC AAB96038;  
XX 25-JUN-2001 (first entry)  
XX Endoplasmic reticulum retention signal peptide SEQ ID 111.  
DE  
DE Epitope; tumor antigen; antiviral; immunostimulatory; cervical cancer;  
KW human papillomavirus-associated disease; condyloma; cervical dysplasia;  
KW cervical dysplasia; major histocompatibility complex; MHC I.  
XX Unidentified.  
OS WO200119408-A1.  
PN 22-MAR-2001.  
XX 18-SEP-2000; 2000WO-US025559.  
PF 16-SEP-1999; 99US-00398534.  
PR 16-SEP-1999; 99US-0154665P.  
PR 09-DEC-1999; 99US-00458173.  
PR

XX PR 16-JUL-1999; 99DE-01033492.  
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX PI Braun K, Friedrich E, Waldeck W, Peschke P, Pipkorn R, Debus J;  
 XX WPI; 2001-235973/25.  
 XX DR New conjugates for mediating cell, compartment or membrane-specific  
 XX PT transport, comprising transport mediator, specific address protein or  
 XX PT peptide and active agent, useful in therapy or diagnosis, e.g. gene  
 XX PT therapy.  
 XX PS Disclosure; Page 3; 10pp; German.  
 XX CC This invention describes a novel conjugate (I) for mediating cell-,  
 XX CC compartment- or membrane-specific transport, comprising a transport  
 XX CC mediator for the cell membrane, a cell-, compartment- or membrane-  
 XX CC specific address protein or peptide, and an active agent to be  
 XX CC transported. The method also describes the preparation of (I) which  
 XX CC comprises (a) separate peptide synthesis of the transport protein,  
 XX CC address protein, and optionally a spacer (preferably by Merrifield  
 XX CC synthesis); (b) covalent coupling of the address protein to an active  
 XX CC agent, optionally via a spacer; and (c) redox coupling of the product of  
 XX CC (b) with the transport protein, preferably in aqueous dimethylsulfoxide  
 XX CC solution, the product is purified, especially by high performance liquid  
 XX CC chromatography (HPLC). The products of the invention can be used for cell  
 XX CC -, compartment- or membrane-specific transport of the active agent, in  
 XX CC diagnosis and/or therapy. (I) is useful in gene therapy, where a whole  
 XX CC gene (including the regulatory elements) can be transported. Targeting  
 XX CC using (I) is widely applicable and highly effective. (I) have low  
 XX CC immunogenicity, minimal risk of infection and a long duration of action.  
 XX CC The specific transportation of the active agent to the required cell  
 XX CC compartment gives improved diagnostic or therapeutic results, including  
 XX CC reduced side-effects, in human or veterinary medicine  
 XX SQ Sequence 4 AA;  
 Query Match 100.0%; Score 20; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KDEL 4  
 Db ||||  
 1 KDEL 4  
 RESULT 44  
 AAB20214  
 ID AAB20214 standard; peptide; 4 AA.  
 XX AC AAB20214;  
 XX DT 14-MAY-2001 (first entry)  
 XX DE Endoplasmic reticulum retention peptide.  
 XX KW Endoplasmic reticulum retention peptide; human papilloma virus; HPV;  
 XX KW immunogen; E7 protein; vaccine; infection; gene therapy;  
 XX KW exophytic condyloma; flat condyloma; cervical cancer;  
 XX KW respiratory papilloma; conjunctival papilloma; cervical dysplasia.  
 XX OS Unidentified.  
 XX PI US6183746-B1.  
 XX PN 06-FEB-2001.  
 XX PD 09-OCT-1998; 98US-00169425.  
 XX PF 09-OCT-1997; 97US-0061657P.  
 XX PS

PA (ZYCO-) ZYCOS INC.  
 XX PI Urban RG, Chicz RM, Collins EJ, Hedley ML;  
 XX WPI; 2001-190939/19.  
 XX DR Inducing an immune response in a mammal for prophylaxis and treatment of  
 XX PT human papilloma virus infections such as cervical cancer, comprises  
 XX PT administering immunogenic peptides from the papilloma virus type 16 E7  
 XX PT protein.  
 XX XX Disclosure; Col 4; 23pp; English.  
 XX CC The present sequence is that of an endoplasmic reticulum retention  
 XX CC peptide. Claimed methods of the invention involve the administration to a  
 XX CC mammal, such as a human, of a nucleic acid encoding a polypeptide  
 XX CC comprising a first peptide, which controls intracellular trafficking,  
 XX CC e.g. the present sequence, and a second peptide, which is derived from  
 XX CC human papilloma virus type 16 E7 protein and which contains multiple  
 XX CC overlapping class I HLA-binding T-cell epitopes. The immunogenic peptides  
 XX CC and nucleic acids of the invention are used as vaccines prophylactically  
 XX CC or therapeutically in subjects having, suspected of having, or at risk of  
 XX CC exophytic condyloma, flat condyloma, cervical cancer, respiratory  
 XX CC papilloma, conjunctival papilloma, genital-tract HPV infection and  
 XX CC cervical dysplasia (claimed)  
 XX SQ Sequence 4 AA;  
 Query Match 100.0%; Score 20; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KDEL 4  
 Db ||||  
 1 KDEL 4  
 RESULT 45  
 AAB31370  
 ID AAB31370 standard; peptide; 4 AA.  
 XX AC AAB31370;  
 XX DT 20-APR-2001 (first entry)  
 XX DE Amino acid sequence of an endoplasmic reticulum retaining peptide.  
 XX KW Protein production; food processing; protein antibiotic; feed enzyme;  
 XX KW endoplasmic reticulum retaining peptide.  
 XX OS Unidentified.  
 XX PN WO200077174-A1.  
 XX PD 21-DEC-2000.  
 XX XX 07-JUN-2000; 2000WO-IL000330.  
 XX PF 10-JUN-1999; 99US-00329234.  
 XX PR (CBDT-) CBD TECHNOLOGIES LTD.  
 XX PA (VISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX PI Shani Z, Shoseyov O;  
 XX WPI; 2001-112219/12.  
 XX DR Expressing and isolating recombinant protein in a plant, useful for  
 XX PT producing large quantities of recombinant proteins, by expressing a  
 XX PT fusion protein including a cellulose binding peptide fused to a  
 XX PT recombinant protein.  
 XX PS Disclosure; Page 41; 87pp; English.

|           |   |  |           |   |   |
|-----------|---|--|-----------|---|---|
| XX        | CC  | The specification describes a method for expressing and isolating a recombinant protein in a plant. The method comprising expressing a fusion protein including the recombinant protein and a cellulose binding peptide fused to it, where the fusion protein is compartmentalised and sequestered within plant cells, plant derived tissue or cultured plant cells. The method is useful for obtaining large quantities of the recombinant proteins and protein products in a simple and cost-effective manner. Recombinant proteins may be used commercially, such as in the food processing industry, e.g. glucosylases and glucose isomerases are used for converting starch to high fructose corn syrup, proteinases for the hydrolysis of high molecular weight proteins and in manufacturing leather or alcoholic beverages, pectinesterases for pectin hydrolysis in food industry, lipases for cleaving ester linkage in triglycerides, and for effluent treatment. The recombinant proteins may further be used to produce protein antibiotics, which can be used in healing processes, and to produce animal feed enzymes. The present sequence represents an endoplasmic reticulum retaining peptide, which is used to produce the fusion proteins of the inventions | XX        | CC  | helper T-cells that provide helper activity for B-cell antibody-producing response e.g. IgG2a antibody response, in a mammal having an immunodeficiency disease, inflammatory condition or an autoimmune disease, by culturing B7-H1 with the mammalian T-cells in vitro, or administering B7-H1 or a nucleic acid encoding B7-H1 to the T-cells, such that the level of CD40 ligand on the T-cell surface is increased. The method further involves providing a recombinant cell e.g. an antigen presenting cell (APC) which is the progeny of a cell obtained from the mammal and has been transfected or transformed ex vivo with a nucleic acid encoding B7-H1, so that the cell expresses B7-H1, and administering the cell to the mammal. Prior to administration, the APC is pulsed with an antigen or an antigenic peptide. B7-H1 can be used to control pathologic cell mediated conditions (e.g. those induced by infectious agents such as Mycobacterium tuberculosis) or other pathologic cell mediated responses such as those involved in autoimmune diseases (e.g. rheumatoid arthritis) |
| XX        | SQ  | Sequence 4 AA;   | XX        | SQ  | Sequence 4 AA;  |
|           |   | Query Match 100.0%; Score 20; DB 4; Length 4;  |           |   | Query Match 100.0%; Score 20; DB 4; Length 4;   |
|           |   | Best Local Similarity 100.0%; Pred. No. 2e+06;   |           |   | Best Local Similarity 100.0%; Pred. No. 2e+06;  |
|           |   | Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   |           |   | Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  |
| QY        |   | 1 KDEL 4   | QY        |   | 1 KDEL 4  |
| DB        |   |  | DB        |   |   |
|           |   | 1 KDEL 4   |           |   | 1 KDEL 4  |
| RESULT 46 |   |  | RESULT 47 |   |   |
| ID        | AAU03564  |  | ID        | AAB84355  |   |
| AC        | AAU03564 standard; peptide; 4 AA.   |  | AC        | AAB84355 standard; protein; 4 AA.                                       |   |
| XX        | AAU03564;   |  | XX        | AAB84355;   |   |
| DT        | 26-SEP-2001 (first entry)   |  | DT        | 22-AUG-2001 (first entry)   |   |
| DE        | Peptide retention signal for ER.  |  | DE        | Amino acid sequence of an endoplasmic reticulum retention peptide.      |   |
| XX        | Human; immunoregulatory protein; B7-H1; co-stimulating T-cell;            |  | XX        | Surface receptor-dependent infection; pathogenic agent; antibody.       |   |
| KW        | B-cell antibody-producing response; IgG2a antibody response; APC;         |  | XX        | Synthetic.  |   |
| KW        | immunodeficiency disease; inflammatory disease; autoimmune disease;       |  | XX        | WO200142308-A2.   |   |
| KW        | endoplasmic reticulum; ER.  |  | XX        | 14-JUN-2001.  |   |
| OS        | Homo sapiens.   |  | XX        | 08-DEC-2000; 2000WO-EP012419.   |   |
| XX        | WO200139722-A2.   |  | XX        | 08-DEC-1999; 99US-0169653P.   |   |
| PN        | 07-JUN-2001.  |  | XX        | (NOVS ) NOVARTIS AG.  |   |
| PD        |   |  | PA        | (SCRI ) SCRIPPS RES INST.   |   |
| XX        | 30-NOV-2000; 2000WO-US032583.   |  | XX        | Barbas CF, Steinberger P;   |   |
| PF        |   |  | PI        | WPI; 2001-381649/40.  |   |
| XX        | 30-NOV-1999; 99US-00451291.   |  | XX        | Inhibiting, preventing or treating pathogenic infection of cells        |   |
| PR        | 28-AUG-2000; 2000US-00649108.   |  | XX        | comprises expressing recombinant antibody specific for surface receptor |   |
| XX        | (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.                               |  | PT        | of cells necessary for pathogenic infection, fused to intracellular     |   |
| PA        | Chen L;   |  | PT        | anchor means.   |   |
| PI        |   |  | XX        | Claim 5; Page 51; 69pp; English.  |   |
| XX        | WPI; 2001-397926/42.  |  | XX        | The specification describes a method for inhibiting, diminishing,       |   |
| DR        | Novel DNA encoding immunoregulatory molecule B7-H1, is useful for co-     |  | XX        | preventing or treating surface receptor-dependent infection of cells by |   |
| PT        | stimulating a T cell for augmenting immunoregulation and for controlling  |  | CC        | pathogenic agents. The method comprises a recombinant antibody protein  |   |
| PT        | pathologic cell mediated conditions.                                      |  | CC        | fused to an intracellular anchor means, where the antibody is specific  |   |
| XX        | Disclosure; Page 25; 85pp; English.                                       |  | CC        | for a surface receptor of the cells necessary for pathogenic infection. |   |
| PS        |   |  | CC        | The anchor means may be an endoplasmic reticulum retention peptide. The |   |
| XX        | The present sequence represents the peptide retention signal for the      |  | CC        | present sequence represents an endoplasmic reticulum retention peptide, |   |
| CC        | endoplasmic reticulum (ER). The present sequence is described relating to |  | CC        | which is used to produce antibody proteins of the invention             |   |
| CC        | the invention of novel human and mouse immunoregulatory protein B7-H1     |  | XX        |   |   |
| CC        | (AAU03559, AAU03560). B7-H1 is useful for co-stimulating T-cells such as  |  |           |   |   |

SQ Sequence 4 AA;  
Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
DB 1 KDEL 4  
RESULT 48  
ABG99144  
ID ABG99144 standard; peptide; 4 AA.  
XX AC ABG99144;  
XX DT 14-JAN-2003 (first entry)  
XX DE Calreticulin endoplasmic reticulum sequence.  
XX KW Intein; intein-catalysed cyclic peptide library; cancer; tumour cell;  
KW cardiovascular disease; obesity; neurological disorder; apoptosis;  
KW cell death; cell division; cell growth; arrhythmia potential;  
KW cardiomyocyte; heart failure; sarcolemmal calcium cycling; stroke;  
KW cell proliferation; atherosclerosis; metabolism; skin disorder;  
KW bone morphogenetic protein; endocrinology; infectious disease;  
KW viral infection; bacterial infection; diabetic ulcer; wound healing;  
KW keloid formation; skin connective tissue cell; antibiotic transport;  
KW drug resistance; cyclostatic; anorectic; neuroprotective; cardiac;  
KW haemostatic; nuclear localisation signal; targeting signal;  
KW secretory signal.  
XX OS Unidentified.  
XX PN WO200166565-A2.  
XX PD 13-SEP-2001.  
XX PF 06-MAR-2001; 2001WO-US007162.  
XX PR 06-MAR-2000; 2000US-0187130P.  
XX PA (RIGE-) RIGEL PHARM INC.  
XX PI Kinsella TM;  
XX PS WPI; 2001-589926/66.  
XX DR Fusion polypeptide for generating libraries of cyclic peptides in vivo,  
XX PT comprises terminal intein motifs and a random peptide.  
XX PS Disclosure; Page 20; 115pp; English.  
XX CC The present invention relates to methods and compositions utilising  
CC inteins to generate libraries of cyclic peptides in vivo. The  
CC compositions of the invention are useful for making cyclic peptides in  
CC vivo. Libraries of cells can be transformed with libraries of fusion  
CC nucleic acids. Intein-catalysed cyclic peptide libraries are useful for  
CC screening for an altered phenotype and identifying target molecules. The  
CC library is introduced into a cell, screened for an altered phenotype and  
CC target molecules that bind to the cyclic peptide are isolated. The method  
CC is useful for making cyclic peptides which retain biological activity,  
CC and for screening for cyclic peptides capable of altering the phenotype  
CC of a cell. The cyclic peptides are useful for altering cellular  
CC phenotypes and/or physiology, in screening assays to identify target  
CC molecules associated with changes in cellular phenotype or physiology and  
CC as drugs to treat a number of disease state, such as cancer.  
CC cardiovascular diseases, obesity and neurological disorders. The  
CC bioactive cyclic peptide is useful as the starting point for  
CC designing/synthesising derivative molecules with similar or more  
CC favourable properties for use as a drug and to pull out target molecules.  
CC By introducing random libraries into any tumour cell, peptides which

CC induce apoptosis, cell death, loss of cell division or decreased cell  
CC growth can be identified and this method is useful in cancer  
CC applications. The methods are also useful in cardiovascular applications,  
CC to screen for diminished arrhythmia potential in cardiomyocytes, for  
CC enhanced contractile properties of cardiomyocytes and diminish heart  
CC failure potential and to identify agents that regulate the intracellular  
CC and sarcolemmal calcium cycling in cardiomyocytes to prevent arrhythmias  
CC and agents that diminish embolic phenomena in arteries and arterioles  
CC leading to stroke. Candidate bioactive peptide libraries are inserted  
CC into these cell types and their proliferation in response to specific  
CC stimuli is monitored. Furthermore, the methods are also useful in  
CC screening for decreases in atherosclerosis, in screens to regulate  
CC obesity by controlling food intake mechanisms or reducing the responses  
CC of the receptor signalling pathways that regulate metabolism, in  
CC neurobiology applications, to screen for agonists of bone morphogenetic  
CC proteins, in skin biology applications, endocrinology applications,  
CC infectious disease applications including viral and bacterial infection,  
CC to screen for cyclic peptides which block HIV-1 infection, regulation or  
CC inhibition of keloid formation and wound healing for diabetic ulcers.  
CC Candidate libraries are inserted into skin connective tissue cells and  
CC bioactive peptides which promote the growth of these cells are isolated.  
CC Further applications include screening for bioactive peptides that block  
CC antibiotic transport mechanisms, drug toxicities and drug resistance,  
CC improving the performance of existing or developmental drugs, and in  
CC biotechnology. ABG99123-ABG99153 represent various targeting signals that  
CC may be fused to intein motifs or peptides  
XX SQ Sequence 4 AA;  
Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
DB 1 KDEL 4  
RESULT 49  
AAB48315  
ID AAB48315 standard; peptide; 4 AA.  
XX AC AAB48315;  
XX DT 20-APR-2001 (first entry)  
XX DE Endoplasmic reticulum retaining peptide.  
XX KW Recombinant; fusion protein; cellulose binding peptide; CBP; cellulose;  
KW food industry; alcoholic beverage; hydrolysis; whey lactose; aspartame;  
KW artificial sweetener; milk; animal feed enzyme; heparin; heparan sulfate;  
KW protein fiber; effluent treatment; detergent; leather;  
KW endoplasmic reticulum.  
XX OS Unidentified.  
XX PN WO200077175-A1.  
XX PD 21-DEC-2000.  
XX PF 17-MAY-2000; 2000WO-US013434.  
XX PR 10-JUN-1999; 99US-00329234.  
XX PA (CBDT-) CBD TECHNOLOGIES LTD.  
XX PA (YISS ) YISSUM RES & DEV CO.  
XX PA (FRIE/) FRIEDMAN M M.  
XX PI Shani Z, Shoseyov O;  
XX DR WPI; 2001-080683/09.  
XX PT Expressing and isolating recombinant protein from plant e.g for use in

PT food industry, involves homogenizing a plant expressing fusion protein  
PT including recombinant protein and cellulose binding peptide being fused  
PT to it.  
XX  
PS Disclosure; Page 44; 64pp; English.  
XX  
CC The invention relates to a process of expressing a recombinant protein in  
CC a plant and isolating the recombinant protein from the plant. The method  
CC comprises: (a) providing a plant, a plant derived tissue or cultured  
CC plant cells expressing a fusion protein (FP) including a recombinant  
CC protein and a cellulose binding peptide (CBP) being fused to it, FP being  
CC compartmentalized so as to be sequestered from the cell walls; (b)  
CC homogenizing the plant, plant derived tissue or cultured plant cells such  
CC that FP is brought into contact with a plant derived cellulosic matter  
CC (CM) to effect affinity binding of FP via CBP to CM and forming a FP-CM  
CC complex; and (c) isolating the FP-CM complex. The recombinant protein  
CC isolated by this method is useful commercially in the food industry, for  
CC the hydrolysis of high molecular weight protein, in the manufacture of  
CC alcoholic beverages, for the hydrolysis of whey lactose, in the  
CC production of the artificial sweetener aspartame, in the reduction of the  
CC cooked flavor of milk, in the production of animal feed enzymes, in the  
CC sterilization and oxidation of plastics and rubbers, for the production  
CC of heparin and heparan sulfate oligosaccharides, for purification in  
CC industrial processes, for production of protein fibers, for effluent  
CC treatment, in combination with detergents in cleaning applications, and  
CC in leather manufacturing processes. The present sequence represents a  
CC endoplasmic reticulum retaining peptide  
XX  
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KDEL 4

RESULT 50  
AAB50814  
ID AAB50814 standard; peptide; 4 AA.  
XX  
AC AAB50814;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Human endoplasmic reticulum localisation sequence.  
XX  
KW Fluorescent protein indicator; green fluorescent protein; GFP;  
KW linker moiety; sensor; calmodulin-binding domain.  
XX  
OS Homo sapiens.  
XX  
FN WO2000071565-A2.  
XX  
PD 30-NOV-2000.  
XX  
PF 17-MAY-2000; 2000WO-US013694.  
XX  
PR 21-MAY-1999; 99US-00316919.  
PR 21-MAY-1999; 99US-00316920.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Tsien RY, Baird GA;  
XX  
DR WPI; 2001-032017/04.  
XX  
XX Novel fluorescent proteins comprising a sensor protein inserted into  
PT them, useful for measuring the response of a sensor biological, chemical,  
PT electrical or physiological parameter in vivo or in vitro.  
XX

PS Disclosure; Page 32; 94pp; English.  
XX  
CC The present sequence is a localisation signal sequence used in the  
CC construction of a fluorescent protein indicator. The indicator comprises  
CC a sensor polypeptide that is responsive to a chemical, biological,  
CC electrical or physiological parameter, and a fluorescence protein  
CC functional group. The sensor polypeptide is operatively inserted into the  
CC fluorescent moiety. The fluorescent indicator is useful for detecting the  
CC presence of a response inducing member in a sample. The method involves  
CC contacting the sample with the indicator and detecting a change in  
CC fluorescence, in which a change is indicative of the effect of the  
CC parameter on the sensor polypeptide. The novel fluorescent proteins are  
CC advantageous due to their reduced size as compared to the FRET  
CC (fluorescence resonance energy transfer)-based sensors  
XX  
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|||  
Db 1 KDEL 4

Search completed: March 20, 2006, 07:52:21  
Job time : 83.5 secs



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:51:44 ; Search time 18.5 Seconds  
(without alignments)  
17.876 Million cell updates/sec

Title: US-09-673-707-9  
Perfect score: 20  
Sequence: 1 KDEL 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCITUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                  | Description        |
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| 1          | 20    | 100.0       | 4      | 1 US-08-328-961-6   | Sequence 6, Appli  |
| 2          | 20    | 100.0       | 4      | 1 US-07-872-673B-5  | Sequence 5, Appli  |
| 3          | 20    | 100.0       | 4      | 1 US-08-405-615-16  | Sequence 16, Appli |
| 4          | 20    | 100.0       | 4      | 1 US-08-331-398A-51 | Sequence 51, Appli |
| 5          | 20    | 100.0       | 4      | 1 US-08-462-397-6   | Sequence 6, Appli  |
| 6          | 20    | 100.0       | 4      | 1 US-08-270-314-3   | Sequence 3, Appli  |
| 7          | 20    | 100.0       | 4      | 1 US-08-406-192-28  | Sequence 28, Appli |
| 8          | 20    | 100.0       | 4      | 1 US-08-082-269D-7  | Sequence 7, Appli  |
| 9          | 20    | 100.0       | 4      | 1 US-08-593-865-1   | Sequence 1, Appli  |
| 10         | 20    | 100.0       | 4      | 1 US-08-461-234-16  | Sequence 16, Appli |
| 11         | 20    | 100.0       | 4      | 1 US-08-480-190-152 | Sequence 152, App  |
| 12         | 20    | 100.0       | 4      | 1 US-08-545-151-28  | Sequence 28, Appli |
| 13         | 20    | 100.0       | 4      | 1 US-08-373-190-17  | Sequence 17, Appli |
| 14         | 20    | 100.0       | 4      | 1 US-08-463-480-16  | Sequence 16, Appli |
| 15         | 20    | 100.0       | 4      | 1 US-08-470-566B-51 | Sequence 51, Appli |
| 16         | 20    | 100.0       | 4      | 1 US-08-488-379-152 | Sequence 152, App  |
| 17         | 20    | 100.0       | 4      | 1 US-08-821-840-5   | Sequence 5, Appli  |
| 18         | 20    | 100.0       | 4      | 1 US-08-713-528B-15 | Sequence 15, Appli |
| 19         | 20    | 100.0       | 4      | 1 US-08-407-900B-6  | Sequence 6, Appli  |
| 20         | 20    | 100.0       | 4      | 1 US-08-419-075-28  | Sequence 28, Appli |
| 21         | 20    | 100.0       | 4      | 1 US-08-438-190A-17 | Sequence 17, Appli |
| 22         | 20    | 100.0       | 4      | 1 US-08-923-536A-2  | Sequence 2, Appli  |
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| 25         | 20    | 100.0       | 4      | 1 US-08-809-668-9   | Sequence 9, Appli  |
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| 27         | 20    | 100.0       | 4      | 1 US-08-759-804A-51 | Sequence 51, Appli |

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| 30  | 20 | 100.0 | 4 | 2 | US-08-722-258-62   | Sequence 62, Appli |
| 31  | 20 | 100.0 | 4 | 2 | US-08-718-904-42   | Sequence 42, Appli |
| 32  | 20 | 100.0 | 4 | 2 | US-08-782-480-44   | Sequence 44, Appli |
| 33  | 20 | 100.0 | 4 | 2 | US-09-287-145A-17  | Sequence 17, Appli |
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| 38  | 20 | 100.0 | 4 | 2 | US-09-172-063-37   | Sequence 37, Appli |
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| 41  | 20 | 100.0 | 4 | 2 | US-09-124-671-37   | Sequence 37, Appli |
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| 43  | 20 | 100.0 | 4 | 2 | US-09-169-425C-23  | Sequence 23, Appli |
| 44  | 20 | 100.0 | 4 | 2 | US-09-131-852-1    | Sequence 1, Appli  |
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| 53  | 20 | 100.0 | 4 | 2 | US-09-459-956-10   | Sequence 10, Appli |
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| 57  | 20 | 100.0 | 4 | 2 | US-09-149-727-11   | Sequence 11, Appli |
| 58  | 20 | 100.0 | 4 | 2 | US-09-208-827-29   | Sequence 29, Appli |
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| 63  | 20 | 100.0 | 4 | 2 | US-09-176-741B-44  | Sequence 44, Appli |
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| 66  | 20 | 100.0 | 4 | 2 | US-08-787-738B-28  | Sequence 28, Appli |
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| 68  | 20 | 100.0 | 4 | 2 | US-09-316-919-22   | Sequence 22, Appli |
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| 92  | 20 | 100.0 | 4 | 2 | US-10-043-142-9    | Sequence 9, Appli  |
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6 1 US-08-373-190-10  
6 1 US-08-438-190A-13

ALIGNMENTS

RESULT 1  
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; Sequence 6, Application US/08328961  
; Patent No. 5501975  
; GENERAL INFORMATION:  
; APPLICANT: Chaudhuri, Bhabatosh  
; APPLICANT: Stephan, Christine  
; APPLICANT: Seebboth, Peter  
; APPLICANT: Reizman, Howard  
; TITLE OF INVENTION: No. 5501975e1 DNA Molecules and Hosts  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ciba-Geigy Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10532

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/328,961  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/989,260  
; FILING DATE: 11-DSC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCES/DOCKET NUMBER: 4-18885/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8614  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Domain  
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; OTHER INFORMATION: /note= "ER retention signal KDEL"  
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Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KDEL 4  
Db 1 KDEL 4  
|||||  
1 KDEL 4  
  
RESULT 2  
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; Sequence 5, Application US/07872673B  
; Patent No. 5578466  
; GENERAL INFORMATION:  
; APPLICANT: Toshiya HAYANO, Setsuko KATO, No. 5578466uhiro TAKAHASHI, and Masanori  
; TITLE OF INVENTION: Co-expression System of Protein Disulfide Isomerase Gene an  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Type 2DD, 3.50 inch, 720 KB  
; COMPUTER: Apple Macintosh SE  
; OPERATING SYSTEM: Apple DOS  
; SOFTWARE: Microsoft Word Version 4.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/872,673B  
; FILING DATE: 19920417  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: Japanese Patent Application No. 5578466. 114074/91 and 311.  
; FILING DATE: 18-APR-1991 and 30-OCT-1991  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE:

DESCRIPTION: peptide  
FRAGMENT TYPE: C-terminal fragment  
FEATURE:

NAME/KEY: ER retention signal  
LOCATION: C-terminus  
IDENTIFICATION METHOD: ER retention of proteins having this signal  
OTHER INFORMATION: located at the C-terminus of rat PDI  
PUBLICATION INFORMATION:  
AUTHORS: Edman, Jeffrey C., Ellis, Leland, Blacher, Russell W., Roth, Richa  
TITLE: Sequence of protein disulphide isomerase and implications of its rel  
Patent No. 5578466  
JOURNAL: Nature  
VOLUME: 317  
PAGES: 267-270  
DATE: 19-Sep-1985  
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 486 to 489  
US-07-872-673B-5

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 3

US-08-405-615-16  
Sequence 16, Application US/08405615  
Patent No. 5602095  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: FitzGerald, David J.  
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with  
TITLE OF INVENTION: Increased Activity  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ellen L. Weber  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/405,615  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/901,709  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-36  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-405-615-16

Query Match 100.0%; Score 20; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 4

US-08-331-398A-51  
Sequence 51, Application US/08331398A  
Patent No. 5608039  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Willingham, Mark  
APPLICANT: FitzGerald, David  
APPLICANT: Brinkmann, Ulrich  
APPLICANT: Pai, Lee  
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
TITLE OF INVENTION: and Their Uses (as amended)  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,398A  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-331-398A-51

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 5

US-08-462-397-6  
Sequence 6, Application US/08462397  
Patent No. 5618690  
GENERAL INFORMATION:

Mon Mar 20 08:51:26 2006

us-09-673-707-9.ra1

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; APPLICANT: Chaudhuri, Bhabatosh
; APPLICANT: Stephan, Christine
; APPLICANT: Seebach, Peter
; APPLICANT: Reizman, Howard
; TITLE OF INVENTION: No. 5618690e1 DNA Molecules and Hosts
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,397
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,260
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 4-18885/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 1..4
; OTHER INFORMATION: /note= "ER retention signal KDEL"
;
US-08-462-397-6
;
Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 6
US-08-270-314-3
; Sequence 3, Application US/08270314
; Patent No. 5683888
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, Anthony K.
; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND
; TITLE OF INVENTION: THEIR USE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: US
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/270,314
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 89 16806.6
; FILING DATE: 22-JUL-1989
; APPLICATION NUMBER: PCT/GB90/01131
; FILING DATE: 23-JUL-1990
; APPLICATION NUMBER: US 07/820,867
; FILING DATE: 22-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-270-314-3
;
Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 7
US-08-406-192-28
; Sequence 28, Application US/08406192
; Patent No. 5739287
; GENERAL INFORMATION:
; APPLICANT: Wilbur, D. Scott
; APPLICANT: Prathare, Pradip M
; TITLE OF INVENTION: Biotinylated Cobalamins
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: WA 98101-2333
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,192
; FILING DATE: 16-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,831
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Renzoni, George E
; REGISTRATION NUMBER: 37,919
; REFERENCE/DOCKET NUMBER: RECL18947
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682 8100
; TELEFAX: (206) 224 0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 28:

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; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-406-192-28

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 8

US-08-082-269D-7  
; Sequence 7, Application US/08082269D  
; Patent No. 5773227  
; GENERAL INFORMATION:  
; APPLICANT: Kuhn, Michael  
; APPLICANT: Meyer, Tobias  
; APPLICANT: Allbritton, Nancy  
; TITLE OF INVENTION: Bifunctional Chelating Polysaccharides  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Molecular Probes, Inc.  
; STREET: 4849 Pitchford Avenue  
; CITY: Eugene  
; STATE: Oregon  
; COUNTRY: USA  
; ZIP: 97402-9144

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch  
; COMPUTER: IBM  
; OPERATING SYSTEM: MS-DOS 6.2  
; SOFTWARE: Text Editor  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082,269D  
; FILING DATE: 23-June-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Helfenstein, Allegra J.  
; REGISTRATION NUMBER: 34,179  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (503)465-8300  
; TELEFAX: (503)344-6504  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 AMINO ACIDS  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
; HYPOTHETICAL: no  
; FRAGMENT TYPE:  
; PUBLICATION INFORMATION:  
; AUTHORS: Munro, Sean and Pelham Hugh, R.B.  
; TITLE: A C-Terminal Signal Prevents Secretion of Luminal ER Proteins  
; JOURNAL: Cell  
; VOLUME: 48  
; ISSUE: 13 March 1987  
; PAGES: 899-907  
; DATE: 1987

## US-08-082-269D-7

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

Db 1 KDEL 4

## RESULT 9

US-08-593-865-1  
; Sequence 1, Application US/08593865  
; Patent No. 5776772  
; GENERAL INFORMATION:  
; APPLICANT: Paulson, James C.  
; APPLICANT: Uita-Lee, Eryn  
; APPLICANT: Colley, Karen J.  
; APPLICANT: Adler, Beverly  
; APPLICANT: Browne, Jeffrey K.  
; APPLICANT: Weinstein, Jasminder  
; TITLE OF INVENTION: Method for Producing Secrettable  
; TITLE OF INVENTION: Glycosyltransferases and Other Golgi Processing Enzymes  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Poms, Smith, Lande & Rose  
; STREET: 2029 Century Park East, 38th Floor  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90067

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/593,865  
; FILING DATE: January 30, 1996  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO 91/06635  
; FILING DATE: 16 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oldenkamp, David J.  
; REGISTRATION NUMBER: 29,421  
; REFERENCE/DOCKET NUMBER: 117-033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (310)788-5000  
; TELEFAX: (310) 277-1297  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-593-865-1

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 10

US-08-461-234-16  
; Sequence 16, Application US/08461234  
; Patent No. 5821238  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira H.  
; APPLICANT: FitzGerald, David J.  
; TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with  
; TITLE OF INVENTION: Increased Activity  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Stewart Street Tower

Mon Mar 20 08:51:26 2006

us-09-673-707-9.ra1

```

; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,234
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,709
; FILING DATE: 18-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/405,615
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-36-3
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-461-234-16

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4
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RESULT 11
US-08-480-190-152
; Sequence 152, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 152:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-480-190-152

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4
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RESULT 12
US-08-545-151-28
; Sequence 28, Application US/08545151
; Patent No. 5840712
; GENERAL INFORMATION:
; APPLICANT: Morgan Jr, A. Charles
; APPLICANT: Wilbur, D. Scott
; APPLICANT: Prathare, Pradip M
; TITLE OF INVENTION: Water Soluble Vitamin B12 Receptor
; TITLE OF INVENTION: Modulating Agents and Methods Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson & Kindness PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: WA 98101-2333
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,151
; FILING DATE: 19-OCT-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04404
; FILING DATE: 07-APR-1995
; APPLICATION NUMBER: US 08/406,192
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: US 08/406,194
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: US 08/406,191
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: US 08/224,831
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Renzoni, George E
; REGISTRATION NUMBER: 37,919
; REFERENCE/DOCKET NUMBER: RECL18878

```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682 8100  
TELEFAX: (206) 224 0779  
TELEX: 4938023  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-545-151-28

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
Db 1 KDEL 4

RESULT 13  
US-08-373-190-17  
Sequence 17, Application US/08373190  
Patent No. 5851829  
GENERAL INFORMATION:  
APPLICANT: MARASCO, WAYNE  
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/373,190  
FILING DATE: 17-JAN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06735  
FILING DATE: 16-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 41956-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: STRE UR 2002  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-373-190-17

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
Db 1 KDEL 4

RESULT 14  
US-08-463-480-16  
Sequence 16, Application US/08463480  
Patent No. 5854044  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira H.  
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with  
TITLE OF INVENTION: Increased Activity  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,480  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,709  
FILING DATE: 18-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/405,615  
FILING DATE: 15-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-36-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-463-480-16

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
Db 1 KDEL 4

RESULT 15  
US-08-470-566B-51  
Sequence 51, Application US/08470566B  
Patent No. 5872212  
GENERAL INFORMATION:  
APPLICANT: Warren, Gregory W  
APPLICANT: Koziel, Michael G  
APPLICANT: Mullins, Martha A

Mon Mar 20 08:51:26 2006

us-09-673-707-9.ra1

```

; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5872212el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5872212artis Corporation
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,566B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC169S/CIP3/DIV4 - SOLv4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-470-566B-51

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 16
US-08-488-379-152
; Sequence 152, Application US/08488379
; Patent No 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger

```

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; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 152:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-152

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 17
US-08-821-840-5
; Sequence 5, Application US/08821840
; Patent No. 5919456
; GENERAL INFORMATION:
; APPLICANT: Puri, Raj K.
; APPLICANT: Debinski, Waldemar
; APPLICANT: Pastan, Ira
; APPLICANT: Obiri, Nicholas
; TITLE OF INVENTION: IL-13 Receptor Specific Chimeric
; TITLE OF INVENTION: Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/821,840  
; FILING DATE: 21-MAR-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/404,685  
; FILING DATE: 15-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-217100US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-821-840-5

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 18  
US-08-713-928B-15  
; Sequence 15, Application US/08713928B  
; Patent No. 5929304  
; GENERAL INFORMATION:  
; APPLICANT: RADIN, DAVID N.  
; APPLICANT: CRAMER, CAROLE L.  
; APPLICANT: OISHI, KAREN K.  
; APPLICANT: WEISSENBORN, DEBORAH L.  
; TITLE OF INVENTION: PRODUCTION OF LYSSOSOMAL ENZYMES IN  
; TITLE OF INVENTION: PLANT-BASED EXPRESSION SYSTEMS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,928B  
; FILING DATE: 13-SEP-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/003,737  
; FILING DATE: 14-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cotuzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7956-0011-999  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids

; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-713-928B-15  
Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 19  
US-08-407-900B-6  
; Sequence 6, Application US/08407900B  
; Patent No. 5935822  
; GENERAL INFORMATION:  
; APPLICANT: Staehlin, Andrew  
; APPLICANT: Galbraith, David  
; APPLICANT: Giddings, Thomas  
; TITLE OF INVENTION: PRODUCT AND PROCESS FOR MEMBRANE AND  
; TITLE OF INVENTION: SOLUBLE POLYPEPTIDE SEGREGATION  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheridan Ross P.C.  
; STREET: 1700 Lincoln Street, Suite 3500  
; CITY: Denver  
; STATE: CO  
; COUNTRY: U.S.A.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/407,900B  
; FILING DATE: 03-MAR-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kovarik, Joseph E.  
; REGISTRATION NUMBER: 33,005  
; REFERENCE/DOCKET NUMBER: 2848-12  
; TELEPHONE: 303/863-9700  
; TELEFAX: 303/863-0223  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-407-900B-6  
Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 20  
US-08-419-075-28  
; Sequence 28, Application US/08419075  
; Patent No. 5939599  
; GENERAL INFORMATION:  
; APPLICANT: Saverio C. Falco

```

; APPLICANT: Chok-Pun Chui
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: A High Sulfur Seed
; TITLE OF INVENTION: Protein Gene and
; TITLE OF INVENTION: Method for Increasing
; TITLE OF INVENTION: the Sulfur Amino Acid
; TITLE OF INVENTION: Content of Plants
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; ADDRESSEE: and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,1.0MB
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,075
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/098,371
; FILING DATE:
; APPLICATION NUMBER: 07/656,687
; FILING DATE: 14-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1027-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-419-075-28

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 22
US-08-923-536A-2
; Sequence 2, Application US/08923536A
; Patent No. 5965426
; GENERAL INFORMATION:
; APPLICANT: SAKAI, Yasuyoshi
; APPLICANT: KATO, No. 5965426uo
; APPLICANT: SHIBANO, Yuji
; TITLE OF INVENTION: PROTEIN DISULFIDE ISOMERASE GENE DERIVED
; TITLE OF INVENTION: FROM STRAIN OF METHYLOTROPIC YEAST
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,536A
; FILING DATE: 04-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-234287
; FILING DATE: 04-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 001560-317
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids

```

```

; APPLICANT: Chok-Pun Chui
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: A High Sulfur Seed
; TITLE OF INVENTION: Protein Gene and
; TITLE OF INVENTION: Method for Increasing
; TITLE OF INVENTION: the Sulfur Amino Acid
; TITLE OF INVENTION: Content of Plants
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; ADDRESSEE: and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,1.0MB
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,075
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/098,371
; FILING DATE:
; APPLICATION NUMBER: 07/656,687
; FILING DATE: 14-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1027-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-419-075-28

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 21
US-08-438-190A-17
; Sequence 17, Application US/08438190A
; Patent No. 5965371
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; APPLICANT: HASELTINE, WILLIAM
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109

```

;  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-923-536A-2

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

## RESULT 23

US-08-491-988-29  
; Sequence 29 Application US/08491988  
; Patent No. 5973116

; GENERAL INFORMATION:

; APPLICANT: EPENETOS, AGAMEMNON A.

; APPLICANT: SPOONER, ROBERT A.

; APPLICANT: DEONARAIN, MAHENDRA

; TITLE OF INVENTION: Compounds for targeting

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP

; STREET: 261 MADISON AVENUE

; CITY: NEW YORK

; STATE: NY

; COUNTRY: USA

; ZIP: 10016-2391

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/491,988

; FILING DATE: 18-DEC-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: GOLDBERG, JULES E.

; REGISTRATION NUMBER: 24,408

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-986-4090

; TELEFAX: 212-818-9479

; INFORMATION FOR SEQ ID NO: 29:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

US-08-491-988-29

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

## RESULT 24

US-08-665-202-29

; Sequence 29 Application US/08665202

; Patent No. 5977322

; GENERAL INFORMATION:

; APPLICANT: Marks, James D.

; APPLICANT: Schier, Robert

; TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/665,202

; FILING DATE: 13-JUN-1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/000,238

; FILING DATE: 14-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/000,250

; FILING DATE: 15-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Hunter, Tom

; REGISTRATION NUMBER: 38,498

; REFERENCE/DOCKET NUMBER: 02307E-061410

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 29:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-665-202-29

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

## RESULT 25

US-08-809-668-9

; Sequence 9, Application US/08809668

; Patent No. 5980895

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira

; APPLICANT: Kuan, Chien-Tsun

; TITLE OF INVENTION: Immunotoxin Containing a

; TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a

; TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 5980895 Require Proteolytic

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,668
; FILING DATE: 21-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,388
; FILING DATE: 13-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16327
; FILING DATE: 11-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-253100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-809-668-9

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 26
US-08-331-397B-51
; Sequence 51, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US

US-08-759-804A-51
; Sequence 51, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

```

US-08-759-804A-51

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 28

US-08-818-253-49

; Sequence 49, Application US/08818253

; Patent No. 5998204

; GENERAL INFORMATION:

; APPLICANT: Tsien, Roger Y.

; APPLICANT: Miyawaki, Atsushi

; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR

; DETECTION OF ANALYTES

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/818,253

; FILING DATE: 14-MAR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Haile, Ph.D., Lisa A.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07257/043001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-818-253-49

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 29

US-08-350-215-17

; Sequence 17, Application US/08350215

; Patent No. 6004940

; GENERAL INFORMATION:

; APPLICANT: MARASCO, WAYNE A.

; APPLICANT: RICHARDSON, JENNIFER

; TITLE OF INVENTION: INTRACELLULAR TARGETING OF ENDOGENOUS

; PROTEINS

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &amp;

; ADDRESSEE: CUSHMAN

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/350,215

; FILING DATE: 12-DEC-1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: EISENSTEIN, RONALD I.

; REGISTRATION NUMBER: 30628

; REFERENCE/DOCKET NUMBER: 41956-CP3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 523-3400

; TELEFAX: (617) 523-6440

; TELETYPE: 200291 STRE UR

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-350-215-17

Query Match

100.0%; Score 20; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4

Db 1 KDEL 4

RESULT 30

US-08-722-258-62

; Sequence 62, Application US/08722258

; Patent No. 6011002

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira

; APPLICANT: Kreitman, Robert J.

; APPLICANT: Puri, Raj K.

; TITLE OF INVENTION: Circularly Permuted Ligands and

; Circularly Permuted Chimeric Molecules

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/722,258

; FILING DATE: 08-JAN-1997

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US95/04468

; FILING DATE: 06-APR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/225,224

; FILING DATE: 08-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-193100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-722-258-62

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 31  
US-08-718-904-42  
; Sequence 42, Application US/08718904  
; Patent No. 6037329  
; GENERAL INFORMATION:  
; APPLICANT: Baird, J. Andrew  
; APPLICANT: Chandler, Lois Ann  
; APPLICANT: Sosnowski, Barbara A.  
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 24-SEP-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6037329tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.415C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: /note="Cytoplasmic Translocation"  
; OTHER INFORMATION: "Signal"  
; US-08-718-904-42

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 32  
US-08-782-480-44  
; Sequence 44, Application US/08782480  
; Patent No. 6045774  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew C.  
; APPLICANT: Hein, Mich B.  
; APPLICANT: Fitchen, John H.  
; TITLE OF INVENTION: NOVEL EPITHELIAL TISSUE IMAGING AGENT  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/782,480  
; FILING DATE: 10-JAN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 310098.402  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-782-480-44

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 33  
US-09-287-145A-17  
; Sequence 17, Application US/09287145A  
; Patent No. 6072036  
; GENERAL INFORMATION:  
; APPLICANT: MARASCO, WAYNE  
; APPLICANT: HASELTINE, WILLIAM  
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESS: CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US

; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/09/287,145A  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/438,190  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EISENSTEIN, RONALD I.  
; REGISTRATION NUMBER: 30628  
; REFERENCE/DOCKET NUMBER: 41956  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-09-287-145A-17

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 34  
US-09-397-951-9  
; Sequence 9, Application US/09397951  
; Patent No. 6074644  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; TITLE OF INVENTION: Immunotoxin Containing a  
; TITLE OF INVENTION: Disulfide-Stabilized Antibody Fragment Joined to a  
; TITLE OF INVENTION: Pseudomonas Exotoxin that Does No. 6074644 Require Proteolytic  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/397,951  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/809,668  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US96/16327  
; FILING DATE: 11-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom

; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-253100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-397-951-9

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 35  
US-08-776-271-7  
; Sequence 7, Application US/08776271  
; Patent No. 6083502  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen  
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers  
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/776,271  
; FILING DATE: 01-DEC-1998  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/00224  
; FILING DATE: 03-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/010,166  
; FILING DATE: 05-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paris, Susan K.  
; REGISTRATION NUMBER: 41,739  
; REFERENCE/DOCKET NUMBER: 015280-259100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-776-271-7

Query Match 100.0%; Score 20; DB 2; Length 4;

```

; CURRENT FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-094-359-17

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 36
US-09-047-148-12
; Sequence 12, Application US/09047148
; Patent No. 6086900
; GENERAL INFORMATION:
; APPLICANT: Draper, Rockford
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USING
; TITLE OF INVENTION: MEMBRANE-PENETRATING PROTEINS TO CARRY MATERIALS ACROSS
; TITLE OF INVENTION: CELL MEMBRANES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/047,148
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,056
; FILING DATE: 26-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSP:072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-047-148-12

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 37
US-09-094-359-17
; Sequence 17, Application US/09094359
; Patent No. 6140132
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Liopis, Juan
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
; FILE REFERENCE: 07257/067001
; CURRENT APPLICATION NUMBER: US/09/094,359

; CURRENT FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-063-37

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 38
US-09-172-063-37
; Sequence 37, Application US/09172063
; Patent No. 6150176
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Liopis, Juan
; APPLICANT: Wachter, Rebekka M.
; APPLICANT: Remington, S. James
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
; FILE REFERENCE: 07257/071001
; CURRENT APPLICATION NUMBER: US/09/172,063
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 09/094,359
; EARLIER FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-063-37

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 39
US-08-789-333F-28
; Sequence 28, Application US/08789333F
; Patent No. 6153380
; GENERAL INFORMATION:
; APPLICANT: No. 6153380an, Garry P
; APPLICANT: Rothenberg, S. M.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A642601DJBRMSOSS
; CURRENT APPLICATION NUMBER: US/08/789,333F
; CURRENT FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 4
; TYPE: PRT
```



```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum sequence.
US-08-789-333F-28

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 40
US-09-215-035-7
; Sequence 7, Application US/09215035
; Patent No. 6153430
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Chang, Kai
; TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
; TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
; TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,035
; FILING DATE: No. 6153430 yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/776,271
; FILING DATE: 01-DEC-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/00224
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,166
; FILING DATE: 05-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-259110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-215-035-7

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

US-09-124-671-37
; Sequence 37, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recognition sequence of KDEL receptor
US-09-124-671-37

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 41
US-09-124-671-37
; Sequence 37, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recognition sequence of KDEL receptor
US-09-124-671-37

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 42
US-09-169-015-38
; Sequence 38, Application US/09169015
; Patent No. 6180343
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides
; FILE REFERENCE: A66900/DJB/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/169,015
; CURRENT FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; PUBLICATION INFORMATION:
; JOURNAL: Royal Society London Transaction B
; PAGES: 1-10
US-09-169-015-38

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 43
US-09-169-425C-23
; Sequence 23, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
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; APPLICANT: Chicx, Roman M.
; APPLICANT: Colline, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Frazer, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-169-425C-23

Query Match 100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 44
US-09-191-852-1
; Sequence 1, Application US/09191852
; Patent No. 6194560
; GENERAL INFORMATION:
; APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tariq A. Haq
; TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/191,852
; FILING DATE:
; CLASSIFICATION:

; APPLICANT: Chicx, Roman M.
; APPLICANT: Colline, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Frazer, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-169-425C-23

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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 45
US-08-818-252-49
; Sequence 49, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-818-252-49

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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 46
US-08-957-001B-2
; Sequence 2, Application US/08957001B
; Patent No. 6228621
; GENERAL INFORMATION:
; APPLICANT: Williams, William V.
; APPLICANT: Madaio, Michael
; APPLICANT: Weiner, David B.
; TITLE OF INVENTION: IMPROVED VACCINES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania

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; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: windows  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/957,001B  
; FILING DATE: 23-OCT-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/029,592  
; FILING DATE: 23-OCT-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeLuca, Mark  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: UPN-3303  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: both  
; MOLECULE TYPE: peptide  
; US-08-957-001B-2

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Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 47  
US-09-496-301-2  
; Sequence 2, Application US/09496301  
; Patent No. 6248565  
; GENERAL INFORMATION:  
; APPLICANT: Williams, William V.  
; APPLICANT: Madaio, Michael  
; APPLICANT: Weiner, David B.  
; TITLE OF INVENTION: IMPROVED VACCINES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565ris  
; STREET: One Liberty Place, 46th floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: windows  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/496,301  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/957,001  
; FILING DATE: 23-OCT-1997  
; APPLICATION NUMBER: US 60/029,592  
; FILING DATE: 23-OCT-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeLuca, Mark

; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: UPN-3303  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: both  
; MOLECULE TYPE: peptide  
; US-09-496-301-2

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 48  
US-08-954-211-44  
; Sequence 44, Application US/08954211  
; Patent No. 6251392  
; GENERAL INFORMATION:  
; APPLICANT: Hein, Mich B.  
; APPLICANT: Hiatt, Andrew C.  
; APPLICANT: Fitcher, John H.  
; TITLE OF INVENTION: NOVEL EPITHELIAL CELL TARGETING AGENT  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/954,211  
; FILING DATE: 10-JAN-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 310098.403  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-954-211-44

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 49

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Job time : 20.5 secs

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US-09-133-944-27
; Sequence 27, Application US/09133944
; Patent No. 6280937
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Yu, Pei Wen
; APPLICANT: Lorens, James
; TITLE OF INVENTION: SHUTTLE VECTORS
; FILE REFERENCE: A66252/DJB/DAV
; CURRENT APPLICATION NUMBER: US/09/133,944
; CURRENT FILING DATE: 1999-08-14
; EARLIER APPLICATION NUMBER: 09/133,949
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: endoplasmic
; OTHER INFORMATION: reticulum sequence
; PUBLICATION INFORMATION:
; JOURNAL: Royal Society London Transactions B
; VOLUME: B
; PAGES: 1-10
; DATE: 1992
; US-09-133-944-27

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      1 KDEL 4

RESULT 50
US-09-613-182-12
; Sequence 12, Application US/09613182
; Patent No. 6294653
; GENERAL INFORMATION:
; APPLICANT: Mayfield, Stephen
; TITLE OF INVENTION: RNA BINDING PROTEIN AND BINDING SITE USEFUL FOR
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT MOLECULES
; FILE REFERENCE: SCR2177S
; CURRENT APPLICATION NUMBER: US/09/613,182
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/341,550
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: PCT/US98/00840
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/035,955
; PRIOR FILING DATE: 1997-01-17
; PRIOR APPLICATION NUMBER: 60/069,400
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
; US-09-613-182-12

Query Match      100.0%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      1 KDEL 4
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

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(without alignments)  
26.741 Million cell updates/sec

Title: US-09-673-707-9  
Perfect score: 20  
Sequence: 1 KDEL 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 segs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

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2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pcp:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 3          | 20    | 100.0       | 4      | 3  | US-09-157-748-30  |
| 4          | 20    | 100.0       | 4      | 3  | US-09-749-959-37  |
| 5          | 20    | 100.0       | 4      | 3  | US-09-759-960-23  |
| 6          | 20    | 100.0       | 4      | 3  | US-09-789-652A-25 |
| 7          | 20    | 100.0       | 4      | 3  | US-09-208-827-29  |
| 8          | 20    | 100.0       | 4      | 3  | US-09-854-122-2   |
| 9          | 20    | 100.0       | 4      | 3  | US-09-881-165-5   |
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| 13         | 20    | 100.0       | 4      | 3  | US-09-785-921A-16 |
| 14         | 20    | 100.0       | 4      | 3  | US-09-997-956-2   |
| 15         | 20    | 100.0       | 4      | 3  | US-09-781-804-2   |
| 16         | 20    | 100.0       | 4      | 3  | US-09-916-940-28  |
| 17         | 20    | 100.0       | 4      | 3  | US-09-270-983-5   |
| 18         | 20    | 100.0       | 4      | 3  | US-09-917-154-1   |
| 19         | 20    | 100.0       | 4      | 3  | US-09-480-236-8   |
| 20         | 20    | 100.0       | 4      | 3  | US-09-984-183-3   |
| 21         | 20    | 100.0       | 4      | 3  | US-09-999-745-22  |
| 22         | 20    | 100.0       | 4      | 3  | US-09-967-772-10  |
| 23         | 20    | 100.0       | 4      | 3  | US-09-554-000-49  |
| 24         | 20    | 100.0       | 4      | 3  | US-09-178-286-19  |
| 25         | 20    | 100.0       | 4      | 3  | US-09-792-630-77  |
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|            |       |             |        |    | Sequence 24, Appl |
|            |       |             |        |    | Sequence 30, Appl |
|            |       |             |        |    | Sequence 37, Appl |
|            |       |             |        |    | Sequence 23, Appl |
|            |       |             |        |    | Sequence 25, Appl |
|            |       |             |        |    | Sequence 29, Appl |
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|            |       |             |        |    | Sequence 35, Appl |
|            |       |             |        |    | Sequence 5, Appl  |
|            |       |             |        |    | Sequence 2, Appl  |
|            |       |             |        |    | Sequence 16, Appl |
|            |       |             |        |    | Sequence 2, Appl  |
|            |       |             |        |    | Sequence 28, Appl |
|            |       |             |        |    | Sequence 5, Appl  |
|            |       |             |        |    | Sequence 1, Appl  |
|            |       |             |        |    | Sequence 8, Appl  |
|            |       |             |        |    | Sequence 3, Appl  |
|            |       |             |        |    | Sequence 22, Appl |
|            |       |             |        |    | Sequence 10, Appl |
|            |       |             |        |    | Sequence 49, Appl |
|            |       |             |        |    | Sequence 17, Appl |
|            |       |             |        |    | Sequence 10, Appl |
|            |       |             |        |    | Sequence 6, Appl  |

Sequence 3, Appl  
Sequence 8, Appl  
Sequence 699, Appl  
Sequence 97, Appl  
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Sequence 1383, Appl  
Sequence 8, Appl  
Sequence 10, Appl  
Sequence 163, Appl  
Sequence 46, Appl

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132 20 100.0 4 5 US-10-795-676-67  
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140 20 100.0 4 5 US-10-916-460-1  
141 20 100.0 4 5 US-10-890-789-9  
142 20 100.0 4 5 US-10-823-254-9  
143 20 100.0 4 5 US-10-844-711-4  
144 20 100.0 4 5 US-10-659-036-13  
145 20 100.0 4 5 US-10-873-594-37  
146 20 100.0 4 5 US-10-831-901A-8  
147 20 100.0 4 5 US-10-751-845-111  
148 20 100.0 4 5 US-10-499-184-26  
149 20 100.0 4 5 US-10-490-535-5  
150 20 100.0 4 5 US-10-700-971C-18

Sequence 159, Appl  
Sequence 8, Appl  
Sequence 5, Appl  
Sequence 17, Appl  
Sequence 6, Appl  
Sequence 141, Appl  
Sequence 2, Appl  
Sequence 1, Appl  
Sequence 20, Appl  
Sequence 8, Appl  
Sequence 16, Appl  
Sequence 9, Appl  
Sequence 32, Appl  
Sequence 26, Appl  
Sequence 11, Appl  
Sequence 2, Appl  
Sequence 22, Appl  
Sequence 6, Appl  
Sequence 40, Appl  
Sequence 8, Appl  
Sequence 33, Appl  
Sequence 19, Appl  
Sequence 15, Appl  
Sequence 29, Appl  
Sequence 20, Appl  
Sequence 37, Appl  
Sequence 23, Appl  
Sequence 106, Appl  
Sequence 37, Appl  
Sequence 4, Appl  
Sequence 67, Appl  
Sequence 1, Appl  
Sequence 42, Appl  
Sequence 52, Appl  
Sequence 28, Appl  
Sequence 150, Appl  
Sequence 2, Appl  
Sequence 9, Appl  
Sequence 1, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 4, Appl  
Sequence 13, Appl  
Sequence 37, Appl  
Sequence 8, Appl  
Sequence 111, Appl  
Sequence 26, Appl  
Sequence 5, Appl  
Sequence 18, Appl

US-08-765-244-16  
; Sequence 16, Application US/08765244  
; Publication No. US20010008771A1  
; GENERAL INFORMATION:  
; APPLICANT: Seibel, Peter  
; APPLICANT: Seibel, Andrea  
; TITLE OF INVENTION: CHEMICAL PEPTIDE-NUCLEIC ACID  
; TITLE OF INVENTION: FRAGMENT, PROCESS FOR PRODUCING THE SAME AND ITS USES FOR  
; TITLE OF INVENTION: APPROPRIATELY INTRODUCING NUCLEIC ACIDS INTO CELL ORGANELLES  
; TITLE OF INVENTION: AND CELLS  
; FILE REFERENCE: 8484-0018-999  
; CURRENT APPLICATION NUMBER: US/08/765,244  
; CURRENT FILING DATE: 1997-10-30  
; PRIOR APPLICATION NUMBER: PCT/DE95/00775  
; PRIOR FILING DATE: 1995-06-11  
; PRIOR APPLICATION NUMBER: DE P 44 21 079.5  
; PRIOR FILING DATE: 1994-06-16

; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic sequence  
US-08-765-244-16

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 2  
US-08-873-601-24  
; Sequence 24, Application US/08873601  
; Publication No. US20020064798A1  
; GENERAL INFORMATION:  
; APPLICANT: Pavan, Donald  
; TITLE OF INVENTION: COMBINATORIAL ENZYMATIC COMPLEXES  
; FILE REFERENCE: A-63915/DJB/RMS  
; CURRENT APPLICATION NUMBER: US/08/873,601  
; CURRENT FILING DATE: 1997-06-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: UNKNOWN  
US-08-873-601-24

Query Match 100.0%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 3  
US-09-157-748-30  
; Sequence 30, Application US/09157748  
; Patent No. US20010003042A1  
; GENERAL INFORMATION:  
; APPLICANT: Lorens, James  
; TITLE OF INVENTION: Multiparameter FACS Assays to Detect Alterations in  
; TITLE OF INVENTION: Cell Cycle Regulation  
; FILE REFERENCE: A66587/DJB/RMS  
; CURRENT APPLICATION NUMBER: US/09/157,748  
; CURRENT FILING DATE: 1998-09-21  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; JOURNAL: Royal Society London Transaction B  
; PAGES: 1-1-  
; DATE: 1992  
US-09-157-748-30

Query Match 100.0%; Score 20; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;  
Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 4  
US-09-749-959-37  
; Sequence 37, Application US/09749959  
; Publication No. US20010003650A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; TITLE OF INVENTION: GREEN FLUORESCENT PROTEIN FUSIONS WITH RANDOM PEPTIDES  
; FILE REFERENCE: A-66900-5/RMS/AMS  
; CURRENT APPLICATION NUMBER: US/09/749,959  
; CURRENT FILING DATE: 2000-12-27  
; PRIOR APPLICATION NUMBER: US 09/169,015  
; PRIOR FILING DATE: 1998-10-08  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-749-959-37

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 5  
US-09-759-960-23  
; Sequence 23, Application US/09759960  
; Patent No. US20010006639A1  
; GENERAL INFORMATION:  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chicz, Roman M.  
; APPLICANT: Collins, Edward J.  
; APPLICANT: Hedley, Mary Lynn  
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA: US/09/759,960  
; APPLICATION NUMBER: 09/169,425  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/169,425  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 08191/004002  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070  
TELEFAX: 617-543-8906  
TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-759-960-23

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 6  
US-09-789-652A-25  
; Sequence 25, Application US/09789652A  
; Publication No. US20010036638A1  
; GENERAL INFORMATION:  
; APPLICANT: Nolan, Garry P.  
; APPLICANT: Pavan, Donald  
; TITLE OF INVENTION: COMBINATORIAL ENZYMATIC COMPLEXES  
; FILE REFERENCE: A-63915--1/RMS/CYO  
; CURRENT APPLICATION NUMBER: US/09/789,652A  
; CURRENT FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: US 08/873,601  
; PRIOR FILING DATE: 1997-06-12  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-789-652A-25

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 7  
US-09-208-827-29  
; Sequence 29, Application US/09208827  
; Publication No. US2002001830A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Ying  
; APPLICANT: Yu, Pei Wen  
; APPLICANT: Lorens, James  
; TITLE OF INVENTION: SHUTTLE VECTORS  
; FILE REFERENCE: A66252-1/DJB/DAV  
; CURRENT APPLICATION NUMBER: US/09/208,827  
; CURRENT FILING DATE: 1998-12-09  
; EARLIER APPLICATION NUMBER: 09/133,949  
; EARLIER FILING DATE: 1998-08-14  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: endoplasmic  
; OTHER INFORMATION: reticulum sequence

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; PUBLICATION INFORMATION:
; JOURNAL: Royal Society London Transactions B
; VOLUME: B
; PAGES: 1-10
; DATE: 1992
US-09-208-827-29

Query Match          100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 8
US-09-854-122-2
; Sequence 2, Application US/09854122
; Patent No. US20020016980A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTE, RANDALL S.
; TITLE OF INVENTION: TRANSGENIC PLANTS INCORPORATING TRAIT OF ZOSTERA MARINA
; FILE REFERENCE: PHA-007.01
; CURRENT APPLICATION NUMBER: US/09/854,122
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/202,529
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 4
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-854-122-2

Query Match          100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 9
US-09-881-165-5
; Sequence 5, Application US/09881165
; Publication No. US20020039772A1
; GENERAL INFORMATION:
; APPLICANT: HOOD, ELIZABETH
; APPLICANT: HOWARD, JOHN
; APPLICANT: BAILEY, MICHELE
; APPLICANT: GASTEL, FRANS VAN
; APPLICANT: WANG, HUAMING
; APPLICANT: WARD, MICHAEL
; APPLICANT: WOODARD, SUSAN
; TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE
; FILE REFERENCE: 10032R
; CURRENT APPLICATION NUMBER: US/09/881,165
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/211,732
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
US-09-881-165-5

; PUBLICATION INFORMATION:
; JOURNAL: Royal Society London Transactions B
; VOLUME: B
; PAGES: 1-10
; DATE: 1992
US-09-208-827-29

Query Match          100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 10
US-09-347-064-35
; Sequence 35, Application US/09347064A
; Patent No. US20020045208A1
; GENERAL INFORMATION:
; APPLICANT: Eck, Jurgen
; APPLICANT: Schmidt, Arno
; APPLICANT: Zinke, Holger
; TITLE OF INVENTION: Recombinant Fusion Proteins Based on
; TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
; FILE REFERENCE: 09282-5
; CURRENT APPLICATION NUMBER: US/09/347,064A
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: PCT/EP98/00009
; EARLIER FILING DATE: 1998-01-02
; EARLIER APPLICATION NUMBER: EP 97 10 0012.0
; EARLIER FILING DATE: 1997-01-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modulator
US-09-347-064-35

Query Match          100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 11
US-09-910-639-2
; Sequence 2, Application US/09910639
; Publication No. US20020048550A1
; GENERAL INFORMATION:
; APPLICANT: Vallera, Daniel A.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: RADIOLABELED IMMUNOTOXINS
; FILE REFERENCE: 09531-023001
; CURRENT APPLICATION NUMBER: US/09/910,639
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/219,759
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-639-2

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Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 12

US-09-333-527-2  
; Sequence 2, Application US/09333527  
; Patent No. US20020078472A1  
; GENERAL INFORMATION:  
; APPLICANT: Paul CHRISTOU; Eva STROGER; Rainer FISCHER; Carmen MARTIN-VAQUERO; Stef  
; TITLE OF INVENTION: METHODS AND MEANS FOR EXPRESSION OF MAMMALIAN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 666 Fifth Avenue  
; CITY: New York City  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/333,527  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/089,322  
; FILING DATE: June 15, 1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mary Anne Schofield  
; REGISTRATION NUMBER: 36,669  
; REFERENCE/DOCKET NUMBER: KL/JIC 202.1 - JEL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 318-3000  
; TELEFAX: (212) 752-5958  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-333-527-2

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 13

US-09-785-921A-16  
; Sequence 16, Application US/09785921A  
; Patent No. US2002009434A1  
; GENERAL INFORMATION:  
; APPLICANT: Keener, William K.  
; APPLICANT: Ward, Thomas E.  
; TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN  
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS  
; FILE REFERENCE: LIT-PI-529  
; CURRENT APPLICATION NUMBER: US/09/785,921A  
; CURRENT FILING DATE: 2001-02-15  
; NUMBER OF SEQ ID NOS: 17

; SEQ ID NO 16  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-785-921A-16

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 14

US-09-997-956-2  
; Sequence 2, Application US/09997956  
; Patent No. US20020106714A1  
; GENERAL INFORMATION:  
; APPLICANT: Jalink, Kees  
; TITLE OF INVENTION: Membrane Molecule Indicator Compositions  
; TITLE OF INVENTION: and Methods  
; FILE REFERENCE: P-NS 5045  
; CURRENT APPLICATION NUMBER: US/09/997,956  
; CURRENT FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 60/250,679  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/256,559  
; PRIOR FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-997-956-2

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 15

US-09-781-804-2  
; Sequence 2, Application US/09781804  
; Patent No. US20020107189A1  
; GENERAL INFORMATION:  
; APPLICANT: Ariad Gene Therapeutics, Inc.  
; TITLE OF INVENTION: Regulation of Biological Events Using No. US20020107189A1e1 Con  
; FILE REFERENCE: 374 USD1  
; CURRENT APPLICATION NUMBER: US/09/781,804  
; CURRENT FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: organelle binding domain  
; NAME/KEY: DOMAIN  
; LOCATION: (1)..(4)  
; OTHER INFORMATION: organelle binding domain  
US-09-781-804-2

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mon Mar 20 08:51:26 2006

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Qy      1 KDEL 4
Db      1 KDEL 4

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

RESULT 16
US-09-916-940-28
; Sequence 28, Application US/09916940
; Patent No. US20020127564A1
; GENERAL INFORMATION:
; APPLICANT: NO. US20020127564Alan, Garry P
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A-64260-6/RMS/RMS
; CURRENT FILING DATE: 2001-07-27
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 1997-11-03
; PRIOR FILING DATE: 1996-01-23
; PRIOR FILING DATE: 1996-01-23
; PRIOR FILING DATE: 1996-01-23
; PRIOR FILING DATE: 1997-01-23
; PRIOR FILING DATE: 1997-01-23
; PRIOR FILING DATE: 1997-01-23
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic
; OTHER INFORMATION: reticulum sequence.
US-09-916-940-28

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 17
US-09-270-983-5
; Sequence 5, Application US/09270983
; Publication No. US20020132327A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: HAY, Bruce A.
; APPLICANT: HAWKINS, Christine V.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING PROTEASES, PROTEASE TARGET SITES AND REGU
; TITLE OF INVENTION: OF PROTEASE ACTIVITY IN LIVING CELLS
; FILE REFERENCE: CIT1130-1
; CURRENT APPLICATION NUMBER: US/09/270,983
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: US 60/078,721
; PRIOR FILING DATE: 1998-03-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Product Synthesis, such as solid phase synthesis
US-09-270-983-5

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 18
US-09-917-154-1
; Sequence 1, Application US/09917154
; Publication No. US20020137707A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wolff, Jon A
; APPLICANT: Hagstrom, James E
; APPLICANT: Monahan, Sean D
; APPLICANT: Siattum, Paul M
; APPLICANT: Rozema, David B
; APPLICANT: Budker, Vladimir G
; TITLE OF INVENTION: Intravascular Delivery of Non-Viral Nucleic Acid
; FILE REFERENCE: Mirus.013.04.03
; CURRENT APPLICATION NUMBER: US/09/917,154
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-917-154-1

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 19
US-09-480-236-8
; Sequence 8, Application US/09480236
; Patent No. US20020142000A1
; GENERAL INFORMATION:
; APPLICANT: Digan, Mary Ellen
; APPLICANT: Lake, Philip
; APPLICANT: Wright, Richard M.
; TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor
; FILE REFERENCE: CGC 4-31157A/USN
; CURRENT APPLICATION NUMBER: US/09/480,236
; CURRENT FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PE peptide
US-09-480-236-8

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy      1 KDEL 4
Db      1 KDEL 4
```

```

RESULT 20
US-09-984-183-3
; Sequence 3, Application US/09984183
; Patent No. US20020142983A1
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, BABITA
; APPLICANT: LONGENECKER, MICHAEL B.
; TITLE OF INVENTION: MUC-1 ANTAGONISTS AND METHODS OF TREATING IMMUNE
; DISORDERS
; FILE REFERENCE: 042881/0130
; CURRENT APPLICATION NUMBER: US/09/984,183
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/457,354
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/111,973
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Retrograde
; transport peptide
US-09-984-183-3

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 21
US-09-999-745-22
; Sequence 22, Application US/09999745
; Patent No. US20020157120A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: REGEN1470-1
; CURRENT APPLICATION NUMBER: US/09/999,745
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/316,920
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-999-745-22

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 22
US-09-967-772-10
; Sequence 10, Application US/09967772
; Patent No. US20020164577A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Martin
; APPLICANT: Gonzalez, Ana Maria
; APPLICANT: Baird, Andrew
; GENERAL INFORMATION:
; Patent No. US20020168338A1
; Sequence 19, Application US/09178286
US-09-178-286-19

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 23
US-09-554-000-49
; Sequence 49, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-554-000-49

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 24
US-09-178-286-19
; Sequence 19, Application US/09178286
; Patent No. US20020168338A1
; GENERAL INFORMATION:
; APPLICANT: Baird, Andrew
; APPLICANT: Gonzalez, Ana Maria
; APPLICANT: Berry, Martin

```

Mon Mar 20 08:51:26 2006

us-09-673-707-9.rapbm

US-09-915-789A-10  
Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
Db 1 KDEL 4  
RESULT 27  
US-09-807-721-6  
; Sequence 6, Application US/09807721  
; Patent No. US20020174453A1  
; GENERAL INFORMATION:  
; APPLICANT: AUBURN UNIVERSITY  
; APPLICANT: UNIVERSITY OF CENTRAL FLORIDA  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS  
; FILE REFERENCE: 1463-PCT-US-00  
; CURRENT APPLICATION NUMBER: US/09/807,721  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: PCT/US01/06274  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-807-721-6  
Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
Db 1 KDEL 4

US-09-178-286-19  
Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
Db 1 KDEL 4

US-09-792-630-77  
; Sequence 77, Application US/09792630  
; Patent No. US20020168640A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Min  
; APPLICANT: Dahiyat, Bassil I.  
; TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES  
; FILE REFERENCE: A-70295/RFT/RMS/RMK  
; CURRENT APPLICATION NUMBER: US/09/792,630  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 77  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-792-630-77  
Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
Db 1 KDEL 4

US-09-915-789A-10  
; Sequence 10, Application US/09915789A  
; Patent No. US20020168762A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Lieping  
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY  
; TITLE OF INVENTION: MOLECULES  
; FILE REFERENCE: 07039-219001  
; CURRENT APPLICATION NUMBER: US/09/915,789A  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 60/220,991  
; PRIOR FILING DATE: 2000-07-27  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus

US-09-915-789A-10

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
Db 1 KDEL 4

US-09-807-721-6  
; Sequence 6, Application US/09807721  
; Patent No. US20020174453A1  
; GENERAL INFORMATION:  
; APPLICANT: AUBURN UNIVERSITY  
; APPLICANT: UNIVERSITY OF CENTRAL FLORIDA  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS  
; FILE REFERENCE: 1463-PCT-US-00  
; CURRENT APPLICATION NUMBER: US/09/807,721  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: PCT/US01/06274  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-807-721-6  
Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
Db 1 KDEL 4

US-09-925-803-3  
; Sequence 3, Application US/09925803  
; Publication No. US20020198166A1  
; GENERAL INFORMATION:  
; APPLICANT: ROTHMAN, James E.  
; APPLICANT: HARTL, Ulrich F.  
; APPLICANT: HOE, Mee E.  
; APPLICANT: HOUGHTON, Alan  
; APPLICANT: TEKECHI, Yoshizumi  
; APPLICANT: MAYHEW, Mark  
; TITLE OF INVENTION: METHOD OF TREATMENT OF CANCER AND  
; TITLE OF INVENTION: INFECTIOUS DISEASES AND COMPOSITIONS USEFUL IN SAME  
; FILE REFERENCE: 31568-PCT-USA-III / 065360.0163  
; CURRENT APPLICATION NUMBER: US/09/925,803  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/511,453  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 09/011,648  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: PCT/US96/13233  
; PRIOR FILING DATE: 1996-08-16  
; PRIOR APPLICATION NUMBER: 60/002,479  
; PRIOR FILING DATE: 1995-08-18  
; PRIOR APPLICATION NUMBER: 60/002,490  
; PRIOR FILING DATE: 1995-08-18  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3

; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: eukaryotic  
US-09-925-803-3

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|||  
Db 1 KDEL 4

## RESULT 29

US-09-575-847-8  
; Sequence 8, Application US/09575847  
; Publication No. US20030013149A1  
; GENERAL INFORMATION:  
; APPLICANT: WACHTER, Rebekka  
; APPLICANT: REMINGTON, James  
; TITLE OF INVENTION: LONG WAVELENGTH ENGINEERED FLUORESCENT PROTEINS  
; FILE REFERENCE: REG1250-5  
; CURRENT APPLICATION NUMBER: US/09/575,847  
; CURRENT FILING DATE: 2000-05-19  
; PRIOR FILING DATE: 1997-11-19  
; PRIOR APPLICATION NUMBER: US 08/974,737  
; PRIOR FILING DATE: 1997-11-19  
; PRIOR APPLICATION NUMBER: US 08/911,825  
; PRIOR FILING DATE: 1997-08-15  
; PRIOR APPLICATION NUMBER: US 08/706,408  
; PRIOR FILING DATE: 1996-08-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Targeting sequence  
US-09-575-847-8

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|||  
Db 1 KDEL 4

## RESULT 30

US-09-935-430-699  
; Sequence 699, Application US/09935430  
; Publication No. US20030017466A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-BID, PIA  
; APPLICANT: JAKOBOVITZ, AVA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/09/935,430  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 699

; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-935-430-699

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|||  
Db 1 KDEL 4

## RESULT 31

US-09-991-209-97  
; Sequence 97, Application US/09991209  
; Publication No. US20030024009A1  
; GENERAL INFORMATION:  
; APPLICANT: Dunn-Coleman, Nigel  
; APPLICANT: Langdon, Timothy  
; APPLICANT: Morse, Phillip  
; TITLE OF INVENTION: Manipulation of the Phenolic Acid  
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted  
; FILE REFERENCE: GC648-2  
; CURRENT APPLICATION NUMBER: US/09/991,209  
; CURRENT FILING DATE: 2002-07-02  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: US 60/249,608  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: retention sequence  
US-09-991-209-97

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|||  
Db 1 KDEL 4

## RESULT 32

US-09-999-686-24  
; Sequence 24, Application US/09999686  
; Publication No. US20030028000A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Nazneen  
; APPLICANT: Hedley, Mary Lynne  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Tomlinson, Andrew J.  
; APPLICANT: Cole, Geoffrey  
; TITLE OF INVENTION: CYP1B1 NUCLEIC ACIDS AND METHODS OF USE  
; FILE REFERENCE: 08191-021001  
; CURRENT APPLICATION NUMBER: US/09/999,686  
; CURRENT FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 60/298,428  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/261,719  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 60/244,501

```
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-999-686-24

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 33
US-09-906-393A-1
; Sequence 1, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906.393A
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-906-393A-1

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 34
US-09-861-257-19
; Sequence 19, Application US/09861257
; Publication No. US20030040496A1
; GENERAL INFORMATION:
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; APPLICANT: Baird, J. Andrew
; APPLICANT: Pierce, Glenn
; TITLE OF INVENTION: TREATMENT OF TUMORS USING
; TITLE OF INVENTION: LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/861,257
; FILING DATE: 17-MAY-2001
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen Ph.D., William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 760100.423C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: /note= "Cytoplasmic Translocation
; OTHER INFORMATION: Signal"
US-09-861-257-19

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 35
US-09-913-238-63
; Sequence 63, Application US/09913238
; Publication No. US20030049251A1
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Steinberger, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
; TITLE OF INVENTION: INHIBITING CCR5-DEPENDENT INFECTION OF CELLS BY HIV-1
; FILE REFERENCE: TSRI 728.1
; CURRENT APPLICATION NUMBER: US/09/913,238
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: PCT/EPO 0/12419
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/169,653
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthesized
US-09-913-238-63

Query Match      100.0%; Score 20; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 36
US-09-462-713-13
; Sequence 13, Application US/09462713
; Publication No. US20030054012A1
; GENERAL INFORMATION:
; APPLICANT: FitzGerald, David J.
; APPLICANT: Mreny, Randall J.
; APPLICANT: The Government of the United States of America
```

; APPLICANT: Genentech, Inc.  
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens  
; FILE REFERENCE: 015280-361100US  
; CURRENT APPLICATION NUMBER: US/09/462,713  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: PCT/US98/14336  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/056,924  
; PRIOR FILING DATE: 1997-07-11  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic  
; OTHER INFORMATION: reticulum (ER) retention sequence  
US-09-462-713-13

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 37  
US-09-932-165-1508  
; Sequence 1508, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND Cat-F2E11 USEFUL IN TREATMENT AND  
; TITLE OF INVENTION: DETECTION OF CANCER  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1508  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative  
; OTHER INFORMATION: peptide  
US-09-932-165-1508

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 38

US-09-935-384-781  
; Sequence 781, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 781  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-935-384-781

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 39  
US-09-824-200-9  
; Sequence 9, Application US/09824200  
; Publication No. US20030167531A1  
; GENERAL INFORMATION:  
; APPLICANT: RUSSELL, DOUGLAS A.  
; APPLICANT: SCHLITTLER, MICHAEL  
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF BIOACTIVE, AUTHENTIC  
; TITLE OF INVENTION: POLYPEPTIDES FROM PLANTS  
; FILE REFERENCE: 16712.0031  
; CURRENT APPLICATION NUMBER: US/09/824,200  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/194,217  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-824-200-9

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 40  
US-09-942-052-708  
; Sequence 708, Application US/09942052

Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 708  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative  
; OTHER INFORMATION: peptide  
US-09-942-052-708

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 41  
US-09-293-670-34  
; Sequence 34, Application US/09293670  
; Publication No. US20030190684A1  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Joseph  
; APPLICANT: Lorens, James  
; APPLICANT: Payan, Donald  
; APPLICANT: Rossi, Alexander  
; TITLE OF INVENTION: Multiparameter Facs Assays to Detect Alterations in  
; TITLE OF INVENTION: Cellular Parameters and to Screen Small Molecule  
; TITLE OF INVENTION: Libraries  
; FILE REFERENCE: A68104/DJB/RMS/DAV  
; CURRENT APPLICATION NUMBER: US/09/293,670  
; CURRENT FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; PUBLICATION INFORMATION:  
; JOURNAL: Royal Society London Transaction B  
; PAGES: 1-10  
; DATE: 19992  
US-09-293-670-34

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 42  
US-09-872-836-116  
; Sequence 116, Application US/09872836  
; Publication No. US20040142475A1  
; GENERAL INFORMATION:  
; APPLICANT: Barman, Shikha P.  
; APPLICANT: McKeever, Una  
; APPLICANT: Hedley, Mary Lynne  
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS  
; FILE REFERENCE: 08191-018001  
; CURRENT APPLICATION NUMBER: US/09/872,836  
; CURRENT FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/208,830  
; PRIOR FILING DATE: 2000-06-02  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 116  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-872-836-116

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
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Db 1 KDEL 4

RESULT 43  
US-09-800-770-81  
; Sequence 81, Application US/09800770  
; Publication No. US20050233456A1  
; GENERAL INFORMATION:  
; APPLICANT: Kinsella, Todd  
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES  
; FILE REFERENCE: A-68614-1/DJB/RMS/RMK  
; CURRENT APPLICATION NUMBER: US/09/800,770  
; CURRENT FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: US 60/187,130  
; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 81  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-800-770-81

Query Match 100.0%; Score 20; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 44  
US-10-043-142-9  
; Sequence 9, Application US/10043142  
; Publication No. US20020150969A1  
; GENERAL INFORMATION:  
; APPLICANT: DEXX, PATRICK M.F.  
; APPLICANT: MADRID, SUSAN M.  
; TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES  
; FILE REFERENCE: 078883/0128  
; CURRENT APPLICATION NUMBER: US/10/043,142  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER: 09/806,399  
; PRIOR FILING DATE: 2002-03-30



; PRIOR APPLICATION NUMBER: PCT/IB99/01669  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: GB 9821198.0  
; PRIOR FILING DATE: 1998-09-30  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative ER  
; OTHER INFORMATION: retention  
; OTHER INFORMATION: signal  
US-10-043-142-9

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 45

US-10-154-801-3  
; Sequence 3, Application US/10154801  
; Publication No. US200201510141  
; GENERAL INFORMATION:  
; APPLICANT: CAMPBELL, ANTHONY KEITH  
; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND THEIR USE  
; FILE REFERENCE: 09/225,302  
; CURRENT APPLICATION NUMBER: US/10/154,801  
; CURRENT FILING DATE: 2002-05-28  
; PRIOR APPLICATION NUMBER: 08/957,135  
; PRIOR FILING DATE: 1998-09-14  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-154-801-3

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 46

US-10-080-376-77  
; Sequence 77, Application US/10080376  
; Publication No. US20020172968A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Min  
; APPLICANT: Dahiya, Basail I.  
; TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES  
; FILE REFERENCE: A-70295-2/RT/RMS/RMK  
; CURRENT APPLICATION NUMBER: US/10/080,376  
; CURRENT FILING DATE: 2000-02-19  
; PRIOR APPLICATION NUMBER: US 09/792,630  
; PRIOR FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 77

; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-080-376-77

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 47

US-10-061-395-25  
; Sequence 25, Application US/10061395  
; Publication No. US20020192675A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice  
; APPLICANT: Smith, Ernest S.  
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules  
; FILE REFERENCE: 1821.0080003  
; CURRENT APPLICATION NUMBER: US/10/061,395  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/271,423  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 60/265,880  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: 60/265,589  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Endoplasmic reticulum sequence from calreticulin  
US-10-061-395-25

Query Match 100.0%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 48

US-10-061-395-35  
; Sequence 35, Application US/10061395  
; Publication No. US20020192675A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice  
; APPLICANT: Smith, Ernest S.  
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules  
; FILE REFERENCE: 1821.0080003  
; CURRENT APPLICATION NUMBER: US/10/061,395  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/271,423  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 60/265,880  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: 60/265,589  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Heterologous signal sequence for the endoplasmic reticulum
US-10-061-395-35

Query Match      100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
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Db      1 KDEL 4

RESULT 49
US-10-043-074-29
; Sequence 29, Application US/10043074
; Publication No. US20030017601A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Yu, Pei Wen
; APPLICANT: Lorens, James
; TITLE OF INVENTION: SHUTTLE VECTORS
; FILE REFERENCE: A66252-1/DJB/DAV
; CURRENT APPLICATION NUMBER: US/10/043,074
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,827
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/133,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: endoplasmic
; OTHER INFORMATION: reticulum sequence
; PUBLICATION INFORMATION:
; JOURNAL: Royal Society London Transactions B
; VOLUME: B
; PAGES: 1-10
; DATE: 1992
US-10-043-074-29

Query Match      100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
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Db      1 KDEL 4

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Job time : 65.5 secs
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; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-096-339-24

Query Match      100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
      ||||
Db      1 KDEL 4

Search completed: March 20, 2006, 07:55:12
Job time : 65.5 secs
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; FEATURE:
; OTHER INFORMATION: Heterologous signal sequence for the endoplasmic reticulum
US-10-061-395-35

Query Match      100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
      ||||
Db      1 KDEL 4

RESULT 50
US-10-096-339-24
; Sequence 24, Application US/10096339
; Publication No. US20030022196A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Kinsella, Todd
; APPLICANT: Masuda, Esteban
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Liao, X. Charlene
; APPLICANT: Pearsall, Denise
; APPLICANT: Freira, Annabelle
; APPLICANT: Chu, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ALTERED CELLULAR PHENOC
; FILE REFERENCE: A-71158/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/096,339
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/076,624
; PRIOR FILING DATE: 1998-05-12
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:53:30 ; Search time 8.5 Seconds  
(without alignments)  
13.470 Million cell updates/sec

Title: US-09-673-707-9  
Perfect score: 20  
Sequence: 1 KDEL 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
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6: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1          | 20    | 100.0       | 4      | 6     | US-10-444-662-3    |
| 2          | 20    | 100.0       | 4      | 6     | US-10-667-295-262  |
| 3          | 20    | 100.0       | 4      | 6     | US-10-475-204-23   |
| 4          | 20    | 100.0       | 4      | 6     | US-10-989-767A-699 |
| 5          | 20    | 100.0       | 4      | 6     | US-10-757-832-52   |
| 6          | 20    | 100.0       | 4      | 6     | US-10-909-957-10   |
| 7          | 20    | 100.0       | 4      | 6     | US-10-962-951-4    |
| 8          | 20    | 100.0       | 4      | 6     | US-10-537-061-11   |
| 9          | 20    | 100.0       | 4      | 7     | US-11-042-988-14   |
| 10         | 20    | 100.0       | 4      | 7     | US-11-057-058-2    |
| 11         | 20    | 100.0       | 4      | 7     | US-11-179-844-4    |
| 12         | 20    | 100.0       | 4      | 7     | US-11-018-106-1    |
| 13         | 20    | 100.0       | 4      | 7     | US-11-069-642-159  |
| 14         | 20    | 100.0       | 4      | 7     | US-11-189-321-8    |
| 15         | 20    | 100.0       | 4      | 7     | US-11-019-027-1    |
| 16         | 20    | 100.0       | 4      | 7     | US-11-102-883-42   |
| 17         | 20    | 100.0       | 4      | 7     | US-11-214-613-97   |
| 18         | 20    | 100.0       | 4      | 7     | US-11-029-188-16   |
| 19         | 20    | 100.0       | 4      | 7     | US-11-141-725-47   |
| 20         | 20    | 100.0       | 4      | 7     | US-11-219-180-12   |
| 21         | 20    | 100.0       | 4      | 7     | US-11-174-413-62   |
| 22         | 20    | 100.0       | 4      | 7     | US-11-126-817-17   |
| 23         | 20    | 100.0       | 4      | 7     | US-11-108-088-70   |
| 24         | 20    | 100.0       | 4      | 7     | US-11-255-677-17   |
| 25         | 20    | 100.0       | 4      | 7     | US-11-033-030-2    |
|            |       |             |        |       | Sequence 3, Appli  |
|            |       |             |        |       | Sequence 262, App  |
|            |       |             |        |       | Sequence 23, Appl  |
|            |       |             |        |       | Sequence 699, App  |
|            |       |             |        |       | Sequence 52, Appl  |
|            |       |             |        |       | Sequence 10, Appl  |
|            |       |             |        |       | Sequence 4, Appli  |
|            |       |             |        |       | Sequence 11, Appl  |
|            |       |             |        |       | Sequence 14, Appl  |
|            |       |             |        |       | Sequence 2, Appli  |
|            |       |             |        |       | Sequence 4, Appli  |
|            |       |             |        |       | Sequence 1, Appli  |
|            |       |             |        |       | Sequence 159, App  |
|            |       |             |        |       | Sequence 8, Appli  |
|            |       |             |        |       | Sequence 42, Appl  |
|            |       |             |        |       | Sequence 97, Appl  |
|            |       |             |        |       | Sequence 16, Appl  |
|            |       |             |        |       | Sequence 17, Appl  |
|            |       |             |        |       | Sequence 12, Appl  |
|            |       |             |        |       | Sequence 62, Appl  |
|            |       |             |        |       | Sequence 70, Appl  |
|            |       |             |        |       | Sequence 17, Appl  |
|            |       |             |        |       | Sequence 2, Appli  |

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Sequence 4, Appli  
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Sequence 13, Appli  
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Sequence 9747, Ap  
Sequence 34, Appli  
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Sequence 6, Appli  
Sequence 414, App  
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Sequence 125, App  
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Sequence 14892, A  
Sequence 14507, A  
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Sequence 9746, Ap  
Sequence 5274, Ap  
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Sequence 1153, Ap  
Sequence 26333, A  
Sequence 849, App  
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Sequence 14506, A  
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Sequence 13, Appli  
Sequence 9132, Ap  
Sequence 2662, Ap  
Sequence 24430, A  
Sequence 9, Appli  
Sequence 1291, Ap  
Sequence 10497, A  
Sequence 5501, Ap  
Sequence 14891, A  
Sequence 25463, A  
Sequence 19079, A  
Sequence 860, App  
Sequence 848, App  
Sequence 5, Appli  
Sequence 11708, A  
Sequence 3, Appli  
Sequence 5910, Ap  
Sequence 7560, Ap  
Sequence 10191, A  
Sequence 26332, A  
Sequence 11707, A  
Sequence 21284, A  
Sequence 1651, Ap  
Sequence 4222, Ap  
Sequence 6, Appli  
Sequence 9661, Ap  
Sequence 2237, Ap

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102 20 100.0 204 7 US-11-096-568A-4223
103 20 100.0 205 7 US-11-096-568A-10657
104 20 100.0 210 6 US-10-986-501-126
105 20 100.0 210 6 US-10-793-626-2210
106 20 100.0 212 7 US-11-096-568A-30079
107 20 100.0 214 7 US-11-096-568A-29876
108 20 100.0 215 7 US-11-124-367A-381
109 20 100.0 215 7 US-11-124-367A-383
110 20 100.0 217 7 US-11-096-568A-29878
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112 20 100.0 221 7 US-11-087-099-10926
113 20 100.0 221 7 US-11-087-099-10926
114 20 100.0 222 7 US-11-096-568A-7214
115 20 100.0 222 7 US-11-096-568A-16266
116 20 100.0 224 7 US-11-087-099-4273
117 20 100.0 224 7 US-11-096-568A-29875
118 20 100.0 225 7 US-11-096-568A-14890
119 20 100.0 225 7 US-11-096-568A-29874
120 20 100.0 226 7 US-11-185-342-8
121 20 100.0 226 7 US-11-096-568A-10973
122 20 100.0 227 7 US-11-096-568A-25462
123 20 100.0 232 7 US-11-067-323-504
124 20 100.0 232 7 US-11-067-323-658
125 20 100.0 232 7 US-11-067-323-660
126 20 100.0 232 7 US-11-067-323-662
127 20 100.0 232 7 US-11-024-959-431
128 20 100.0 233 7 US-11-072-512-3056
129 20 100.0 234 7 US-11-100-183-36
130 20 100.0 235 7 US-11-096-568A-10275
131 20 100.0 238 7 US-11-096-568A-16265
132 20 100.0 244 7 US-11-087-099-4893
133 20 100.0 246 7 US-11-087-099-4022
134 20 100.0 246 7 US-11-087-099-6753
135 20 100.0 247 7 US-11-087-099-9422
136 20 100.0 248 7 US-11-096-568A-12320
137 20 100.0 249 7 US-11-096-568A-26331
138 20 100.0 250 7 US-11-096-568A-5335
139 20 100.0 251 7 US-11-096-568A-10274
140 20 100.0 252 7 US-11-067-323-18
141 20 100.0 252 7 US-11-067-323-28
142 20 100.0 254 7 US-11-067-323-2
143 20 100.0 254 7 US-11-067-323-4
144 20 100.0 254 7 US-11-067-323-6
145 20 100.0 254 7 US-11-067-323-8
146 20 100.0 254 7 US-11-067-323-10
147 20 100.0 254 7 US-11-067-323-12
148 20 100.0 254 7 US-11-067-323-16
149 20 100.0 254 7 US-11-067-323-20
150 20 100.0 254 7 US-11-067-323-22

SEQUENCE 5337, Ap
SEQUENCE 3655, Ap
SEQUENCE 5336, Ap
SEQUENCE 4223, Ap
SEQUENCE 10657, A
SEQUENCE 126, Ap
SEQUENCE 2210, Ap
SEQUENCE 30079, A
SEQUENCE 29876, A
SEQUENCE 381, Ap
SEQUENCE 383, Ap
SEQUENCE 29878, A
SEQUENCE 100, Ap
SEQUENCE 10926, A
SEQUENCE 7214, Ap
SEQUENCE 16266, A
SEQUENCE 4273, Ap
SEQUENCE 29875, A
SEQUENCE 14890, A
SEQUENCE 29874, A
SEQUENCE 8, Appli
SEQUENCE 10973, A
SEQUENCE 25462, A
SEQUENCE 504, Ap
SEQUENCE 656, Ap
SEQUENCE 658, Ap
SEQUENCE 660, Ap
SEQUENCE 662, Ap
SEQUENCE 431, Ap
SEQUENCE 3056, Ap
SEQUENCE 36, Appl
SEQUENCE 10275, A
SEQUENCE 16265, A
SEQUENCE 4893, Ap
SEQUENCE 4022, Ap
SEQUENCE 6753, Ap
SEQUENCE 9422, Ap
SEQUENCE 12320, A
SEQUENCE 26331, A
SEQUENCE 5335, Ap
SEQUENCE 10274, A
SEQUENCE 18, Appl
SEQUENCE 28, Appl
SEQUENCE 2, Appli
SEQUENCE 4, Appli
SEQUENCE 6, Appli
SEQUENCE 8, Appli
SEQUENCE 10, Appl
SEQUENCE 12, Appl
SEQUENCE 16, Appl
SEQUENCE 20, Appl
SEQUENCE 22, Appl

ALIGNMENTS

RESULT 1
US-10-444-662-3
; Sequence 3, Application US/10444662
; Publication No. US20050250683A9
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Rozema, David
; APPLICANT: Wolff, Jon
; APPLICANT: Wakefield, Darren
; APPLICANT: Ekena, Kirk
; APPLICANT: Hagstrom, James
; TITLE OF INVENTION: Reversible Modification of Membrane Interaction
; FILE REFERENCE: Mirus.035.01
; CURRENT APPLICATION NUMBER: US/10/444,662
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-444-662-3

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 2
US-10-667-295-262
; Sequence 262, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target sequence
US-10-667-295-262

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 3
US-10-475-204-23
; Sequence 23, Application US/10475204
; Publication No. US20050277116A1
; GENERAL INFORMATION:
; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION OF
; FILE REFERENCE: HMV-056.25
; CURRENT APPLICATION NUMBER: US/10/475,204
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/US02/13008
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/285,509
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Calreticulin
; OTHER INFORMATION: targeting sequence
US-10-475-204-23
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Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|  
|  
|  
|  
Db 1 KDEL 4

## RESULT 4

US-10-989-767A-699  
; Sequence 699, Application US/10989767A  
; Publication No. US20060018917A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AVA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 511582005004  
; CURRENT APPLICATION NUMBER: US/10/989,767A  
; CURRENT FILING DATE: 2004-11-15  
; PRIOR APPLICATION NUMBER: 10/277,292  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: 09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 699  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized peptide motif  
US-10-989-767A-699

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|  
|  
|  
|  
Db 1 KDEL 4

## RESULT 5

US-10-757-832-52  
; Sequence 52, Application US/10757832  
; Publication No. US20060024319A2  
; GENERAL INFORMATION:  
; APPLICANT: VIRGIN, HERBERT W.  
; TITLE OF INVENTION: MURINE CALICIVIRUS  
; FILE REFERENCE: 56029-45752  
; CURRENT APPLICATION NUMBER: US/10/757,832  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: 60/440,016  
; PRIOR FILING DATE: 2003-01-14  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 52  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Illustrative MNV-1 ORF1 motif  
US-10-757-832-52

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
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|  
|  
|  
Db 1 KDEL 4

## RESULT 6

US-10-909-957-10  
; Sequence 10, Application US/10909957  
; Publication No. US20060024332A1  
; GENERAL INFORMATION:  
; APPLICANT: Waters, Wade R  
; APPLICANT: Palmer, Mitchell V  
; APPLICANT: Minion, Frank C  
; TITLE OF INVENTION: Recombinant ESAT-6:CFP-10 Fusion Protein Useful for  
; TITLE OF INVENTION: Specific Diagnosis of Tuberculosis  
; FILE REFERENCE: 0072.04 - Waters et al.  
; CURRENT APPLICATION NUMBER: US/10/909,957  
; CURRENT FILING DATE: 2004-08-02  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Signal Peptide  
US-10-909-957-10

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|  
|  
|  
|  
Db 1 KDEL 4

## RESULT 7

US-10-962-951-4  
; Sequence 4, Application US/10962951  
; Publication No. US20060029610A1  
; GENERAL INFORMATION:  
; APPLICANT: Argon, Yair  
; APPLICANT: Gidalevitz, Tali  
; APPLICANT: Biswas, Chhanda  
; APPLICANT: Simen, Birgitte B.  
; APPLICANT: Wanderling, Sherry  
; APPLICANT: Ostrovsky, Olga  
; TITLE OF INVENTION: GRP94-BASED COMPOSITIONS AND METHODS OF  
; TITLE OF INVENTION: USE THEREOF  
; FILE REFERENCE: 3460-CHOP.C-206US  
; CURRENT APPLICATION NUMBER: US/10/962,951  
; CURRENT FILING DATE: 2004-10-12  
; PRIOR APPLICATION NUMBER: US/10/844,711  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/469,723  
; PRIOR FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/477,990  
; PRIOR FILING DATE: 2003-06-12  
; PRIOR APPLICATION NUMBER: 60/478,149  
; PRIOR FILING DATE: 2003-06-12  
; PRIOR APPLICATION NUMBER: 60/556,362  
; PRIOR FILING DATE: 2004-04-28  
; PRIOR APPLICATION NUMBER: 60/566,363  
; PRIOR FILING DATE: 2004-04-28  
; NUMBER OF SEQ ID NOS: 27

Mon Mar 20 08:51:26 2006

us-09-673-707-9.rapbn

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ER retrieval signal
US-10-962-951-4

Query Match          100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 8
US-10-537-061-11
; Sequence 11, Application US/10537061
; Publication No. US20060051359A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: HUMAN SERVICES
; APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
; APPLICANT: Pastan, Ira
; APPLICANT: Onda, Masanori
; APPLICANT: Cheung, Nai-Kong
; TITLE OF INVENTION: IN-VIVO CYTOTOXIC ACTIVITIES OF RECOMBINANT IMMUNOTOXIN B9
; FILE REFERENCE: (FV)-P938 AGAINST BREAST CANCER, OSTEOCARCINOMA AND NEUROBLASTOM
; CURRENT APPLICATION NUMBER: US/10/537,061
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: PCT/US03/038227
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/430,305
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-537-061-11

Query Match          100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 9
US-11-042-988-14
; Sequence 14, Application US/11042988
; Publication No. US20050244618A1
; GENERAL INFORMATION:
; APPLICANT: SILICIANO, ROBERT
; APPLICANT: ZHANG, HAILI
; APPLICANT: ZHOU, YAN
; TITLE OF INVENTION: SINGLE CELL ANALYSIS OF HIV REPLICATION CAPACITY AND
; FILE REFERENCE: 62760(71699)
; CURRENT APPLICATION NUMBER: US/11/042,988
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/540,716
; PRIOR FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-042-988-14

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 10
US-11-057-058-2
; Sequence 2, Application US/11057058
; Publication No. US20050244400A1
; GENERAL INFORMATION:
; APPLICANT: Lebowitz, Jonathan
; APPLICANT: Maga, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
; FILE REFERENCE: SYM-011
; CURRENT APPLICATION NUMBER: US/11/057,058
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: US 60/543,812
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A C-terminal sequence of a targeting domain
US-11-057-058-2

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 11
US-11-179-844-4
; Sequence 4, Application US/11179844
; Publication No. US20050249738A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Goldenberg, David M.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Immunotoxins Directed Against Malignant Cells
; FILE REFERENCE: 015280-325200US
; CURRENT APPLICATION NUMBER: US/11/179,844
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: US/09/918,887
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US 60/046,895
; PRIOR FILING DATE: 1997-05-02
; PRIOR APPLICATION NUMBER: US 09/071,672
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:carboxy terminal
; OTHER INFORMATION: sequence of rFB4-PE35KDEL and LL2-PE38KDEL chimeric
; OTHER INFORMATION: immunotoxins with Pseudomonas exotoxin A (PE) modified
; OTHER INFORMATION: by KDEL endoplasmic reticulum retention sequence
US-11-179-844-4

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 12
US-11-018-106-1
; Sequence 1, Application US/11018106
; Publication No. US2005025550A1
; GENERAL INFORMATION:
; APPLICANT: IMPERIAL COLLEGE INNOVATIONS LIMITED
; APPLICANT: RAMAKHA, PUNIT
; APPLICANT: GEORGE, ANDREW
; APPLICANT: HASKARD, DORIAN
; APPLICANT: LECHLER, ROBERT
; APPLICANT: DORLING, ANTHONY
; TITLE OF INVENTION: SUPPRESSION OF XENOTRANSPLANT REJECTION
; FILE REFERENCE: REV 1021
; CURRENT APPLICATION NUMBER: US/11/018,106
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: US 09/856,322
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: PCT/GB99/03888
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: GB9825555.7
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: targeting
; OTHER INFORMATION: sequence
US-11-018-106-1

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 13
US-11-069-642-159
; Sequence 159, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: RIGL-022CIP3
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; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-069-642-159

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 14
US-11-189-321-8
; Sequence 8, Application US/11189321
; Publication No. US20050272154A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Bio Corporation
; APPLICANT: Wolff, Jon A
; APPLICANT: Hagstrom, James E
; APPLICANT: Budker, Vladimir G
; APPLICANT: Slattum, Paul M
; TITLE OF INVENTION: Gene Expression with Covalently Modified Polynucleotides
; FILE REFERENCE: Mirus 017.01.1
; CURRENT APPLICATION NUMBER: US/11/189,321
; CURRENT FILING DATE: 2005-07-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-189-321-8

Query Match          100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 1 KDEL 4

RESULT 15
US-11-019-027-1
; Sequence 1, Application US/11019027
; Publication No. US20050282181A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Wei
; APPLICANT: SHEN, Wenyan
; APPLICANT: ZHOU, Hongxing
; APPLICANT: ZHOU, Chen
; APPLICANT: COSMAN, David J.
; APPLICANT: CARTER, Paul
; APPLICANT: MARTIN, Francis H.
; TITLE OF INVENTION: METHODS OF IDENTIFYING FUNCTIONAL ANTIBODIES
; FILE REFERENCE: A-890A
; CURRENT APPLICATION NUMBER: US/11/019,027
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; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/11/214,613
; CURRENT FILING DATE: 2005-08-30
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: retention sequence
; US-11-214-613-97

Query Match      100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 18
US-11-029-188-16
; Sequence 16, Application US/11029188
; Publication No. US20060013832A1
; GENERAL INFORMATION:
; APPLICANT: JUNE, CARL H.
; APPLICANT: THOMPSON, CRAIG B.
; APPLICANT: NABEL, GARY J.
; APPLICANT: GRAY, GARY S.
; APPLICANT: RENNERT, PAUL D.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING PROLIFERATION OF T
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 36119.125 US13
; CURRENT APPLICATION NUMBER: US/11/029,188
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: 08/592,711
; PRIOR FILING DATE: 1996-01-26
; PRIOR APPLICATION NUMBER: 08/435,816
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: 08/403,253
; PRIOR FILING DATE: 1995-03-10
; PRIOR APPLICATION NUMBER: 08/253,964
; PRIOR FILING DATE: 1994-06-03
; PRIOR APPLICATION NUMBER: 08/073,223
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: 07/864,866
; PRIOR FILING DATE: 1992-04-07
; PRIOR APPLICATION NUMBER: 07/864,807
; PRIOR FILING DATE: 1992-04-07
; PRIOR APPLICATION NUMBER: 07/864,805
; PRIOR FILING DATE: 1992-04-07
; PRIOR APPLICATION NUMBER: 07/275,433
; PRIOR FILING DATE: 1988-11-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-11-029-188-16

Query Match      100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: 60/605,902
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: 60/531,714
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: ER localization signal
; US-11-019-027-1

Query Match      100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 16
US-11-102-883-42
; Sequence 42, Application US/11102883
; Publication No. US20050281816A1
; GENERAL INFORMATION:
; APPLICANT: Lamping, Norbert
; APPLICANT: Cramer, Reto
; APPLICANT: Fluckiger, Sabina
; APPLICANT: Daigle, Isabelle
; TITLE OF INVENTION: Modular Antigen Transporter Molecules (MAT Molecules) for
; TITLE OF INVENTION: Modulating Immune Reactions, Associated Constructs, Methods and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 03100234pa
; CURRENT APPLICATION NUMBER: US/11/102,883
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: EP02022774.0
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/011190
; PRIOR FILING DATE: 2003-10-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: partial sequence form calreticulin
; US-11-102-883-42

Query Match      100.0%; Score 20; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 17
US-11-214-613-97
; Sequence 97, Application US/11214613
; Publication No. US20060005270A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; US-11-214-613-97
```



Db 1 KDEL 4  
||||

## RESULT 19

US-11-141-725-47  
; Sequence 47, Application US/11141725  
; Publication No. US20060014712A1  
; GENERAL INFORMATION:  
; APPLICANT: Neuman, Tomas  
; TITLE OF INVENTION: Controlled Delivery of Therapeutic Compounds  
; FILE REFERENCE: 34211/US/2 (473322-00024)  
; CURRENT APPLICATION NUMBER: US/11/141,725  
; PRIOR FILING DATE: 2005-05-31  
; PRIOR APPLICATION NUMBER: US 60/575,660  
; PRIOR FILING DATE: 2004-05-30  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 47  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-141-725-47

Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
||||

Db 1 KDEL 4  
||||

## RESULT 20

US-11-219-180-12  
; Sequence 12, Application US/11219180  
; Publication No. US20060026715A1  
; GENERAL INFORMATION:  
; APPLICANT: HOOD, ELIZABETH  
; APPLICANT: HOWARD, JOHN  
; TITLE OF INVENTION: COMMERCIAL PRODUCTION OF POLYSACCHARIDE DEGRADING  
; FILE REFERENCE: AB0007  
; CURRENT APPLICATION NUMBER: US/11/219,180  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: 60/607,098  
; PRIOR FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: 10/310,292  
; PRIOR FILING DATE: 2002-12-05  
; PRIOR APPLICATION NUMBER: 60/340,035  
; PRIOR FILING DATE: 2001-12-06  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 12  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-11-219-180-12

Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
||||

Db 1 KDEL 4  
||||

## RESULT 21

US-11-174-413-62

; Sequence 62, Application US/11174413  
; Publication No. US20060031962A1  
; GENERAL INFORMATION:  
; APPLICANT: Altier, Daniel J.  
; APPLICANT: Dahlbacka, Glen  
; APPLICANT: Elleskaya, I.A.  
; APPLICANT: Herrmann, Rafael  
; APPLICANT: Hunter-Cevera, Jennie  
; APPLICANT: McCutchen, Billy F.  
; APPLICANT: Prensail, James  
; APPLICANT: Rice, Janet  
; APPLICANT: Schepers, Eric  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Torok, Tamas  
; APPLICANT: Valpani, Nasser  
; TITLE OF INVENTION: Antifungal Polypeptides  
; FILE REFERENCE: 035718/293488  
; CURRENT APPLICATION NUMBER: US/11/174,413  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: 60/585,267  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Endoplasmic reticulum retention sequence  
US-11-174-413-62

Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
||||

Db 1 KDEL 4  
||||

## RESULT 22

US-11-126-817-17  
; Sequence 17, Application US/11126817  
; Publication No. US20060034834A1  
; GENERAL INFORMATION:  
; APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.  
; APPLICANT: MARASCO, Wayne  
; APPLICANT: MEASHILKAR, Abner  
; TITLE OF INVENTION: INTRABODY-MEDIATED CONTROL OF IMMUNE REACTIONS  
; FILE REFERENCE: 47577 C  
; CURRENT APPLICATION NUMBER: US/11/126,817  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US/09/522,727  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: PCT/US98/19563  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/059,339  
; PRIOR FILING DATE: 1997-09-19  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: human  
US-11-126-817-17

Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
||||

Db 1 KDEL 4  
||||

Mon Mar 20 08:51:26 2006

US-11-108-088-70  
; Sequence 70, Application US/11108088  
; Publication No. US20060040353A1  
; GENERAL INFORMATION:  
; APPLICANT: DAVIDSON, ROBERT  
; APPLICANT: GERNGROSS, TILLMAN  
; APPLICANT: WILDT, STEFAN  
; APPLICANT: CHOI, BYUNG-KWON  
; APPLICANT: NETT, JUERGEN  
; APPLICANT: BOBROWICZ, PIOTR  
; APPLICANT: HAMILTON, STEPHEN  
; TITLE OF INVENTION: PRODUCTION OF GALACTOSYLATED GLYCOPROTEINS IN LOWER  
; FILE REFERENCE: GPI-12  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US/11/108,088  
; PRIOR FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: 60/214,358  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/215,638  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/279,997  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: PCT/US02/41510  
; PRIOR FILING DATE: 2002-12-24  
; PRIOR APPLICATION NUMBER: 60/344,169  
; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/562,424  
; PRIOR FILING DATE: 2004-04-15  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: Patentin Ver. 3.3  
; SEQ ID NO 70  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-11-108-088-70  
Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KDEL 4  
Db 1 KDEL 4  
RESULT 24  
US-11-255-677-17  
; Sequence 17, Application US/11255677  
; Publication No. US20060040359A1  
; GENERAL INFORMATION:  
; APPLICANT: The State of Oregon acting by and through the State Board  
; APPLICANT: of Higher Education on behalf of the University of Oregon  
; APPLICANT: Remington, S. James  
; APPLICANT: Hanson, George T.  
; TITLE OF INVENTION: OXIDATION -REDUCTION SENSITIVE GREEN FLUORESCENT PROTEIN VARIANTS  
; FILE REFERENCE: 1505-66506-01  
; CURRENT APPLICATION NUMBER: US/11/255,677  
; CURRENT FILING DATE: 2005-10-20  
; PRIOR APPLICATION NUMBER: US/10/471,857  
; PRIOR FILING DATE: 2004-03-08  
; PRIOR APPLICATION NUMBER: 60/275,200  
; PRIOR FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: PCT/US02/07374  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: 60/293,427  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: 60/302,894  
US-11-033-030-2  
; Sequence 2, Application US/11033030  
; Publication No. US20060053510A1  
; GENERAL INFORMATION:  
; APPLICANT: ALBERTE, RANDALL S.  
; APPLICANT: SMITH, ROBERT  
; TITLE OF INVENTION: TRANSGENIC PLANTS INCORPORATING TRAIT OF ZOSTERA MARINA  
; FILE REFERENCE: PHA-007.01  
; CURRENT APPLICATION NUMBER: US/11/033,030  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: US/09/854,122  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/202,529  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-11-033-030-2  
Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KDEL 4  
Db 1 KDEL 4  
RESULT 26  
US-11-081-140-8  
; Sequence 8, Application US/11081140  
; Publication No. US20050261225A1  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Cy A  
; APPLICANT: Benimetskaya, Lyuba  
; APPLICANT: Guzzo-Pernell, Nancy  
; TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DOWN  
; TITLE OF INVENTION: PKC-PROTEIN EXPRESSION IN CELLS  
; FILE REFERENCE: 0575/63293  
; CURRENT APPLICATION NUMBER: US/11/081,140  
; CURRENT FILING DATE: 2005-03-15  
; PRIOR APPLICATION NUMBER: US/10/002,884  
; PRIOR FILING DATE: 2001-11-02  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentin version 3.1

US-11-108-088-70  
; Sequence 70, Application US/11108088  
; Publication No. US20060040353A1  
; GENERAL INFORMATION:  
; APPLICANT: DAVIDSON, ROBERT  
; APPLICANT: GERNGROSS, TILLMAN  
; APPLICANT: WILDT, STEFAN  
; APPLICANT: CHOI, BYUNG-KWON  
; APPLICANT: NETT, JUERGEN  
; APPLICANT: BOBROWICZ, PIOTR  
; APPLICANT: HAMILTON, STEPHEN  
; TITLE OF INVENTION: PRODUCTION OF GALACTOSYLATED GLYCOPROTEINS IN LOWER  
; FILE REFERENCE: GPI-12  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US/11/108,088  
; PRIOR FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: 60/214,358  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/215,638  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/279,997  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: PCT/US02/41510  
; PRIOR FILING DATE: 2002-12-24  
; PRIOR APPLICATION NUMBER: 60/344,169  
; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/562,424  
; PRIOR FILING DATE: 2004-04-15  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: Patentin Ver. 3.3  
; SEQ ID NO 70  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-11-108-088-70  
Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KDEL 4  
Db 1 KDEL 4  
RESULT 24  
US-11-255-677-17  
; Sequence 17, Application US/11255677  
; Publication No. US20060040359A1  
; GENERAL INFORMATION:  
; APPLICANT: The State of Oregon acting by and through the State Board  
; APPLICANT: of Higher Education on behalf of the University of Oregon  
; APPLICANT: Remington, S. James  
; APPLICANT: Hanson, George T.  
; TITLE OF INVENTION: OXIDATION -REDUCTION SENSITIVE GREEN FLUORESCENT PROTEIN VARIANTS  
; FILE REFERENCE: 1505-66506-01  
; CURRENT APPLICATION NUMBER: US/11/255,677  
; CURRENT FILING DATE: 2005-10-20  
; PRIOR APPLICATION NUMBER: US/10/471,857  
; PRIOR FILING DATE: 2004-03-08  
; PRIOR APPLICATION NUMBER: 60/275,200  
; PRIOR FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: PCT/US02/07374  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: 60/293,427  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: 60/302,894

; SEQ ID NO 8  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: ER-RETAINING PEPTIDE, SOURCE UNKNOWN  
US-11-081-140-8

Query Match 100.0%; Score 20; DB 7; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 2 KDEL 5

## RESULT 27

US-10-493-909-4  
; Sequence 4, Application US/10493909  
; Publication No. US20060015969A1  
; GENERAL INFORMATION:  
; APPLICANT: LARRICK, JAMES W.  
; APPLICANT: WYCOFF, KEITH L.  
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICITY  
; TITLE OF INVENTION: AND PATHOGEN-MEDIATED DISEASES  
; FILE REFERENCE: 41514-20004.01  
; CURRENT APPLICATION NUMBER: US/10/493,909  
; CURRENT FILING DATE: 2004-04-26  
; PRIOR APPLICATION NUMBER: PCT/US01/13932  
; PRIOR FILING DATE: 2001-04-28  
; PRIOR APPLICATION NUMBER: 60/200,298  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-493-909-4

Query Match 100.0%; Score 20; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 3 KDEL 6

## RESULT 28

US-11-019-027-58  
; Sequence 58, Application US/11019027  
; Publication No. US20050282181A1  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Wei  
; APPLICANT: SHEN, Wenyan  
; APPLICANT: ZHOU, Hongxing  
; APPLICANT: ZHOU, Chen  
; APPLICANT: COSMAN, David J.  
; APPLICANT: CARTER, Paul  
; APPLICANT: MARTIN, Francis H.  
; TITLE OF INVENTION: METHODS OF IDENTIFYING FUNCTIONAL ANTIBODIES  
; FILE REFERENCE: A-890A  
; CURRENT APPLICATION NUMBER: US/11/019,027  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: 60/605,902  
; PRIOR FILING DATE: 2004-08-31  
; PRIOR APPLICATION NUMBER: 60/531,714  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 58

; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: ER localization signal  
US-11-019-027-58

Query Match 100.0%; Score 20; DB 7; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 3 KDEL 6

## RESULT 29

US-11-174-413-63  
; Sequence 63, Application US/11174413  
; Publication No. US20060031962A1  
; GENERAL INFORMATION:  
; APPLICANT: Altier, Daniel J.  
; APPLICANT: Dahlbacka, Glen  
; APPLICANT: Elleskaya, I.A.  
; APPLICANT: Herrmann, Rafael  
; APPLICANT: Hunter-Cevera, Jennie  
; APPLICANT: McCutchen, Billy F.  
; APPLICANT: Presnail, James  
; APPLICANT: Rice, Janet  
; APPLICANT: Schepers, Eric  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Torok, Tamas  
; APPLICANT: Valpani, Nasser  
; TITLE OF INVENTION: Antifungal Polypeptides  
; FILE REFERENCE: 035718/293488  
; CURRENT APPLICATION NUMBER: US/11/174,413  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: 60/585,267  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 63  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Endoplasmic reticulum retention sequence  
US-11-174-413-63

Query Match 100.0%; Score 20; DB 7; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 3 KDEL 6

## RESULT 30

US-11-126-817-13  
; Sequence 13, Application US/11126817  
; Publication No. US20060034834A1  
; GENERAL INFORMATION:  
; APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.  
; APPLICANT: MARASCO, Wayne  
; APPLICANT: MHASHILKAR, Abner  
; TITLE OF INVENTION: INTRABODY-MEDIATED CONTROL OF IMMUNE REACTIONS  
; FILE REFERENCE: 47577 C  
; CURRENT APPLICATION NUMBER: US/11/126,817  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US/09/522,727  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: PCT/US98/19563

Mon Mar 20 08:51:26 2006

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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/059,339
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: human
US-11-126-817-13

Query Match          100.0%; Score 20; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      3 KDEL 6

RESULT 31
US-10-493-909-5
; Sequence 5, Application US/10493909
; Publication No. US20060015969A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICITY
; TITLE OF INVENTION: AND PATHOGEN-MEDIATED DISEASES
; FILE REFERENCE: 41514-20004.01
; CURRENT APPLICATION NUMBER: US/10/493,909
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-493-909-5

Query Match          100.0%; Score 20; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      4 KDEL 7

RESULT 32
US-11-042-988-16
; Sequence 16, Application US/11042988
; Publication No. US20050244818A1
; GENERAL INFORMATION:
; APPLICANT: SILICIANO, ROBERT
; APPLICANT: ZHANG, HAILI
; APPLICANT: ZHOU, YAN
; TITLE OF INVENTION: SINGLE CELL ANALYSIS OF HIV REPLICATION CAPACITY AND
; TITLE OF INVENTION: DRUG RESISTANCE
; FILE REFERENCE: 62760(71699)
; CURRENT APPLICATION NUMBER: US/11/042,988
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/540,716
; PRIOR FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-042-988-16

Query Match          100.0%; Score 20; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      4 KDEL 7

RESULT 33
US-11-214-613-85
; Sequence 85, Application US/11214613
; Publication No. US20060005270A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/11/214,613
; CURRENT FILING DATE: 2005-08-30
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDEL fusion peptide
US-11-214-613-85

Query Match          100.0%; Score 20; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      4 KDEL 7

RESULT 34
US-11-214-613-86
; Sequence 86, Application US/11214613
; Publication No. US20060005270A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/11/214,613
; CURRENT FILING DATE: 2005-08-30
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

; OTHER INFORMATION: designated KDEL fusion peptide  
US-11-214-613-86

Query Match 100.0%; Score 20; DB 7; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Length 7;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 4 KDEL 7

## RESULT 35

US-11-214-613-90  
; Sequence 90, Application US/11214613  
; Publication No. US2006005270A1  
; GENERAL INFORMATION:  
; APPLICANT: Dunn-Coleman, Nigel  
; APPLICANT: Langdon, Timothy  
; APPLICANT: Morse, Phillip  
; TITLE OF INVENTION: Manipulation of the Phenolic Acid  
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted  
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes  
; FILE REFERENCE: GC648-2  
; CURRENT APPLICATION NUMBER: US/11/214,613  
; CURRENT FILING DATE: 2005-08-30  
; PRIOR APPLICATION NUMBER: US 60/249,608  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 90  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: ER retention vector  
US-11-214-613-90

Query Match 100.0%; Score 20; DB 7; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Length 7;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 4 KDEL 7

## RESULT 36

US-11-214-613-5  
; Sequence 5, Application US/11214613  
; Publication No. US2006005270A1  
; GENERAL INFORMATION:  
; APPLICANT: Dunn-Coleman, Nigel  
; APPLICANT: Langdon, Timothy  
; APPLICANT: Morse, Phillip  
; TITLE OF INVENTION: Manipulation of the Phenolic Acid  
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted  
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes  
; FILE REFERENCE: GC648-2  
; CURRENT APPLICATION NUMBER: US/11/214,613  
; CURRENT FILING DATE: 2005-08-30  
; PRIOR APPLICATION NUMBER: US 60/249,608  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: retention sequence  
US-11-214-613-5

Query Match 100.0%; Score 20; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 7 KDEL 10

## RESULT 37

US-10-952-535A-32  
; Sequence 32, Application US/10952535A  
; Publication No. US20050255113A1  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Messer, Anne  
; APPLICANT: Leceref, Jean-Michel  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE  
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS  
; FILE REFERENCE: INR-004CP  
; CURRENT APPLICATION NUMBER: US/10/952,535A  
; CURRENT FILING DATE: 2004-09-27  
; PRIOR APPLICATION NUMBER: 60/146,047  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: construct  
US-10-952-535A-32

Query Match 100.0%; Score 20; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 12 KDEL 15

## RESULT 38

US-11-206-138-2  
; Sequence 2, Application US/11206138  
; Publication No. US20060039919A1  
; GENERAL INFORMATION:  
; APPLICANT: HealthBanks Biotech CO. LTD.  
; TITLE OF INVENTION: Fusion protein for inhibiting cervical cancer  
; FILE REFERENCE: P7819/0613  
; CURRENT APPLICATION NUMBER: US/11/206,138  
; CURRENT FILING DATE: 2005-08-18  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Pseudomonas sp.  
US-11-206-138-2

Query Match 100.0%; Score 20; DB 7; Length 18;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 7 KDEL 10

## RESULT 39

US-11-193-654-18

```
; Sequence 18, Application US/11193654
; Publication No. US20060019316A1
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahiyat, Bassil L.
; APPLICANT: Gordon, D. Benjamin
; APPLICANT: Street, Arthur
; APPLICANT: Su, Yaoying
; TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
; FILE REFERENCE: A65353-4/RT/RMS/SJR
; CURRENT APPLICATION NUMBER: US/11/193,654
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/09/127,926
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/043,464
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/054,678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061,097
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: 09/058,459
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/087,561
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;
US-11-193-654-18

Query Match      100.0%; Score 20; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 56;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      15 KDEL 18

RESULT 40
US-11-096-568A-9747
; Sequence 9747, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Thetby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 9747
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(38)
; OTHER INFORMATION: Ceres Seq. ID no. 12619229
US-11-096-568A-9747

Query Match      100.0%; Score 20; DB 7; Length 38;
Best Local Similarity 100.0%; Pred. No. 78;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      35 KDEL 38

; Sequence 18, Application US/11193654
; Publication No. US20060019316A1
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahiyat, Bassil L.
; APPLICANT: Gordon, D. Benjamin
; APPLICANT: Street, Arthur
; APPLICANT: Su, Yaoying
; TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
; FILE REFERENCE: A65353-4/RT/RMS/SJR
; CURRENT APPLICATION NUMBER: US/11/193,654
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/09/127,926
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/043,464
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/054,678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061,097
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: 09/058,459
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/087,561
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;
US-11-193-654-18

Query Match      100.0%; Score 20; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 56;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      15 KDEL 18

RESULT 40
US-11-096-568A-9747
; Sequence 9747, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Thetby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 9747
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(38)
; OTHER INFORMATION: Ceres Seq. ID no. 12619229
US-11-096-568A-9747

Query Match      100.0%; Score 20; DB 7; Length 38;
Best Local Similarity 100.0%; Pred. No. 78;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      35 KDEL 38

; Sequence 34, Application US/11245400
; Publication No. US20060040357A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasehkar
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Melanoma
; TITLE OF INVENTION: Associated Antigen Molecules, Aminotransferase
; TITLE OF INVENTION: Molecules, ATPase Molecules, Acyltransferase Molecules,
; TITLE OF INVENTION: Pyridoxal-Phosphate Dependant Enzyme Molecules and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/247400
; CURRENT APPLICATION NUMBER: US/11/245,400
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US/10/164,966
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 10/034,864
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/258,517
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 09/996,194
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/250,348
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250,073
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/253,878
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,338
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/908,928
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,465
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pfam consensus sequence
;
US-11-245-400-34

Query Match      100.0%; Score 20; DB 7; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      9 KDEL 12

RESULT 42
US-11-174-413-38
; Sequence 38, Application US/11174413
; Publication No. US20060031962A1
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Dahlbacka, Glen
; APPLICANT: Elleskaya, I. A.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Hunter-Cevera, Jennie
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Prensail, James
; APPLICANT: Rice, Janet
; APPLICANT: Schepers, Eric
; APPLICANT: Simmons, Carl R.
```

```
; APPLICANT: Torok, Tamás
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Antifungal Polypeptides
; FILE REFERENCE: 035718/293488
; CURRENT APPLICATION NUMBER: US/11/174,413
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: 60/585,267
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of SEQ ID NO:1 (LEML 5220)
; OTHER INFORMATION: joined with a carboxy-terminal KDEL sequence (SEQ
; OTHER INFORMATION: ID NO:62)
US-11-174-413-38

Query Match      100.0%; Score 20; DB 7; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      56 KDEL 59

RESULT 43
US-11-195-459-6
; Sequence 6, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Meeley, Robert
; APPLICANT: Hantke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Zea mays
US-11-195-459-6

Query Match      100.0%; Score 20; DB 7; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      47 KDEL 50

RESULT 44
US-10-467-657-414
; Sequence 414, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
```

```
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 414
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-414

Query Match      100.0%; Score 20; DB 6; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      17 KDEL 20

RESULT 45
US-11-022-562-224
; Sequence 224, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 224
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-11-022-562-224

Query Match      100.0%; Score 20; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      27 KDEL 30

RESULT 46
US-10-986-501-200
; Sequence 200, Application US/10986501
; Publication No. US2005024845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
```

```
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-200

Query Match          100.0%; Score 20; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. NO. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      58 KDEL 61

RESULT 47
US-10-517-696-99
; Sequence 99, Application US/10517696
; Publication No. US20060051759A1
; GENERAL INFORMATION:
; APPLICANT: diadexus, Inc.
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto A.
; APPLICANT: Turner, Leah R.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
; FILE REFERENCE: DEX-0432
; CURRENT APPLICATION NUMBER: US/10/517,696
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/389,327
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 171
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-517-696-99

Query Match          100.0%; Score 20; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. NO. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      46 KDEL 49

RESULT 48
US-10-986-501-125
; Sequence 125, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-986-501-125

Query Match          100.0%; Score 20; DB 6; Length 103;
Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      39 KDEL 42

RESULT 49
US-11-096-568A-19081
; Sequence 19081, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19081
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(111)
; OTHER INFORMATION: Ceres Seq. ID no. 12368808
US-11-096-568A-19081

Query Match          100.0%; Score 20; DB 7; Length 111;
Best Local Similarity 100.0%; Pred. NO. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



Qy 1 KDEL 4  
|||  
Db 33 KDEL 36

RESULT 50  
US-10-467-657-6306  
; Sequence 6306, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 6306  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6306

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Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 73 KDEL 76

Search completed: March 20, 2006, 07:53:54  
Job time : 8.5 secs

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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:52:41 ; Search time 401.5 Seconds  
(without alignments)  
13.768 Million cell-updates/sec

Title: US-09-673-707-9  
Perfect score: 20  
Sequence: 1 KDEL 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues  
Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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| 1             | 20    | 100.0      | 4               | 1  | PCT-US00-06588-66   | Sequence 66, Appl |
| 2             | 20    | 100.0      | 4               | 1  | PCT-US00-13684-22   | Sequence 22, Appl |
| 3             | 20    | 100.0      | 4               | 1  | PCT-US00-25559-111  | Sequence 111, App |
| 4             | 20    | 100.0      | 4               | 1  | PCT-US00-32583-9    | Sequence 9, Appli |
| 5             | 20    | 100.0      | 4               | 1  | PCT-US01-06769-7    | Sequence 7, Appli |
| 6             | 20    | 100.0      | 4               | 1  | PCT-US01-41430-10   | Sequence 10, Appl |
| 7             | 20    | 100.0      | 4               | 1  | PCT-US01-43588-97   | Sequence 97, Appl |
| 8             | 20    | 100.0      | 4               | 1  | PCT-US01-02814-25   | Sequence 25, Appl |
| 9             | 20    | 100.0      | 4               | 1  | PCT-US02-02814-35   | Sequence 35, Appl |
| 10            | 20    | 100.0      | 4               | 1  | PCT-US02-10132-5    | Sequence 5, Appli |
| 11            | 20    | 100.0      | 4               | 1  | PCT-US02-13008-23   | Sequence 23, Appl |
| 12            | 20    | 100.0      | 4               | 1  | PCT-US02-15520-43   | Sequence 43, Appl |
| 13            | 20    | 100.0      | 4               | 1  | PCT-US02-16391-15   | Sequence 15, Appl |
| 14            | 20    | 100.0      | 4               | 1  | PCT-US02-16906-17   | Sequence 17, Appl |
| 15            | 20    | 100.0      | 4               | 1  | PCT-US02-19297-163  | Sequence 163, App |
| 16            | 20    | 100.0      | 4               | 1  | PCT-US02-21677-31   | Sequence 31, Appl |
| 17            | 20    | 100.0      | 4               | 1  | PCT-US02-21677-41   | Sequence 41, Appl |
| 18            | 20    | 100.0      | 4               | 1  | PCT-US02-21677-118  | Sequence 118, App |
| 19            | 20    | 100.0      | 4               | 1  | PCT-US02-26837-33   | Sequence 33, Appl |
| 20            | 20    | 100.0      | 4               | 1  | PCT-US02-27628-30   | Sequence 30, Appl |
| 21            | 20    | 100.0      | 4               | 1  | PCT-US02-27628A-30  | Sequence 30, Appl |
| 22            | 20    | 100.0      | 4               | 1  | PCT-US02-29560-411  | Sequence 411, App |
| 23            | 20    | 100.0      | 4               | 1  | PCT-US02-29560A-411 | Sequence 411, App |
| 24            | 20    | 100.0      | 4               | 1  | PCT-US02-30118-8    | Sequence 8, Appli |
| 25            | 20    | 100.0      | 4               | 1  | PCT-US02-30116-5    | Sequence 5, Appli |
| 26            | 20    | 100.0      | 4               | 1  | PCT-US02-38763-4    | Sequence 4, Appli |
| 27            | 20    | 100.0      | 4               | 1  | PCT-US02-38849-8    | Sequence 8, Appli |
| 28            | 20    | 100.0      | 4               | 1  | PCT-US02-41158-26   | Sequence 26, Appl |
| 29            | 20    | 100.0      | 4               | 1  | PCT-US02-41158A-26  | Sequence 26, Appl |
| 30            | 20    | 100.0      | 4               | 1  | PCT-US02-41510-102  | Sequence 102, App |
| 31            | 20    | 100.0      | 4               | 1  | PCT-US03-04631-23   | Sequence 23, Appl |
| 32            | 20    | 100.0      | 4               | 1  | PCT-US03-10081-4    | Sequence 4, Appli |
| 33            | 20    | 100.0      | 4               | 1  | PCT-US03-10630-3    | Sequence 3, Appli |
| 34            | 20    | 100.0      | 4               | 1  | PCT-US03-10630A-3   | Sequence 3, Appli |
| 35            | 20    | 100.0      | 4               | 1  | PCT-US03-15809-26   | Sequence 26, Appl |
| 36            | 20    | 100.0      | 4               | 1  | PCT-US03-16360-3    | Sequence 3, Appli |
| 37            | 20    | 100.0      | 4               | 1  | PCT-US03-18373-30   | Sequence 30, Appl |
| 38            | 20    | 100.0      | 4               | 1  | PCT-US03-18373A-30  | Sequence 30, Appl |
| 39            | 20    | 100.0      | 4               | 1  | PCT-US03-23691-262  | Sequence 262, App |
| 40            | 20    | 100.0      | 4               | 1  | PCT-US03-23968-33   | Sequence 33, Appl |
| 41            | 20    | 100.0      | 4               | 1  | PCT-US03-35088A-18  | Sequence 18, Appl |
| 42            | 20    | 100.0      | 4               | 1  | PCT-US03-38227-11   | Sequence 11, Appl |
| 43            | 20    | 100.0      | 4               | 1  | PCT-US03-39476-5    | Sequence 5, Appli |
| 44            | 20    | 100.0      | 4               | 1  | PCT-US04-08866-1955 | Sequence 1955, Ap |
| 45            | 20    | 100.0      | 4               | 1  | PCT-US04-10059-103  | Sequence 103, App |
| 46            | 20    | 100.0      | 4               | 1  | PCT-US04-11481-9    | Sequence 9, Appli |
| 47            | 20    | 100.0      | 4               | 1  | PCT-US04-11482-9    | Sequence 9, Appli |
| 48            | 20    | 100.0      | 4               | 1  | PCT-US04-23191-12   | Sequence 12, Appl |
| 49            | 20    | 100.0      | 4               | 1  | PCT-US04-23192-12   | Sequence 12, Appl |
| 50            | 20    | 100.0      | 4               | 1  | PCT-US04-41020A-73  | Sequence 73, Appl |
| 51            | 20    | 100.0      | 4               | 1  | PCT-US04-41023A-89  | Sequence 89, Appl |
| 52            | 20    | 100.0      | 4               | 1  | PCT-US05-01382-52   | Sequence 52, Appl |
| 53            | 20    | 100.0      | 4               | 1  | PCT-US05-16746-18   | Sequence 18, Appl |
| 54            | 20    | 100.0      | 4               | 1  | PCT-US05-22321-10   | Sequence 10, Appl |
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
PCT-US00-25559-111
; Sequence 111, Application PC/TUS0025559
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; CURRENT APPLICATION NUMBER: PCT/US00/25559
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/25559
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-25559-111

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
PCT-US00-32583-9
; Sequence 9, Application PC/TUS0032583
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; TITLE OF INVENTION: B7-H1, A NOVEL IMMUNOREGULATORY MOLECULE
; FILE REFERENCE: 07039-220W01
; CURRENT APPLICATION NUMBER: PCT/US00/32583
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 09/649,108
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/451,291
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Rattus rattus
PCT-US00-32583-9

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PCT-US01-06769-7
; Sequence 7, Application PC/TUS0106769
; GENERAL INFORMATION:
; APPLICANT: Mayo Medical Ventures
; TITLE OF INVENTION: h87-H2, A NOVEL CO-STIMULATORY MOLECULE
; FILE REFERENCE: 07039-202W01
; CURRENT APPLICATION NUMBER: PCT/US01/06769
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/186,519
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Rattus norvegicus
PCT-US01-06769-7

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RESULT 6
PCT-US01-41430-10
; Sequence 10, Application PC/TUS0141430
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE REFERENCE: 07039-219W01
; CURRENT APPLICATION NUMBER: PCT/US01/41430
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Rattus norvegicus
PCT-US01-41430-10

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; Sequence 97, Application PC/TUS0143588
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE REFERENCE: GC648-2-PCT
; CURRENT APPLICATION NUMBER: PCT/US01/43588
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 4
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: retention sequence
PCT-US01-43588-97

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; Sequence 97, Application PC/TUS0143588A
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2-PCT
; CURRENT APPLICATION NUMBER: PCT/US01/43588A
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: retention sequence
PCT-US01-43588A-97

Query Match      100.0%; Score 20; DB 1; Length 4;
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RESULT 9
PCT-US02-02814-25
; Sequence 25, Application PC/TUS0202814
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice (U.S. Only)
; APPLICANT: Smith, Ernest S. (U.S. Only)
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules
; FILE REFERENCE: 1821.0080003
; CURRENT APPLICATION NUMBER: PCT/US02/02814
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/271,423
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/265,880
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/265,589
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Endoplasmic reticulum sequence from calreticulin
PCT-US02-02814-25

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KDEL 4

RESULT 10
PCT-US02-02814-35
; Sequence 35, Application PC/TUS0202814
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice (U.S. Only)
; APPLICANT: Smith, Ernest S. (U.S. Only)
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules
; FILE REFERENCE: 1821.0080003
; CURRENT APPLICATION NUMBER: PCT/US02/02814
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/271,423
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/265,880
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/265,589
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heterologous signal sequence for the endoplasmic reticulum
PCT-US02-02814-35

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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KDEL 4

RESULT 11
PCT-US02-10132-5
; Sequence 5, Application PC/TUS0210132
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Rubert, Rene S.
; APPLICANT: Morrison, Karen J.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 238P1B2 USEFUL IN TREATMENT AND DETECTION OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 51158-20065.40
; CURRENT APPLICATION NUMBER: PCT/US02/10132
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 8913
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
PCT-US02-10132-5

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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapiens
PCT-US02-15520-43

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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
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RESULT 12
PCT-US02-13008-23
; Sequence 23, Application PC/TUS0213008
; GENERAL INFORMATION:
; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION OF
; FILE REFERENCE: HMV-056.25
; CURRENT APPLICATION NUMBER: PCT/US02/13008
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/285,509
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Calreticulin
; OTHER INFORMATION: targeting sequence
PCT-US02-13008-23

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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
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RESULT 13
PCT-US02-15520-43
; Sequence 43, Application PC/TUS0215520
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Faris
; APPLICANT: Arthur B. Raitano
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Douglas Saffran
; APPLICANT: Wangmao Ge
; APPLICANT: Pia M. Challita-Eid
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS
; TITLE OF INVENTION: ENTITLED 101P3a11 or PHOR-1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.46
; CURRENT APPLICATION NUMBER: PCT/US02/15520
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 10/017,066
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 10/001,469
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 09/680,728
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/157,902
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
```

```
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapiens
PCT-US02-15520-43

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 14
PCT-US02-16391-15
; Sequence 15, Application PC/TUS0216391
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: ATTRACTIN/MAHOGANY-LIKE POLYPEPTIDES, POLYNUCLEOTIDES, ANTIBODI
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 3224-WO
; CURRENT APPLICATION NUMBER: PCT/US02/16391
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/293,608
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/324,626
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Localization Sequence
PCT-US02-16391-15

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 15
PCT-US02-16906-17
; Sequence 17, Application PC/TUS0216906
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Dirk, Anderson M.
; APPLICANT: Marken, John S.
; TITLE OF INVENTION: SIGLEC-12 POLYPEPTIDES, POLYNUCLEOTIDES, AND METHODS OF USE THERE
; FILE REFERENCE: 3290-WO
; CURRENT APPLICATION NUMBER: PCT/US02/16906
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/294,199
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Localization sequence
PCT-US02-16906-17

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KDEL 4  
 Db 1 KDEL 4

RESULT 16  
 PCT-US02-19297-163  
 ; Sequence 163, Application PC/TUS0219297  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mack, David H.  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Eos Biotechnology Inc.  
 ; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions  
 ; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian  
 ; TITLE OF INVENTION: Cancer  
 ; FILE REFERENCE: 018501-002420PC  
 ; CURRENT APPLICATION NUMBER: PCT/US02/19297  
 ; CURRENT FILING DATE: 2002-06-18  
 ; PRIOR APPLICATION NUMBER: US 60/299,234  
 ; PRIOR FILING DATE: 2001-06-18  
 ; PRIOR APPLICATION NUMBER: US 60/315,287  
 ; PRIOR FILING DATE: 2001-08-27  
 ; PRIOR APPLICATION NUMBER: US 60/317,544  
 ; PRIOR FILING DATE: 2001-09-05  
 ; PRIOR APPLICATION NUMBER: US 60/350,666  
 ; PRIOR FILING DATE: 2001-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/372,246  
 ; PRIOR FILING DATE: 2001-04-12  
 ; NUMBER OF SEQ ID NOS: 164  
 ; SOFTWARE: PatentIn ver. 2.1  
 ; SEQ ID NO 163  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:KDEL  
 ; OTHER INFORMATION: endoplasmic reticulum retention sequence  
 PCT-US02-19297-163

Query Match 100.0%; Score 20; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
 Db 1 KDEL 4

RESULT 17  
 PCT-US02-21677-31  
 ; Sequence 31, Application PC/TUS0221677  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Rochester  
 ; APPLICANT: Zauderer, Maurice  
 ; APPLICANT: Wei, Chungwen  
 ; APPLICANT: Smith, Ernest  
 ; TITLE OF INVENTION: Methods of Producing or Identifying Intrabodies in Eukaryotic Cell  
 ; FILE REFERENCE: 1821.009PC05  
 ; CURRENT APPLICATION NUMBER: PCT/US02/21677  
 ; CURRENT FILING DATE: 2003-02-27  
 ; PRIOR APPLICATION NUMBER: 60/298,095  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/271,422  
 ; PRIOR FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: 60/263,200  
 ; PRIOR FILING DATE: 2001-01-24  
 ; PRIOR APPLICATION NUMBER: 60/263,225  
 ; PRIOR FILING DATE: 2001-01-23  
 ; NUMBER OF SEQ ID NOS: 154  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 31

; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: targeting sequence  
 PCT-US02-21677-31

Query Match 100.0%; Score 20; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
 Db 1 KDEL 4

RESULT 18  
 PCT-US02-21677-41  
 ; Sequence 41, Application PC/TUS0221677  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Rochester  
 ; APPLICANT: Zauderer, Maurice  
 ; APPLICANT: Wei, Chungwen  
 ; APPLICANT: Smith, Ernest  
 ; TITLE OF INVENTION: Methods of Producing or Identifying Intrabodies in Eukaryotic Cell  
 ; FILE REFERENCE: 1821.009PC05  
 ; CURRENT APPLICATION NUMBER: PCT/US02/21677  
 ; CURRENT FILING DATE: 2003-02-27  
 ; PRIOR APPLICATION NUMBER: 60/298,095  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/271,422  
 ; PRIOR FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: 60/263,200  
 ; PRIOR FILING DATE: 2001-01-24  
 ; PRIOR APPLICATION NUMBER: 60/263,225  
 ; PRIOR FILING DATE: 2001-01-23  
 ; NUMBER OF SEQ ID NOS: 154  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 41  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: signal sequence  
 PCT-US02-21677-41

Query Match 100.0%; Score 20; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
 Db 1 KDEL 4

RESULT 19  
 PCT-US02-21677-118  
 ; Sequence 118, Application PC/TUS0221677  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Rochester  
 ; APPLICANT: Zauderer, Maurice  
 ; APPLICANT: Wei, Chungwen  
 ; APPLICANT: Smith, Ernest  
 ; TITLE OF INVENTION: Methods of Producing or Identifying Intrabodies in Eukaryotic Cell  
 ; FILE REFERENCE: 1821.009PC05  
 ; CURRENT APPLICATION NUMBER: PCT/US02/21677  
 ; CURRENT FILING DATE: 2003-02-27  
 ; PRIOR APPLICATION NUMBER: 60/298,095  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/271,422  
 ; PRIOR FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: 60/263,200  
 ; PRIOR FILING DATE: 2001-01-24



; PRIOR APPLICATION NUMBER: 60/263,225  
; PRIOR FILING DATE: 2001-01-23  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 118  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: localization signal  
PCT-US02-21677-118

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 30  
PCT-US02-26837-33  
; Sequence 33, Application PC/TUS0226837  
; GENERAL INFORMATION:  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Physalia Fluorescent Proteins  
; FILE REFERENCE: FP-71663-PC/TAL/AXG  
; CURRENT APPLICATION NUMBER: PCT/US02/26837  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: US 60/314,378  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-26837-33

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 21  
PCT-US02-27628-30  
; Sequence 30, Application PC/TUS0227628  
; GENERAL INFORMATION:  
; APPLICANT: Rossi, Alex  
; TITLE OF INVENTION: Production of Cultured Human Mast Cells and Basophils for High Th  
; FILE REFERENCE: A-70882/RMS/AMS  
; CURRENT APPLICATION NUMBER: PCT/US02/27628  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/316,723  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-27628-30

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 22  
PCT-US02-27628A-30  
; Sequence 30, Application PC/TUS0227628A  
; GENERAL INFORMATION:  
; APPLICANT: RIGEL PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: Production of Cultured Human Mast Cells and Basophils for High  
; FILE REFERENCE: FP-70882-PC/RMS/AMS  
; CURRENT APPLICATION NUMBER: PCT/US02/27628A  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/316,723  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 10/053,355  
; PRIOR FILING DATE: 2001-11-08  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-27628A-30

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 23  
PCT-US02-29560-411  
; Sequence 411, Application PC/TUS0229560  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Hevezi, Peter A.  
; APPLICANT: Mack, David H.  
; APPLICANT: Wilson, Keith E.  
; APPLICANT: Zlotnik, Albert  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
; FILE REFERENCE: 018501-002710PC  
; CURRENT APPLICATION NUMBER: PCT/US02/29560  
; CURRENT FILING DATE: 2025-11-01  
; PRIOR APPLICATION NUMBER: US 60/323,469  
; PRIOR FILING DATE: 2001-09-17  
; NUMBER OF SEQ ID NOS: 412  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 411  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: KDEL endoplasmic reticulum retention sequence  
PCT-US02-29560-411

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

Mon Mar 20 08:51:26 2006

```
RESULT 24
PCT-US02-29560A-411
; Sequence 411, Application PC/TUS0229560A
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Ros Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560A
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 411
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDEL endoplasmic reticulum retention sequence
PCT-US02-29560A-411

Query Match          100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      1 KDEL 4

RESULT 25
PCT-US02-30118-8
; Sequence 8, Application PC/TUS0230118
; GENERAL INFORMATION:
; APPLICANT: PRODIGENE, INC.
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS IN PLANTS
; FILE REFERENCE: C-36-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/30118
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/324,308
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: peptide motif
PCT-US02-30118-8

Query Match          100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      1 KDEL 4

RESULT 26
PCT-US02-30316-5
```

```
; Sequence 5, Application PC/TUS0230316
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Salvatore, Giuliana
; APPLICANT: Beers, Richard
; APPLICANT: Kreitman, Robert J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mutated Anti-CD22 Antibodies With Increased Affinity to
; TITLE OF INVENTION: CD22-Expressing Leukemia Cells
; FILE REFERENCE: 015280-438100PC
; CURRENT APPLICATION NUMBER: PCT/US02/30316
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/325,360
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:carboxyl
; OTHER INFORMATION: terminus addition to maintain ability of the
; OTHER INFORMATION: construct to translocate to cytosol
PCT-US02-30316-5

Query Match          100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      1 KDEL 4

RESULT 27
PCT-US02-38763-4
; Sequence 4, Application PC/TUS0238763
; GENERAL INFORMATION:
; APPLICANT: PRODIGENE, INC.
; TITLE OF INVENTION: METHODS FOR THE COST-EFFECTIVE SACCHARIFICATION OF
; TITLE OF INVENTION: LIGNOCELLULOSIC BIOMASS
; FILE REFERENCE: 10038 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/38763
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: 60/340,035
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic KDEL
; OTHER INFORMATION: motif
PCT-US02-38763-4

Query Match          100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      1 KDEL 4

RESULT 28
PCT-US02-38849-8
; Sequence 8, Application PC/TUS0238849
; GENERAL INFORMATION:
```

; APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.  
; TITLE OF INVENTION: ANTIBODY TO LATENT MEMBRANE PROTEINS AND USES THEREOF  
; FILE REFERENCE: 52141-PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/38849  
; CURRENT FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/337,294  
; PRIOR FILING DATE: 2001-04-12  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative motif  
PCT-US02-38849-8

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

## RESULT 29

PCT-US02-41158-26  
; Sequence 26, Application PC/TUS0241158  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNEX CORPORATION  
; APPLICANT: BAUM, Peter R.  
; TITLE OF INVENTION: C-Type Lectin Polypeptide, Polynucleotide and Methods of Making a  
; FILE REFERENCE: 3303-WO  
; CURRENT APPLICATION NUMBER: PCT/US02/41158  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/342,001  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Localization Sequence  
PCT-US02-41158-26

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

## RESULT 30

PCT-US02-41158A-26  
; Sequence 26, Application PC/TUS0241158A  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNEX CORPORATION  
; APPLICANT: BAUM, Peter R.  
; TITLE OF INVENTION: C-Type Lectin Polypeptide, Polynucleotide and Methods of Making a  
; FILE REFERENCE: 3303-WO  
; CURRENT APPLICATION NUMBER: PCT/US02/41158A  
; CURRENT FILING DATE: 2003-03-05  
; PRIOR APPLICATION NUMBER: US 60/342,001  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 26  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Localization Sequence  
PCT-US02-41158A-26

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

## RESULT 31

PCT-US02-41510-102  
; Sequence 102, Application PC/TUS0241510  
; GENERAL INFORMATION:  
; APPLICANT: GLYCOPI, INC.  
; TITLE OF INVENTION: METHODS TO ENGINEER MAMMALIAN-TYPE CARBOHYDRATE  
; FILE REFERENCE: GPI/102 PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/41510  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: 60/344,169  
; PRIOR FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 102  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative  
; OTHER INFORMATION: retention signal peptide  
PCT-US02-41510-102

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 1 KDEL 4

## RESULT 32

PCT-US03-04631-23  
; Sequence 23, Application PC/TUS0304631  
; GENERAL INFORMATION:  
; APPLICANT: Duke University  
; APPLICANT: Nicchitta, Chris  
; APPLICANT: Baker-Lepain, Julie  
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESP  
; FILE REFERENCE: 180/145  
; CURRENT APPLICATION NUMBER: PCT/US03/04631  
; CURRENT FILING DATE: 2003-02-13  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: synthetic construct  
PCT-US03-04631-23

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 33
PCT-US03-10081-4
; Sequence 4, Application PC/TUS0310081
; GENERAL INFORMATION:
; APPLICANT: Selective Genetics, Inc.
; APPLICANT: Abbott, Robert
; APPLICANT: Larocca, David
; APPLICANT: Baird, Andrew
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PORTAL
; FILE REFERENCE: 760100.460PC
; CURRENT APPLICATION NUMBER: PCT/US03/10081
; CURRENT FILING DATE: 2003-04-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ER retention sequence
PCT-US03-10081-4

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 34
PCT-US03-10630-3
; Sequence 3, Application PC/TUS0310630
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
; TITLE OF INVENTION: COLON TUMOR SPECIFIC BINDING PEPTIDES
; FILE REFERENCE: 38509-0015
; CURRENT APPLICATION NUMBER: PCT/US03/10630
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/369,850
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
PCT-US03-10630-3

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 35
PCT-US03-10630A-3
; Sequence 3, Application PC/TUS0310630A
; GENERAL INFORMATION:
; APPLICANT: Kimberly A. Kelly
; APPLICANT: David A. Jones
; TITLE OF INVENTION: COLON TUMOR SPECIFIC BINDING PEPTIDES
; FILE REFERENCE: 38509-0015U1

```

```

; CURRENT APPLICATION NUMBER: PCT/US03/10630A
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: PCT/US03/10630
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/369,850
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
PCT-US03-10630A-3

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 36
PCT-US03-15809-26
; Sequence 26, Application PC/TUS0315809
; GENERAL INFORMATION:
; APPLICANT: Henry, Lu
; APPLICANT: Huang, Peiyong
; APPLICANT: Kinsella, Todd
; APPLICANT: Martinez, Anthony
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING AND IDENTIFYING ANTI-HCV
; FILE REFERENCE: RIGL-016WO
; CURRENT APPLICATION NUMBER: PCT/US03/15809
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 10/152,163
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-15809-26

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 37
PCT-US03-16360-3
; Sequence 3, Application PC/TUS0316360
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Rozema, David
; APPLICANT: Wolff, Jon
; APPLICANT: Wakefield, Darren
; APPLICANT: Ekena, Kirk
; APPLICANT: Hagstrom, James
; TITLE OF INVENTION: Reversible Modification of Membrane Interaction
; FILE REFERENCE: MC.035-01.1
; CURRENT APPLICATION NUMBER: PCT/US03/16360
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4

```

; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-16360-3

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|  
|  
|  
|  
Db 1 KDEL 4

## RESULT 38

PCT-US03-18373-30

; Sequence 30, Application PC/TUS0318373

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira H.

; APPLICANT: Nagata, Satoshi

; APPLICANT: Onda, Masanori

; APPLICANT: Numata, Yoshito

; APPLICANT: Santora, Kenneth

; APPLICANT: Beers, Richard

; APPLICANT: Kreitman, Robert

; APPLICANT: Sinha, Abhishek

; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by The Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Anti-CD30 Stalk and Anti-CD30 Antibodies Suitable for

; TITLE OF INVENTION: Use in Immunotoxins

; FILE REFERENCE: 015280-464100PC

; CURRENT APPLICATION NUMBER: PCT/US03/18373

; CURRENT FILING DATE: 2003-06-09

; PRIOR APPLICATION NUMBER: US 60/387,293

; PRIOR FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: US 60/411,032

; PRIOR FILING DATE: 2002-09-16

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 30

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Pseudomonas

; OTHER INFORMATION: exotoxin (PE) carboxyl terminus addition

PCT-US03-18373-30

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|  
|  
|  
|  
Db 1 KDEL 4

## RESULT 39

PCT-US03-18373A-30

; Sequence 30, Application PC/TUS0318373A

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira H.

; APPLICANT: Nagata, Satoshi

; APPLICANT: Onda, Masanori

; APPLICANT: Numata, Yoshito

; APPLICANT: Santora, Kenneth

; APPLICANT: Beers, Richard

; APPLICANT: Kreitman, Robert

; APPLICANT: Sinha, Abhishek

; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by The Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Anti-CD30 Stalk and Anti-CD30 Antibodies Suitable for

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence universally recognized as signals for protein
; OTHER INFORMATION: retention in the endoplasmic reticulum (ER)
PCT-US03-32968-33

```

```

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KDEL 4
      ||||
DB      1 KDEL 4

```

```

RESULT 42
PCT-US03-35088A-18
; Sequence 18, Application PC/TUS0335088A
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Baker, Brenda
; APPLICANT: Eldrup, Ann
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Griffey, Richard H.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Conjugated Oligomeric Compounds and Their Use in Gene
; TITLE OF INVENTION: Modulation
; FILE REFERENCE: ISIC009-500
; CURRENT APPLICATION NUMBER: PCT/US03/35088A
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: US 10/616,241
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 60/423,760
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically Synthesized Peptide
PCT-US03-35088A-18

```

```

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KDEL 4
      ||||
DB      1 KDEL 4

```

```

RESULT 43
PCT-US03-38227-11
; Sequence 11, Application PC/TUS0338227
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
; APPLICANT: Pastan, Ira
; APPLICANT: Onda, Masanori
; APPLICANT: Cheung, Nai-Kong
; TITLE OF INVENTION: IN-VIVO CYTOTOXIC ACTIVITIES OF RECOMBINANT IMMUNOTOXIN 8H9
; TITLE OF INVENTION: (FV)-PE38 AGAINST BREAST CANCER, OSTEOCARCINOMA AND NEUROBLASTOM
; FILE REFERENCE: 4239-67287
; CURRENT APPLICATION NUMBER: PCT/US03/38227
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/430,305
; PRIOR FILING DATE: 2002-12-02

```

```

; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
PCT-US03-38227-11

```

```

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KDEL 4
      ||||
DB      1 KDEL 4

```

```

RESULT 44
PCT-US03-39476-5
; Sequence 5, Application PC/TUS0339476
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Eglund, Kristi A.
; APPLICANT: Vincent, James J.
; APPLICANT: Lee, Byungkook
; APPLICANT: Strausberg, Robert
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: BASE, a New Cancer Gene, and Uses Thereof
; FILE REFERENCE: 015280-475100PC
; CURRENT APPLICATION NUMBER: PCT/US03/39476
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/432,531
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:carboxyl
; OTHER INFORMATION: terminus addition sequence
PCT-US03-39476-5

```

```

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KDEL 4
      ||||
DB      1 KDEL 4

```

```

RESULT 45
PCT-US04-08866-1955
; Sequence 1955, Application PC/TUS0408866
; GENERAL INFORMATION:
; APPLICANT: Dana Farber Cancer Institute, Inc.
; TITLE OF INVENTION: GENE EXPRESSION IN BREAST CANCER
; FILE REFERENCE: 00530-116W01
; CURRENT APPLICATION NUMBER: PCT/US04/08866
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 60/456,735
; PRIOR FILING DATE: 2003-03-20
; NUMBER OF SEQ ID NOS: 1955
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1955
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-08866-1955

```

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 46

PCT-US04-10059-103  
; Sequence 9, Application PC/TUS0410059  
; GENERAL INFORMATION:  
; APPLICANT: INTRADIGM CORPORATION  
; TITLE OF INVENTION: TARGETS FOR TUMOR GROWTH INHIBITION  
; FILE REFERENCE: 38147-0055  
; CURRENT APPLICATION NUMBER: PCT/US04/10059  
; CURRENT FILING DATE: 2004-04-01  
; PRIOR APPLICATION NUMBER: 60/458,948  
; PRIOR FILING DATE: 2003-04-01  
; PRIOR APPLICATION NUMBER: 60/489,504  
; PRIOR FILING DATE: 2003-07-24  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 103  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
PCT-US04-10059-103

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 47

PCT-US04-11481-9  
; Sequence 9, Application PC/TUS0411481  
; GENERAL INFORMATION:  
; APPLICANT: MedImmune, Inc.  
; TITLE OF INVENTION: EphA2 and Hypoproliferative Cell Disorders and Epithelial and End  
; FILE REFERENCE: 10271-058-228  
; CURRENT APPLICATION NUMBER: PCT/US04/11481  
; CURRENT FILING DATE: 2004-04-20  
; PRIOR APPLICATION NUMBER: 60/462,009  
; PRIOR FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US04-11481-9

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 48

PCT-US04-11482-9  
; Sequence 9, Application PC/TUS0411482  
; GENERAL INFORMATION:  
; APPLICANT: MedImmune, Inc.  
; TITLE OF INVENTION: EphA2 and Hyperproliferative Cell Disorders  
; FILE REFERENCE: 10271-060-228  
; CURRENT APPLICATION NUMBER: PCT/US04/11482  
; CURRENT FILING DATE: 2004-04-20  
; PRIOR APPLICATION NUMBER: 60/462,024  
; PRIOR FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US04-11482-9

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 49

PCT-US04-23191-12  
; Sequence 12, Application PC/TUS0423191  
; GENERAL INFORMATION:  
; APPLICANT: MedImmune, Inc.  
; TITLE OF INVENTION: DIAGNOSIS OF PRE-CANCEROUS CONDITIONS  
; FILE REFERENCE: 10271-131-228  
; CURRENT APPLICATION NUMBER: PCT/US04/23191  
; CURRENT FILING DATE: 2004-07-28  
; PRIOR APPLICATION NUMBER: 60/489,035  
; PRIOR FILING DATE: 2003-07-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Localization signal used to direct intrabody to endoplasmic ret  
PCT-US04-23191-12

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 50

PCT-US04-23192-12  
; Sequence 12, Application PC/TUS0423192  
; GENERAL INFORMATION:  
; APPLICANT: MedImmune, Inc.  
; TITLE OF INVENTION: TREATMENT OF PRE-CANCEROUS CONDITIONS  
; FILE REFERENCE: 10271-110-228  
; CURRENT APPLICATION NUMBER: PCT/US04/23192  
; CURRENT FILING DATE: 2004-07-28  
; PRIOR APPLICATION NUMBER: 60/489,035  
; PRIOR FILING DATE: 2003-07-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 12

Mon Mar 20 08:51:26 2006

```
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Localization signal used to direct intrabody to endoplasmic retic
PCT-US04-23192-12

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
      ||||
Db      1 KDEL 4

Search completed: March 20, 2006, 08:10:46
Job time : 403.5 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:52:40 ; Search time 17.5 Seconds  
(without alignments)  
21.955 Million cell updates/sec

Title: US-09-673-707-9

Perfect score: 20

Sequence: 1 KDEL 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 443638 seqs, 96052105 residues

Total number of hits satisfying chosen parameters: 443638

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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3: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*

4: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*

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8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 20    | 100.0       | 4      | 1  | PCT-US05-38666-9   |
| 2          | 20    | 100.0       | 4      | 1  | PCT-US05-38667-9   |
| 3          | 20    | 100.0       | 4      | 1  | PCT-US05-38668-81  |
| 4          | 20    | 100.0       | 4      | 1  | PCT-US05-39091-268 |
| 5          | 20    | 100.0       | 4      | 1  | PCT-US05-31269A-30 |
| 6          | 20    | 100.0       | 4      | 1  | PCT-US05-21612-262 |
| 7          | 20    | 100.0       | 4      | 1  | PCT-US05-35802-3   |
| 8          | 20    | 100.0       | 4      | 1  | PCT-US04-04340-9   |
| 9          | 20    | 100.0       | 4      | 1  | PCT-US04-41023B-89 |
| 10         | 20    | 100.0       | 4      | 5  | US-09-892-591A-6   |
| 11         | 20    | 100.0       | 4      | 6  | US-11-259-133-81   |
| 12         | 20    | 100.0       | 4      | 6  | US-11-259-266-9    |
| 13         | 20    | 100.0       | 4      | 6  | US-11-259-267-9    |
| 14         | 20    | 100.0       | 4      | 6  | US-11-108-088-70   |
| 15         | 20    | 100.0       | 4      | 6  | US-11-263-230-268  |
| 16         | 20    | 100.0       | 4      | 6  | US-11-240-432-6    |
| 17         | 20    | 100.0       | 4      | 6  | US-11-055-181-7    |
| 18         | 20    | 100.0       | 4      | 6  | US-11-312-319-3    |
| 19         | 20    | 100.0       | 4      | 6  | US-11-326-148-16   |
| 20         | 20    | 100.0       | 4      | 6  | US-11-324-947-44   |
| 21         | 20    | 100.0       | 4      | 6  | US-11-053-045-1    |
| 22         | 20    | 100.0       | 4      | 6  | US-11-046-S90A-12  |
| 23         | 20    | 100.0       | 4      | 6  | US-11-154-103-26   |
| 24         | 20    | 100.0       | 4      | 6  | US-11-334-622-49   |
| 25         | 20    | 100.0       | 4      | 6  | US-11-244-348A-3   |
| 26         | 20    | 100.0       | 4      | 6  | PCT-US05-38666-9   |
| 27         | 20    | 100.0       | 4      | 6  | PCT-US05-38667-9   |
| 28         | 20    | 100.0       | 4      | 6  | PCT-US05-38668-81  |
| 29         | 20    | 100.0       | 4      | 6  | PCT-US05-39091-268 |
| 30         | 20    | 100.0       | 4      | 6  | PCT-US05-31269A-30 |
| 31         | 20    | 100.0       | 4      | 6  | PCT-US05-21612-262 |
| 32         | 20    | 100.0       | 4      | 6  | PCT-US05-35802-3   |
| 33         | 20    | 100.0       | 4      | 6  | PCT-US04-04340-9   |
| 34         | 20    | 100.0       | 4      | 6  | PCT-US04-41023B-89 |
| 35         | 20    | 100.0       | 4      | 6  | US-09-892-591A-6   |
| 36         | 20    | 100.0       | 4      | 6  | US-11-259-133-81   |
| 37         | 20    | 100.0       | 4      | 6  | US-11-259-266-9    |
| 38         | 20    | 100.0       | 4      | 6  | US-11-259-267-9    |
| 39         | 20    | 100.0       | 4      | 6  | US-11-108-088-70   |
| 40         | 20    | 100.0       | 4      | 6  | US-11-263-230-268  |
| 41         | 20    | 100.0       | 4      | 6  | US-11-240-432-6    |
| 42         | 20    | 100.0       | 4      | 6  | US-11-055-181-7    |
| 43         | 20    | 100.0       | 4      | 6  | US-11-312-319-3    |
| 44         | 20    | 100.0       | 4      | 6  | US-11-326-148-16   |
| 45         | 20    | 100.0       | 4      | 6  | US-11-324-947-44   |
| 46         | 20    | 100.0       | 4      | 6  | US-11-053-045-1    |
| 47         | 20    | 100.0       | 4      | 6  | US-11-046-S90A-12  |
| 48         | 20    | 100.0       | 4      | 6  | US-11-154-103-26   |
| 49         | 20    | 100.0       | 4      | 6  | US-11-334-622-49   |
| 50         | 20    | 100.0       | 4      | 6  | US-11-244-348A-3   |
| 51         | 20    | 100.0       | 4      | 6  | PCT-US05-38666-9   |
| 52         | 20    | 100.0       | 4      | 6  | PCT-US05-38667-9   |
| 53         | 20    | 100.0       | 4      | 6  | PCT-US05-38668-81  |
| 54         | 20    | 100.0       | 4      | 6  | PCT-US05-39091-268 |
| 55         | 20    | 100.0       | 4      | 6  | PCT-US05-31269A-30 |
| 56         | 20    | 100.0       | 4      | 6  | PCT-US05-21612-262 |
| 57         | 20    | 100.0       | 4      | 6  | PCT-US05-35802-3   |
| 58         | 20    | 100.0       | 4      | 6  | PCT-US04-04340-9   |
| 59         | 20    | 100.0       | 4      | 6  | PCT-US04-41023B-89 |
| 60         | 20    | 100.0       | 4      | 6  | US-09-892-591A-6   |
| 61         | 20    | 100.0       | 4      | 6  | US-11-259-133-81   |
| 62         | 20    | 100.0       | 4      | 6  | US-11-259-266-9    |
| 63         | 20    | 100.0       | 4      | 6  | US-11-259-267-9    |
| 64         | 20    | 100.0       | 4      | 6  | US-11-108-088-70   |
| 65         | 20    | 100.0       | 4      | 6  | US-11-263-230-268  |
| 66         | 20    | 100.0       | 4      | 6  | US-11-240-432-6    |
| 67         | 20    | 100.0       | 4      | 6  | US-11-055-181-7    |
| 68         | 20    | 100.0       | 4      | 6  | US-11-312-319-3    |
| 69         | 20    | 100.0       | 4      | 6  | US-11-326-148-16   |
| 70         | 20    | 100.0       | 4      | 6  | US-11-324-947-44   |
| 71         | 20    | 100.0       | 4      | 6  | US-11-053-045-1    |
| 72         | 20    | 100.0       | 4      | 6  | US-11-046-S90A-12  |
| 73         | 20    | 100.0       | 4      | 6  | US-11-154-103-26   |
| 74         | 20    | 100.0       | 4      | 6  | US-11-334-622-49   |
| 75         | 20    | 100.0       | 4      | 6  | US-11-244-348A-3   |
| 76         | 20    | 100.0       | 4      | 6  | PCT-US05-38666-9   |
| 77         | 20    | 100.0       | 4      | 6  | PCT-US05-38667-9   |
| 78         | 20    | 100.0       | 4      | 6  | PCT-US05-38668-81  |
| 79         | 20    | 100.0       | 4      | 6  | PCT-US05-39091-268 |
| 80         | 20    | 100.0       | 4      | 6  | PCT-US05-31269A-30 |
| 81         | 20    | 100.0       | 4      | 6  | PCT-US05-21612-262 |
| 82         | 20    | 100.0       | 4      | 6  | PCT-US05-35802-3   |
| 83         | 20    | 100.0       | 4      | 6  | PCT-US04-04340-9   |
| 84         | 20    | 100.0       | 4      | 6  | PCT-US04-41023B-89 |
| 85         | 20    | 100.0       | 4      | 6  | US-09-892-591A-6   |
| 86         | 20    | 100.0       | 4      | 6  | US-11-259-133-81   |
| 87         | 20    | 100.0       | 4      | 6  | US-11-259-266-9    |
| 88         | 20    | 100.0       | 4      | 6  | US-11-259-267-9    |
| 89         | 20    | 100.0       | 4      | 6  | US-11-108-088-70   |
| 90         | 20    | 100.0       | 4      | 6  | US-11-263-230-268  |
| 91         | 20    | 100.0       | 4      | 6  | US-11-240-432-6    |
| 92         | 20    | 100.0       | 4      | 6  | US-11-055-181-7    |
| 93         | 20    | 100.0       | 4      | 6  | US-11-312-319-3    |
| 94         | 20    | 100.0       | 4      | 6  | US-11-326-148-16   |
| 95         | 20    | 100.0       | 4      | 6  | US-11-324-947-44   |
| 96         | 20    | 100.0       | 4      | 6  | US-11-053-045-1    |
| 97         | 20    | 100.0       | 4      | 6  | US-11-046-S90A-12  |
| 98         | 20    | 100.0       | 4      | 6  | US-11-154-103-26   |
| 99         | 20    | 100.0       | 4      | 6  | US-11-334-622-49   |
| 100        | 20    | 100.0       | 4      | 6  | US-11-244-348A-3   |

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Sequence 6, Appli  
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Sequence 17189, A  
Sequence 17891, A  
Sequence 18689, A  
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Sequence 12925, A  
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Sequence 140064, A  
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Sequence 15785, A  
Sequence 28, Appli  
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Sequence 121871, A  
Sequence 127363, A  
Sequence 136631, A  
Sequence 15784, A  
Sequence 12127, A  
Sequence 46, Appli  
Sequence 9465, Appli  
Sequence 132249, A  
Sequence 137313, A  
Sequence 77, Appli  
Sequence 18743, A

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| 99  | 20 | 100.0 | 93  | 7   | US-11-360-355-165903, |                   |
| 100 | 20 | 100.0 | 94  | 7   | Sequence 160863,      |                   |
| 101 | 20 | 100.0 | 95  | 7   | Sequence 129599,      |                   |
| 102 | 20 | 100.0 | 96  | 7   | Sequence 140409,      |                   |
| 103 | 20 | 100.0 | 97  | 6   | Sequence 7271, Ap     |                   |
| 104 | 20 | 100.0 | 98  | 8   | Sequence 13272, A     |                   |
| 105 | 20 | 100.0 | 99  | 8   | Sequence 12408, A     |                   |
| 106 | 20 | 100.0 | 100 | 6   | Sequence 20438, A     |                   |
| 107 | 20 | 100.0 | 101 | 6   | Sequence 1369, Ap     |                   |
| 108 | 20 | 100.0 | 102 | 1   | Sequence 4664, Ap     |                   |
| 109 | 20 | 100.0 | 103 | 8   | Sequence 13485, A     |                   |
| 110 | 20 | 100.0 | 104 | 7   | Sequence 18216, A     |                   |
| 111 | 20 | 100.0 | 105 | 6   | Sequence 164392,      |                   |
| 112 | 20 | 100.0 | 106 | 7   | Sequence 24, Appl     |                   |
| 113 | 20 | 100.0 | 107 | 1   | Sequence 143860,      |                   |
| 114 | 20 | 100.0 | 108 | 7   | Sequence 142924,      |                   |
| 115 | 20 | 100.0 | 109 | 113 | 7                     | Sequence 2318, Ap |
| 116 | 20 | 100.0 | 110 | 8   | Sequence 14528, A     |                   |
| 117 | 20 | 100.0 | 111 | 8   | Sequence 26, Appl     |                   |
| 118 | 20 | 100.0 | 112 | 1   | Sequence 14980, A     |                   |
| 119 | 20 | 100.0 | 113 | 6   | Sequence 147485,      |                   |
| 120 | 20 | 100.0 | 114 | 7   | Sequence 151083,      |                   |
| 121 | 20 | 100.0 | 115 | 7   | Sequence 129834,      |                   |
| 122 | 20 | 100.0 | 116 | 7   | Sequence 134603,      |                   |
| 123 | 20 | 100.0 | 117 | 7   | Sequence 167225,      |                   |
| 124 | 20 | 100.0 | 118 | 7   | Sequence 520, App     |                   |
| 125 | 20 | 100.0 | 118 | 8   | Sequence 129681,      |                   |
| 126 | 20 | 100.0 | 119 | 7   | Sequence 120658,      |                   |
| 127 | 20 | 100.0 | 120 | 7   | Sequence 10754, A     |                   |
| 128 | 20 | 100.0 | 120 | 8   | Sequence 20856, A     |                   |
| 129 | 20 | 100.0 | 120 | 8   | Sequence 155048,      |                   |
| 130 | 20 | 100.0 | 121 | 7   | Sequence 161084,      |                   |
| 131 | 20 | 100.0 | 121 | 7   | Sequence 168152,      |                   |
| 132 | 20 | 100.0 | 121 | 7   | Sequence 50045, A     |                   |
| 133 | 20 | 100.0 | 121 | 8   | Sequence 4058, Ap     |                   |
| 134 | 20 | 100.0 | 121 | 8   | Sequence 42, Appl     |                   |
| 135 | 20 | 100.0 | 122 | 1   | Sequence 20437, A     |                   |
| 136 | 20 | 100.0 | 122 | 6   | Sequence 126836,      |                   |
| 137 | 20 | 100.0 | 123 | 7   | Sequence 20051, A     |                   |
| 138 | 20 | 100.0 | 123 | 8   | Sequence 9166, Ap     |                   |
| 139 | 20 | 100.0 | 123 | 8   | Sequence 11892, A     |                   |
| 140 | 20 | 100.0 | 123 | 8   | Sequence 10786, A     |                   |
| 141 | 20 | 100.0 | 125 | 8   | Sequence 13100, A     |                   |
| 142 | 20 | 100.0 | 126 | 8   | Sequence 1269, Ap     |                   |
| 143 | 20 | 100.0 | 127 | 6   | Sequence 1365, Ap     |                   |
| 144 | 20 | 100.0 | 128 | 1   | Sequence 1366, Ap     |                   |
| 145 | 20 | 100.0 | 128 | 1   | Sequence 1367, Ap     |                   |
| 146 | 20 | 100.0 | 128 | 1   | Sequence 1368, Ap     |                   |
| 147 | 20 | 100.0 | 128 | 1   | Sequence 152058,      |                   |
| 148 | 20 | 100.0 | 128 | 7   | Sequence 13132, A     |                   |
| 149 | 20 | 100.0 | 129 | 6   | Sequence 125331,      |                   |
| 150 | 20 | 100.0 | 129 | 7   |                       |                   |

ALIGNMENTS

RESULT 1  
PCT-US05-38666-9  
; Sequence 9, Application PC/TUS0538666  
; GENERAL INFORMATION:  
; APPLICANT: MedImmune  
; APPLICANT: Kinch, Michael  
; APPLICANT: Carles-Kinch, Kelly  
; TITLE OF INVENTION: Use of Modulators of EphA2 and EphrinA1 for the Treatment and Pre  
; TITLE OF INVENTION: of Infections  
; FILE REFERENCE: EP350PCT  
; CURRENT APPLICATION NUMBER: PCT/US05/38666  
; CURRENT FILING DATE: 2005-11-04  
; PRIOR APPLICATION NUMBER: 60/622,489  
; PRIOR FILING DATE: 2004-10-27  
; PRIOR APPLICATION NUMBER: 60/705,705  
; PRIOR FILING DATE: 2005-08-03

; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US05-38666-9

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 2

PCT-US05-38667-9  
; Sequence 9, Application PC/TUS0538667  
; GENERAL INFORMATION:  
; APPLICANT: MedImmune  
; APPLICANT: Kinch, Michael  
; APPLICANT: Carles-Kinch, Kelly  
; TITLE OF INVENTION: Modulators of EphA2 and EphrinA1 for the Treatment of  
; TITLE OF INVENTION: Fibrosis-Related Disease  
; FILE REFERENCE: EP301PCT  
; CURRENT APPLICATION NUMBER: PCT/US05/38667  
; CURRENT FILING DATE: 2005-11-04  
; PRIOR APPLICATION NUMBER: 60/622,517  
; PRIOR FILING DATE: 2004-10-27  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US05-38667-9

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 3

PCT-US05-38668-81  
; Sequence 81, Application PC/TUS0538668  
; GENERAL INFORMATION:  
; APPLICANT: MedImmune  
; APPLICANT: Dall'Acqua, William  
; APPLICANT: Damschroder, Melissa  
; APPLICANT: Kinch, Michael  
; APPLICANT: Carles-Kinch, Kelly  
; TITLE OF INVENTION: MODULATION OF ANTIBODY SPECIFICITY BY TAILORING THE AFFINITY TO  
; TITLE OF INVENTION: COGNATE ANTIGENS  
; FILE REFERENCE: EP700PCT  
; CURRENT APPLICATION NUMBER: PCT/US05/38668  
; CURRENT FILING DATE: 2005-11-04  
; PRIOR APPLICATION NUMBER: 60/622,711  
; PRIOR FILING DATE: 2004-10-27  
; PRIOR APPLICATION NUMBER: 60/717,209  
; PRIOR FILING DATE: 2005-09-16  
; NUMBER OF SEQ ID NOS: 205  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 81  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US05-38668-81

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Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 4
PCT-US05-39091-268
; Sequence 268, Application PC/TUS0539091
; GENERAL INFORMATION:
; APPLICANT: MedImmune, Inc.
; TITLE OF INVENTION: Methods of Preventing and Treating RSV Infections
; FILE REFERENCE: 10271-174-228
; CURRENT APPLICATION NUMBER: PCT/US05/39091
; CURRENT FILING DATE: 2005-11-07
; PRIOR APPLICATION NUMBER: 60/623,821
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/675,724
; PRIOR FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/681,233
; PRIOR FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: 60/727,042
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/727,043
; PRIOR FILING DATE: 2005-10-14
; NUMBER OF SEQ ID NOS: 1496
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 268
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: intrabody
PCT-US05-39091-268

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 5
PCT-US05-31269A-30
; Sequence 30, Application PC/TUS0531269A
; GENERAL INFORMATION:
; APPLICANT: Swayze, Eric E.
; APPLICANT: Robinson, Dale E. Jr.
; APPLICANT: Jefferson, Elizabeth Ann
; APPLICANT: Dande, Prasad
; APPLICANT: Prakash, Thazha P.
; APPLICANT: Allerson, Charles
; APPLICANT: Bhat, Balakrishen
; TITLE OF INVENTION: PYRROLIDINYL GROUPS FOR ATTACHING
; FILE REFERENCE: CONJUGATES TO OLIGOMERIC COMPOUNDS
; CURRENT APPLICATION NUMBER: PCT/US05/31269A
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/608,201
; PRIOR FILING DATE: 2004-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Delivery peptide
PCT-US05-31269A-30

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 6
PCT-US05-21612-262
; Sequence 262, Application PC/TUS0521612
; GENERAL INFORMATION:
; APPLICANT: Ceres Inc.
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-109W01
; CURRENT APPLICATION NUMBER: PCT/US05/21612
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: 10/873,679
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target sequence
PCT-US05-21612-262

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 7
PCT-US05-35802-3
; Sequence 3, Application PC/TUS0535802
; GENERAL INFORMATION:
; APPLICANT: Mtnsy, Randall J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMMUNIZING
; FILE REFERENCE: 10901-015-999
; CURRENT APPLICATION NUMBER: PCT/US05/35802
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: 60/616,125
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
PCT-US05-35802-3

Query Match      100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      1 KDEL 4

RESULT 8
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PCT-US04-04340-9  
; Sequence 9, Application PC/TUS0404340  
; GENERAL INFORMATION:  
; APPLICANT: Antigenics, Inc.  
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND  
; TITLE OF INVENTION: IMMUNOTHERAPIES  
; FILE REFERENCE: 8449-405-228  
; CURRENT APPLICATION NUMBER: PCT/US04/04340  
; CURRENT FILING DATE: 2004-02-13  
; PRIOR APPLICATION NUMBER: 60/503,417  
; PRIOR FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: 60/463,746  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: 60/462,469  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 60/447,142  
; PRIOR FILING DATE: 2003-02-13  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutated heat shock protein peptide  
PCT-US04-04340-9

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|||  
Db 1 KDEL 4

RESULT 9  
PCT-US04-41023B-89  
; Sequence 89, Application PC/TUS0441023B  
; GENERAL INFORMATION:  
; APPLICANT: MedImmune, Inc.  
; TITLE OF INVENTION: Epha2, EphA4 and LMW-PTP and Methods of  
; TITLE OF INVENTION: Treatment of Hyperproliferative Cell Disorders  
; FILE REFERENCE: 10271-111-228  
; CURRENT APPLICATION NUMBER: PCT/US04/41023B  
; CURRENT FILING DATE: 2004-12-06  
; PRIOR APPLICATION NUMBER: 60/527,154  
; PRIOR FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: 11/004,794  
; PRIOR FILING DATE: 2004-12-03  
; PRIOR APPLICATION NUMBER: 11/004,795  
; PRIOR FILING DATE: 2004-12-03  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 89  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US04-41023B-89

Query Match 100.0%; Score 20; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
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Db 1 KDEL 4

RESULT 10  
US-09-892-591A-6  
; Sequence 6, Application US/09892591A  
; GENERAL INFORMATION:

; APPLICANT: Gerngross, Tillman U.  
; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED  
; TITLE OF INVENTION: GLYCOPROTEINS  
; FILE REFERENCE: GFI 100  
; CURRENT APPLICATION NUMBER: US/09/892,591A  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: US 60/214,358  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: US 60/215,638  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/279,997  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Signal tetrapeptide  
US-09-892-591A-6

Query Match 100.0%; Score 20; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
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Db 1 KDEL 4

RESULT 11  
US-11-259-133-81  
; Sequence 81, Application US/11259133  
; GENERAL INFORMATION:  
; APPLICANT: Dall'Acqua, William  
; APPLICANT: Damschroder, Melissa  
; APPLICANT: Kinch, Michael  
; APPLICANT: Carles-Kinch, Kelly  
; TITLE OF INVENTION: MODULATION OF ANTIBODY SPECIFICITY BY TAILORING THE AFFINITY TO  
; TITLE OF INVENTION: COGNATE ANTIGENS  
; FILE REFERENCE: EP700US  
; CURRENT APPLICATION NUMBER: US/11/259,133  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: 60/622,711  
; PRIOR FILING DATE: 2004-10-27  
; PRIOR APPLICATION NUMBER: 60/717,209  
; PRIOR FILING DATE: 2005-09-16  
; NUMBER OF SEQ ID NOS: 205  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 81  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-259-133-81

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
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Db 1 KDEL 4

RESULT 12  
US-11-259-266-9  
; Sequence 9, Application US/11259266  
; GENERAL INFORMATION:  
; APPLICANT: Kinch, Michael  
; APPLICANT: Carles-Kinch, Kelly  
; TITLE OF INVENTION: Use of Modulators of EphA2 and EphrinA1 for the Treatment and P  
; TITLE OF INVENTION: of Infections

; FILE REFERENCE: EP350US  
; CURRENT APPLICATION NUMBER: US/11/259,266  
; PRIOR FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: 60/622,489  
; PRIOR FILING DATE: 2004-10-27  
; PRIOR APPLICATION NUMBER: 60/705,705  
; PRIOR FILING DATE: 2005-08-03  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-259-266-9

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 13  
US-11-259-267-9  
; Sequence 9, Application US/11259267  
; GENERAL INFORMATION:  
; APPLICANT: Kinch, Michael  
; APPLICANT: Carles-Kinch, Kelly  
; TITLE OF INVENTION: Modulators of EphA2 and EphrinA1 for the Treatment of  
; FILE REFERENCE: EP301US  
; CURRENT APPLICATION NUMBER: US/11/259,267  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: 60/622,517  
; PRIOR FILING DATE: 2004-10-27  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-259-267-9

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 14  
US-11-108-088-70  
; Sequence 70, Application US/11108088  
; GENERAL INFORMATION:  
; APPLICANT: DAVIDSON, ROBERT  
; APPLICANT: GERNGROSS, TILLMAN  
; APPLICANT: WILDT, STEFAN  
; APPLICANT: CHOI, BYUNG-KWON  
; APPLICANT: NETT, JUERGEN  
; APPLICANT: BOBROWICZ, PIOTR  
; APPLICANT: HAMILTON, STEPHEN  
; TITLE OF INVENTION: PRODUCTION OF GALACTOSYLATED GLYCOPROTEINS IN LOWER  
; FILE REFERENCE: GPI-12  
; CURRENT APPLICATION NUMBER: US/11/108,088  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: 60/214,358  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/215,638

; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/279,997  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: PCT/US02/41510  
; PRIOR FILING DATE: 2002-12-24  
; PRIOR APPLICATION NUMBER: 60/344,169  
; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/562,424  
; PRIOR FILING DATE: 2004-04-15  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 70  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-11-108-088-70

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 15  
US-11-263-230-268  
; Sequence 268, Application US/11263230  
; GENERAL INFORMATION:  
; APPLICANT: Losonsky, Genevieve  
; APPLICANT: Connor, Edward M.  
; APPLICANT: Young, James F.  
; APPLICANT: Wu, Herren  
; APPLICANT: Dall'Acqua, William  
; TITLE OF INVENTION: Methods of Preventing and Treating RSV Infections  
; TITLE OF INVENTION: and Related Conditions  
; FILE REFERENCE: 10271-174-999  
; CURRENT APPLICATION NUMBER: US/11/263,230  
; CURRENT FILING DATE: 2005-10-31  
; PRIOR APPLICATION NUMBER: 60/623,821  
; PRIOR FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: 60/675,724  
; PRIOR FILING DATE: 2005-04-27  
; PRIOR APPLICATION NUMBER: 60/681,233  
; PRIOR FILING DATE: 2005-05-13  
; PRIOR APPLICATION NUMBER: 60/718,719  
; PRIOR FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: 60/727,042  
; PRIOR FILING DATE: 2005-10-14  
; PRIOR APPLICATION NUMBER: 60/727,043  
; PRIOR FILING DATE: 2005-10-14  
; NUMBER OF SEQ ID NOS: 1496  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 268  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: intrabody  
US-11-263-230-268

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

|   |  |
|---|--|
| RESULT 16   |  |
| US-11-240-432-6   |  |
| ; Sequence 6, Application US/11240432   |  |
| ; GENERAL INFORMATION:  |  |
| ; APPLICANT: Gerngross, Tillman U.  |  |
| ; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED                                    |  |
| ; FILE OF INVENTION: GLYCOPROTEINS  |  |
| ; FILE REFERENCE: GFI 100 CON   |  |
| ; CURRENT APPLICATION NUMBER: US/11/240,432   |  |
| ; CURRENT FILING DATE: 2005-09-30   |  |
| ; PRIOR APPLICATION NUMBER: US 09/892,591   |  |
| ; PRIOR FILING DATE: 2001-06-27   |  |
| ; PRIOR APPLICATION NUMBER: US 60/214,358   |  |
| ; PRIOR FILING DATE: 2000-06-28   |  |
| ; PRIOR APPLICATION NUMBER: US 60/215,638   |  |
| ; PRIOR FILING DATE: 2000-06-30   |  |
| ; PRIOR APPLICATION NUMBER: US 60/279,997   |  |
| ; PRIOR FILING DATE: 2001-03-30   |  |
| ; NUMBER OF SEQ ID NOS: 6   |  |
| ; SOFTWARE: FastSeq for Windows Version 4.0   |  |
| ; SEQ ID NO 6   |  |
| ; LENGTH: 4   |  |
| ; TYPE: PRT   |  |
| ; ORGANISM: Artificial Sequence   |  |
| ; FEATURE:  |  |
| ; OTHER INFORMATION: Signal tetrapeptide  |  |
| US-11-240-432-6   |  |
| Query Match 100.0%; Score 20; DB 6; Length 4;   |  |
| Best Local Similarity 100.0%; Pred. No. 4e+05;  |  |
| Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                              |  |
| QY 1 KDEL 4   |  |
| DB 1 KDEL 4   |  |
| RESULT 17   |  |
| US-11-055-181-7   |  |
| ; Sequence 7, Application US/11055181   |  |
| ; GENERAL INFORMATION:  |  |
| ; APPLICANT: DENARDO, SALLY J.  |  |
| ; APPLICANT: DENARDO, GERALD L.   |  |
| ; APPLICANT: BALHORN, RODNEY  |  |
| ; TITLE OF INVENTION: SELECTIVE HIGH-AFFINITY POLYDENTATE LIGANDS AND METHODS OF MAKING |  |
| ; FILE OF INVENTION: SUCH   |  |
| ; FILE REFERENCE: 309t-300510US   |  |
| ; CURRENT APPLICATION NUMBER: US/11/055,181   |  |
| ; CURRENT FILING DATE: 2005-02-09   |  |
| ; PRIOR APPLICATION NUMBER: US 60/543,444   |  |
| ; PRIOR FILING DATE: 2004-02-09   |  |
| ; NUMBER OF SEQ ID NOS: 20  |  |
| ; SOFTWARE: PatentIn version 3.3  |  |
| ; SEQ ID NO 7   |  |
| ; LENGTH: 4   |  |
| ; TYPE: PRT   |  |
| ; ORGANISM: Artificial  |  |
| ; FEATURE:  |  |
| ; OTHER INFORMATION: Synthetic translocation signaling sequence.                        |  |
| US-11-055-181-7   |  |
| Query Match 100.0%; Score 20; DB 6; Length 4;   |  |
| Best Local Similarity 100.0%; Pred. No. 4e+05;  |  |
| Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                              |  |
| QY 1 KDEL 4   |  |
| DB 1 KDEL 4   |  |
| RESULT 18   |  |
| US-11-312-319-3   |  |
| ; Sequence 3, Application US/11312319   |  |
| ; GENERAL INFORMATION:  |  |
| ; APPLICANT: Mirus Bio Corporation  |  |
| ; APPLICANT: Rozema, David  |  |
| ; APPLICANT: Wolff, Jon   |  |
| ; APPLICANT: Wakefield, Darren  |  |
| ; APPLICANT: Ekena, Kirk  |  |
| ; APPLICANT: Hagstrom, James  |  |
| ; TITLE OF INVENTION: Reversible Modification of Membrane Interaction                   |  |
| ; FILE REFERENCE: Mirus.035.01.3  |  |
| ; CURRENT APPLICATION NUMBER: US/11/312,319   |  |
| ; CURRENT FILING DATE: 2005-12-20   |  |
| ; NUMBER OF SEQ ID NOS: 9   |  |
| ; SOFTWARE: PatentIn version 3.3  |  |
| ; SEQ ID NO 3   |  |
| ; LENGTH: 4   |  |
| ; TYPE: PRT   |  |
| ; ORGANISM: Homo sapiens  |  |
| US-11-312-319-3   |  |
| Query Match 100.0%; Score 20; DB 6; Length 4;   |  |
| Best Local Similarity 100.0%; Pred. No. 4e+05;  |  |
| Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                              |  |
| QY 1 KDEL 4   |  |
| DB 1 KDEL 4   |  |
| RESULT 19   |  |
| US-11-326-148-16  |  |
| ; Sequence 16, Application US/11326148  |  |
| ; GENERAL INFORMATION:  |  |
| ; APPLICANT: JUNE, CARL H.  |  |
| ; APPLICANT: THOMPSON, CRAIG B.   |  |
| ; APPLICANT: NABEL, GARY J.   |  |
| ; APPLICANT: GRAY, GARY S.  |  |
| ; APPLICANT: RENNERT, PAUL D.   |  |
| ; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING PROLIFERATION OF T            |  |
| ; FILE OF INVENTION: CELLS  |  |
| ; FILE REFERENCE: 36119.125 US13  |  |
| ; CURRENT APPLICATION NUMBER: US/11/326,148   |  |
| ; CURRENT FILING DATE: 2006-01-05   |  |
| ; PRIOR APPLICATION NUMBER: US/11/029,188   |  |
| ; PRIOR FILING DATE: 2005-01-04   |  |
| ; PRIOR APPLICATION NUMBER: 08/592,711  |  |
| ; PRIOR FILING DATE: 1996-01-26   |  |
| ; PRIOR APPLICATION NUMBER: 08/435,816  |  |
| ; PRIOR FILING DATE: 1995-05-04   |  |
| ; PRIOR APPLICATION NUMBER: 08/403,253  |  |
| ; PRIOR FILING DATE: 1995-03-10   |  |
| ; PRIOR APPLICATION NUMBER: 08/253,964  |  |
| ; PRIOR FILING DATE: 1994-06-03   |  |
| ; PRIOR APPLICATION NUMBER: 08/073,223  |  |
| ; PRIOR FILING DATE: 1993-06-04   |  |
| ; PRIOR APPLICATION NUMBER: 07/864,866  |  |
| ; PRIOR FILING DATE: 1992-04-07   |  |
| ; PRIOR APPLICATION NUMBER: 07/864,807  |  |
| ; PRIOR FILING DATE: 1992-04-07   |  |
| ; PRIOR APPLICATION NUMBER: 07/864,805  |  |
| ; PRIOR FILING DATE: 1992-04-07   |  |
| ; PRIOR APPLICATION NUMBER: 07/275,433  |  |
| ; PRIOR FILING DATE: 1988-11-23   |  |
| ; NUMBER OF SEQ ID NOS: 16  |  |
| ; SOFTWARE: PatentIn Ver. 3.3   |  |
| ; SEQ ID NO 16  |  |
| ; LENGTH: 4   |  |
| ; TYPE: PRT   |  |
| ; ORGANISM: Artificial Sequence   |  |
| ; FEATURE:  |  |
| ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic                      |  |
| ; OTHER INFORMATION: peptide  |  |
| US-11-326-148-16  |  |

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 20  
US-11-324-947-44  
; Sequence 44, Application US/11324947  
; GENERAL INFORMATION:  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; APPLICANT: FITCHEN, JOHN H.  
; TITLE OF INVENTION: J CHAIN POLYPEPTIDE TARGETING MOLECULE LINKED TO AN IMAGING AGENT  
; FILE REFERENCE: EPI3003C  
; CURRENT APPLICATION NUMBER: US/11/324,947  
; CURRENT FILING DATE: 2006-01-04  
; PRIOR APPLICATION NUMBER: US/10/062,467  
; PRIOR FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 08/782,480  
; PRIOR FILING DATE: 1997-01-10  
; PRIOR APPLICATION NUMBER: 09/005,167  
; PRIOR FILING DATE: 1998-01-09  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Intracellular  
; OTHER INFORMATION: targeting signal  
US-11-324-947-44

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 21  
US-11-053-045-1  
; Sequence 1, Application US/11053045  
; GENERAL INFORMATION:  
; APPLICANT: Denescke, Jurgen  
; APPLICANT: Jelitto, Edith  
; TITLE OF INVENTION: Enhancing Plant Pathogen Resistance via Increasing BiP Levels  
; FILE REFERENCE: 9052.94  
; CURRENT APPLICATION NUMBER: US/11/053,045  
; CURRENT FILING DATE: 2005-02-08  
; PRIOR APPLICATION NUMBER: US/09/868,434  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: GB9827480.6  
; PRIOR FILING DATE: 1998-12-15  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: mammalian  
US-11-053-045-1

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 22  
US-11-046-590A-12  
; Sequence 12, Application US/11046590A  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Bio Corporation  
; APPLICANT: Trubetskoy, Vladimir  
; APPLICANT: Buckner, Vladimir  
; APPLICANT: Wolff, Jon  
; APPLICANT: Hagstrom, James  
; APPLICANT: Rozema, David  
; APPLICANT: Monahan, Sean  
; TITLE OF INVENTION: Compositions and Methods for Drug Delivery Using pH Sensitive  
; TITLE OF INVENTION: Molecules  
; FILE REFERENCE: Mirus.009.05.8  
; CURRENT APPLICATION NUMBER: US/11/046,590A  
; CURRENT FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: 10/095,680  
; PRIOR FILING DATE: 2002-03-11  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 12  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-046-590A-12

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

RESULT 23  
US-11-154-103-26  
; Sequence 26, Application US/11154103  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, GREGORY P.  
; APPLICANT: HORAK, EVA M.  
; APPLICANT: WEINER, LOUIS M.  
; APPLICANT: JAMES, MARKS D.  
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 407T-000420US  
; CURRENT APPLICATION NUMBER: US/11/154,103  
; CURRENT FILING DATE: 2005-06-15  
; PRIOR APPLICATION NUMBER: US 60/370,276  
; PRIOR FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: US10/406,830  
; PRIOR FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 26  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Translocation signaling sequence.  
US-11-154-103-26

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

Db 1 KDEL 4

RESULT 24  
US-11-334-622-49  
; Sequence 49, Application US/11334622  
; GENERAL INFORMATION:  
; APPLICANT: Tsien, Roger Y.  
; APPLICANT: Miyawaki, Atsushi  
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR  
; TITLE OF INVENTION: DETECTION OF ANALYTES  
; FILE REFERENCE: 07257/042001  
; CURRENT APPLICATION NUMBER: US/11/334,622  
; CURRENT FILING DATE: 2006-01-17  
; PRIOR APPLICATION NUMBER: US/09/554,000  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 08/818,252  
; PRIOR FILING DATE: 1997-03-14  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-334-622-49

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
Db 1 KDEL 4

RESULT 25  
US-11-244-348A-3  
; Sequence 3, Application US/11244348A  
; GENERAL INFORMATION:  
; APPLICANT: Misny, Randall J.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMMUNIZING  
; TITLE OF INVENTION: AGAINST PSEUDOMONAS INFECTION  
; FILE REFERENCE: 10901-015-999  
; CURRENT APPLICATION NUMBER: US/11/244,348A  
; CURRENT FILING DATE: 2005-10-04  
; PRIOR APPLICATION NUMBER: 60/616,125  
; PRIOR FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Pseudomonas sp.  
US-11-244-348A-3

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
Db 1 KDEL 4

RESULT 26  
US-11-211-723-22  
; Sequence 22, Application US/11211723  
; GENERAL INFORMATION:  
; APPLICANT: CLARK, PATRICIA L.  
; APPLICANT: EVANS, MICHAEL S.  
; APPLICANT: UGRINOV, KRASTYU G.  
; APPLICANT: CLARKE, IV, THOMAS F.  
; APPLICANT: FRESE, MARC-ANDRE

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
Db 1 KDEL 4

RESULT 27  
US-11-344-466-6  
; Sequence 6, Application US/11344466  
; GENERAL INFORMATION:  
; APPLICANT: Fey, Georg H.  
; APPLICANT: Peipp, Matthias  
; APPLICANT: Schwemmler, Michael  
; TITLE OF INVENTION: CD19-Specific Immunotoxin and Treatment Method  
; FILE REFERENCE: 59849-8005  
; CURRENT APPLICATION NUMBER: US/11/344,466  
; CURRENT FILING DATE: 2006-01-30  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic transport sequence  
US-11-344-466-6

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
Db 1 KDEL 4

RESULT 28  
US-11-352-733-6  
; Sequence 6, Application US/11352733  
; GENERAL INFORMATION:  
; APPLICANT: AUBURN UNIVERSITY  
; APPLICANT: UNIVERSITY OF CENTRAL FLORIDA  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS  
; FILE REFERENCE: 1463-PCT-US-00  
; CURRENT APPLICATION NUMBER: US/11/352,733  
; CURRENT FILING DATE: 2006-02-13  
; PRIOR APPLICATION NUMBER: US/09/807,721  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: PCT/US01/06274  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
Db 1 KDEL 4



; SEQ ID NO 6  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-11-352-733-6

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 29

US-11-361-631-24  
; Sequence 24, Application US/11361631

; GENERAL INFORMATION:  
; APPLICANT: Lorens, James B.  
; APPLICANT: Kinsella, Todd  
; APPLICANT: Masuda, Esteban  
; APPLICANT: Hitoshi, Yasumichi  
; APPLICANT: Liao, X. Charlene  
; APPLICANT: Pearsall, Denise  
; APPLICANT: Freira, Annabelle  
; APPLICANT: Chu, Peter  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ALTERED CELLULAR PHENOC  
; FILE REFERENCE: A-71158/RMS/DCF  
; CURRENT APPLICATION NUMBER: US/11/361,631  
; CURRENT FILING DATE: 2006-02-24  
; PRIOR APPLICATION NUMBER: US/10/096,339  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: US 09/076,624  
; PRIOR FILING DATE: 1998-05-12  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-361-631-24

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 30

US-10-432-412A-23  
; Sequence 23, Application US/10432412A

; GENERAL INFORMATION:  
; APPLICANT: FitzGerald, David J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: A Chimeric Protein Comprising Non-Toxic Pseudomonas  
; TITLE OF INVENTION: Exocoxin A and Type IV Pilin Sequences  
; FILE REFERENCE: 015280-429100US  
; CURRENT APPLICATION NUMBER: US/10/432,412A  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/257,877  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: WO PCT/US01/49143  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic  
; OTHER INFORMATION: reticulum (ER) retention domain  
US-10-432-412A-23

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 31

US-10-565-771-12  
; Sequence 12, Application US/10565771

; GENERAL INFORMATION:  
; APPLICANT: Kinch, Michael S.  
; TITLE OF INVENTION: DIAGNOSIS OF PRE-CANCEROUS CONDITIONS  
; TITLE OF INVENTION: AND USING PCDF AGENTS  
; FILE REFERENCE: 10271-131-999  
; CURRENT APPLICATION NUMBER: US/10/565,771  
; CURRENT FILING DATE: 2006-01-23  
; PRIOR APPLICATION NUMBER: 60/489,035  
; PRIOR FILING DATE: 2003-07-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Localization signal used to direct intrabody to endoplasmic ret  
US-10-565-771-12

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 1 KDEL 4

## RESULT 32

US-10-147-368B-43  
; Sequence 43, Application US/10147368B

; GENERAL INFORMATION:  
; APPLICANT: JAKOBOVITS, Aya  
; APPLICANT: FARIS, Mary  
; APPLICANT: RAITANO, Arthur B.  
; APPLICANT: MORRISON, Robert Kendall  
; APPLICANT: SAFFRAN, Douglas  
; APPLICANT: GE, Wangmao  
; APPLICANT: CHALITA-EID, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS  
; TITLE OF INVENTION: ENTITLED 101P3A11 or PHOR-1 USEFUL IN TREATMENT AND  
; TITLE OF INVENTION: DETECTION OF CANCER  
; FILE REFERENCE: 51158-20024.21  
; CURRENT APPLICATION NUMBER: US/10/147,368B  
; CURRENT FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: US 10/017,066  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 10/001,469  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: US 60/291,118  
; PRIOR FILING DATE: 2001-05-15

```
; PRIOR APPLICATION NUMBER: US 09/680,728
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/157,902
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-147-368B-43

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 33
US-10-533-266-2
; Sequence 2, Application US/10533266
; GENERAL INFORMATION:
; APPLICANT: FREEMAN, MATTHEW
; TITLE OF INVENTION: PROTOZOAN RHOMBOID PROTEINS
; FILE REFERENCE: MEWE-022
; CURRENT APPLICATION NUMBER: US/10/533,266
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 60/422,861
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic motif
US-10-533-266-2

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 34
US-10-500-264-1
; Sequence 1, Application US/10500264
; GENERAL INFORMATION:
; APPLICANT: Mahn, Andreas
; APPLICANT: Hantke, Sabine
; APPLICANT: Petsch, Dagmar
; TITLE OF INVENTION: Method of Increasing the Transgene-Coded Biomolecule Content in
; TITLE OF INVENTION: Organisms
; FILE REFERENCE: 4121-168
; CURRENT APPLICATION NUMBER: US/10/500,264
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/EP02/14512
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: EP 0 113 0319.5
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial

; FEATURE:
; OTHER INFORMATION: signal polypeptide
US-10-500-264-1

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 35
US-10-189-360A-42
; Sequence 42, Application US/10189360A
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS
; TITLE OF INVENTION: AND LIGANDS FOR THERAPEUTIC TREATMENT
; FILE REFERENCE: 760100.415C4
; CURRENT APPLICATION NUMBER: US/10/189,360A
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/449,249
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: US 08/718,904
; PRIOR FILING DATE: 1996-09-24
; PRIOR APPLICATION NUMBER: US 08/441,979
; PRIOR FILING DATE: 1995-05-16
; PRIOR APPLICATION NUMBER: US 08/305,771
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 08/297,961
; PRIOR FILING DATE: 1994-08-29
; PRIOR APPLICATION NUMBER: US 08/213,446
; PRIOR FILING DATE: 1994-03-15
; PRIOR APPLICATION NUMBER: US 08/213,447
; PRIOR FILING DATE: 1994-03-15
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: Signal sequence in mammalian cells (cytoplasmic
; OTHER INFORMATION: translocation signal)
US-10-189-360A-42

Query Match 100.0%; Score 20; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 1 KDEL 4

RESULT 36
US-10-428-339B-42
; Sequence 42, Application US/10428339B
; GENERAL INFORMATION:
; APPLICANT: KENWARD, Kimberly D.
; APPLICANT: SHAH, Salehzzaman
; TITLE OF INVENTION: Production of Recombinant Epidermal Growth Factor in Plants
; FILE REFERENCE: 07121.0005U2
; CURRENT APPLICATION NUMBER: US/10/428,339B
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,294
; PRIOR FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for windows Version 4.0
```

; SEQ ID NO 42  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; note =  
US-10-428-339B-42  
; OTHER INFORMATION: synthetic construct

Query Match 100.0%; Score 20; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDEL 4  
Db 1 KDEL 4

RESULT 37  
US-11-368-804-52  
; Sequence 52, Application US/11368804  
; GENERAL INFORMATION:  
; APPLICANT: VIRGIN, HERBERT W.  
; TITLE OF INVENTION: MURINE CALICIVIRUS  
; FILE REFERENCE: 56029-45752  
; CURRENT APPLICATION NUMBER: US/11/368,804  
; CURRENT FILING DATE: 2006-03-06  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE: 2006-03-06  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 52  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Illustrative MNV-1 ORF1 motif  
US-11-368-804-52

Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDEL 4  
Db 1 KDEL 4

RESULT 38  
US-11-271-235-6  
; Sequence 6, Application US/11271235  
; GENERAL INFORMATION:  
; APPLICANT: Geirgros, Tillman U.  
; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED  
; TITLE OF INVENTION: GLYCOPROTEINS  
; FILE REFERENCE: GFI 100 DIV3  
; CURRENT APPLICATION NUMBER: US/11/271,235  
; CURRENT FILING DATE: 2005-11-10  
; PRIOR APPLICATION NUMBER: US 09/892,591  
; PRIOR FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: US 60/214,358  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: US 60/215,638  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/279,997  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Signal tetrapeptide  
US-11-271-235-6

Query Match 100.0%; Score 20; DB 7; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDEL 4  
Db 1 KDEL 4

RESULT 39  
US-11-335-891-113  
; Sequence 113, Application US/11335891  
; GENERAL INFORMATION:  
; APPLICANT: HALLENBECK, PAUL  
; TITLE OF INVENTION: SENECA VALLEY VIRUS BASED COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: 287037.127US2  
; CURRENT APPLICATION NUMBER: US/11/335,891  
; CURRENT FILING DATE: 2006-01-19  
; PRIOR APPLICATION NUMBER: 60/506,182  
; PRIOR FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: PCT/US2004/031504  
; PRIOR FILING DATE: 2004-09-23  
; PRIOR APPLICATION NUMBER: 60/664,442  
; PRIOR FILING DATE: 2005-03-23  
; PRIOR APPLICATION NUMBER: 60/726,313  
; PRIOR FILING DATE: 2005-10-13  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 113  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Seneca Valley Virus  
US-11-335-891-113

Query Match 100.0%; Score 20; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDEL 4  
Db 1 KDEL 4

RESULT 40  
US-60-773-847-38  
; Sequence 38, Application US/60773847  
; GENERAL INFORMATION:  
; APPLICANT: Syngentas Participations AG  
; APPLICANT: Johnson, Brian  
; APPLICANT: Chalk, Tanya  
; APPLICANT: Samoylov, Vladimir  
; APPLICANT: Meghji, Moez  
; TITLE OF INVENTION: Corn Event 3272 and Methods of Detection Thereof  
; FILE REFERENCE: 70648  
; CURRENT APPLICATION NUMBER: US/60/773,847  
; CURRENT FILING DATE: 2006-02-16  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 38  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-60-773-847-38

Query Match 100.0%; Score 20; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDEL 4

Db 3 KDEL 6  
|||||

RESULT 41  
PCT-US04-04340-108  
; Sequence 108, Application PC/TUS0404340  
; GENERAL INFORMATION:  
; APPLICANT: Antigenics, Inc.  
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND  
; TITLE OF INVENTION: IMMUNOTHERAPIES  
; FILE REFERENCE: 8449-405-228  
; CURRENT APPLICATION NUMBER: PCT/US04/04340  
; CURRENT FILING DATE: 2004-02-13  
; PRIOR APPLICATION NUMBER: 60/503,417  
; PRIOR FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: 60/463,746  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: 60/462,469  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 60/447,142  
; PRIOR FILING DATE: 2003-02-13  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 108  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: P. falciparum  
PCT-US04-04340-108

Query Match 100.0%; Score 20; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||||  
Db 3 KDEL 6

RESULT 42  
PCT-US04-04340-109  
; Sequence 109, Application PC/TUS0404340  
; GENERAL INFORMATION:  
; APPLICANT: Antigenics, Inc.  
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND  
; TITLE OF INVENTION: IMMUNOTHERAPIES  
; FILE REFERENCE: 8449-405-228  
; CURRENT APPLICATION NUMBER: PCT/US04/04340  
; CURRENT FILING DATE: 2004-02-13  
; PRIOR APPLICATION NUMBER: 60/503,417  
; PRIOR FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: 60/463,746  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: 60/462,469  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 60/447,142  
; PRIOR FILING DATE: 2003-02-13  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 109  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: P. falciparum  
PCT-US04-04340-109

Query Match 100.0%; Score 20; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||||  
Db 3 KDEL 6

RESULT 43  
US-10-537-642-272  
; Sequence 272, Application US/10537642  
; GENERAL INFORMATION:  
; APPLICANT: Epimmune, Inc.  
; APPLICANT: The United States of America as Represented by the  
; APPLICANT: Secretary of the Navy  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Doonan, Denise L.  
; APPLICANT: Carucci, Daniel J.  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE  
; FILE REFERENCE: EPI-103X  
; CURRENT APPLICATION NUMBER: US/10/537,642  
; CURRENT FILING DATE: 2005-06-06  
; PRIOR APPLICATION NUMBER: US 60/431,494  
; PRIOR FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1161  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 272  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Plasmodium falciparum  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(9)  
; OTHER INFORMATION: Peptide No. 98.0257  
US-10-537-642-272

Query Match 100.0%; Score 20; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||||  
Db 5 KDEL 8

RESULT 44  
PCT-US05-40707-26  
; Sequence 26, Application PC/TUS0540707  
; GENERAL INFORMATION:  
; APPLICANT: diadexus, Inc.  
; APPLICANT: Pilkington, Glenn  
; APPLICANT: Keller, Gilbert-Andre  
; APPLICANT: Li, Wenlu  
; APPLICANT: Burcham, Timothy S  
; APPLICANT: Corral, Laura  
; APPLICANT: Simon, Iris  
; APPLICANT: Papkoff, Jackie  
; TITLE OF INVENTION: Ovr110 Antibody Compositions and Methods of Use  
; FILE REFERENCE: DEX0519W0  
; CURRENT APPLICATION NUMBER: PCT/US05/40707  
; CURRENT FILING DATE: 2005-11-17  
; PRIOR APPLICATION NUMBER: US 60/626,817  
; PRIOR FILING DATE: 2004-11-10  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
PCT-US05-40707-26

Query Match 100.0%; Score 20; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4

```
Db      |||||
       7 KDEL 10

RESULT 45
US-60-772-986-9632
; Sequence 9632, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tangyu
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9632
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-9632

Query Match      100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      4 KDEL 7

RESULT 46
US-60-772-986-14015
; Sequence 14015, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tangyu
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14015
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-14015

Query Match      100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      4 KDEL 7

RESULT 47
US-60-772-986-15264
; Sequence 15264, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tangyu
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15264
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-15264

Query Match      100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      14 KDEL 17

RESULT 48
US-60-772-986-15721
; Sequence 15721, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tangyu
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15721
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-15721

Query Match      100.0%; Score 20; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
Db      14 KDEL 17

RESULT 49
US-60-772-986-16508
; Sequence 16508, Application US/60772986
; GENERAL INFORMATION:
; APPLICANT: Dunker, A. Keith
; APPLICANT: Uversky, Vladimir N.
; APPLICANT: Cheng, Yugong
; APPLICANT: Le Gall, Tangyu
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF
; FILE REFERENCE: 670098.405P1
; CURRENT APPLICATION NUMBER: US/60/772,986
; CURRENT FILING DATE: 2006-02-14
; NUMBER OF SEQ ID NOS: 24337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16508
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-772-986-16508

Query Match      100.0%; Score 20; DB 8; Length 19;
```

Best Local Similarity 100.0%; Pred. No. 70;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 14 KDEL 17

RESULT 50  
US-60-772-986-16515  
; Sequence 16515, Application US/60772986  
; GENERAL INFORMATION:  
; APPLICANT: Dunker, A. Keith  
; APPLICANT: Uversky, Vladimir N.  
; APPLICANT: Cheng, Yugong  
; APPLICANT: Le Gall, Tanguy  
; TITLE OF INVENTION: INTRINSICALLY DISORDERED SITES OF  
; FILE REFERENCE: 670098.405P1  
; CURRENT APPLICATION NUMBER: US/60/772,986  
; CURRENT FILING DATE: 2006-02-14  
; NUMBER OF SEQ ID NOS: 24337  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16515  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-772-986-16515

Query Match 100.0%; Score 20; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 14 KDEL 17

Search completed: March 20, 2006, 07:53:22  
Job time : 17.5 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:59 ; Search time 15 Seconds  
(without alignments)  
25.658 Million cell updates/sec

Title: US-09-673-707-9  
Perfect score: 20  
Sequence: 1 KDEL 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID    | Description        |
|------------|-------|---------|--------------|----------|--------------------|
| 1          | 20    | 100.0   | 35           | 2 JX0200 | gummarin - Gymnema |
| 2          | 20    | 100.0   | 38           | 2 C60657 | circumsporozoite p |
| 3          | 20    | 100.0   | 38           | 2 B60657 | circumsporozoite p |
| 4          | 20    | 100.0   | 38           | 2 A38869 | circumsporozoite p |
| 5          | 20    | 100.0   | 41           | 2 B37188 | major body fluid a |
| 6          | 20    | 100.0   | 46           | 2 S39239 | cholera enterotoxi |
| 7          | 20    | 100.0   | 50           | 2 S19624 | ornatin E - leech  |
| 8          | 20    | 100.0   | 50           | 2 AH2496 | transposase asr715 |
| 9          | 20    | 100.0   | 52           | 2 S19623 | ornatin C - leech  |
| 10         | 20    | 100.0   | 54           | 2 E96530 | hypothetical prote |
| 11         | 20    | 100.0   | 58           | 2 A35416 | DNA topoisomerase  |
| 12         | 20    | 100.0   | 58           | 2 AD3018 | conserved hypothet |
| 13         | 20    | 100.0   | 60           | 2 AE2387 | hypothetical prote |
| 14         | 20    | 100.0   | 62           | 2 D69384 | hypothetical prote |
| 15         | 20    | 100.0   | 63           | 2 S11883 | copB protein - Esc |
| 16         | 20    | 100.0   | 65           | 2 AI2513 | hypothetical prote |
| 17         | 20    | 100.0   | 67           | 2 JU0399 | rflA.1 protein - p |
| 18         | 20    | 100.0   | 68           | 2 G97737 | hypothetical prote |
| 19         | 20    | 100.0   | 70           | 2 AC2866 | hypothetical prote |
| 20         | 20    | 100.0   | 71           | 2 D81389 | conserved hypothet |
| 21         | 20    | 100.0   | 72           | 2 E81126 | hypothetical prote |
| 22         | 20    | 100.0   | 76           | 2 D84167 | hypothetical prote |
| 23         | 20    | 100.0   | 77           | 2 D69010 | hypothetical prote |
| 24         | 20    | 100.0   | 78           | 2 S69531 | holin protein - ph |
| 25         | 20    | 100.0   | 79           | 1 JN0246 | calcium-binding pr |
| 26         | 20    | 100.0   | 79           | 2 B90352 | partial ORF from I |
| 27         | 20    | 100.0   | 79           | 2 D75326 | hypothetical prote |
| 28         | 20    | 100.0   | 79           | 2 AG2544 | hypothetical prote |
| 29         | 20    | 100.0   | 80           | 2 C69204 | hypothetical prote |

|     |    |       |     |          |                     |
|-----|----|-------|-----|----------|---------------------|
| 30  | 20 | 100.0 | 81  | 2 S77318 | secretory protein   |
| 31  | 20 | 100.0 | 82  | 2 JT0765 | rapid lysal III pr  |
| 32  | 20 | 100.0 | 82  | 2 D64329 | hypothetical prote  |
| 33  | 20 | 100.0 | 83  | 2 F82891 | hypothetical prote  |
| 34  | 20 | 100.0 | 83  | 2 F82887 | hypothetical prote  |
| 35  | 20 | 100.0 | 85  | 2 I40586 | hypothetical prote  |
| 36  | 20 | 100.0 | 85  | 2 T39536 | probable involveme  |
| 37  | 20 | 100.0 | 86  | 1 WMEC5R | replication contro  |
| 38  | 20 | 100.0 | 89  | 2 S05557 | hypothetical prote  |
| 39  | 20 | 100.0 | 90  | 2 T04077 | probable ribosomal  |
| 40  | 20 | 100.0 | 90  | 2 AC1030 | hypothetical prote  |
| 41  | 20 | 100.0 | 91  | 2 E59100 | hypothetical prote  |
| 42  | 20 | 100.0 | 92  | 2 H84264 | hypothetical prote  |
| 43  | 20 | 100.0 | 92  | 2 H84296 | hypothetical prote  |
| 44  | 20 | 100.0 | 93  | 2 T08319 | conserved hypothet  |
| 45  | 20 | 100.0 | 93  | 2 AG2290 | hypothetical prote  |
| 46  | 20 | 100.0 | 94  | 2 S60798 | M protein precursor |
| 47  | 20 | 100.0 | 94  | 2 G86415 | hypothetical prote  |
| 48  | 20 | 100.0 | 95  | 2 S61076 | M protein precursor |
| 49  | 20 | 100.0 | 95  | 2 F97179 | uncharacterized pr  |
| 50  | 20 | 100.0 | 97  | 1 ZCBPT9 | gene 55.5 protein   |
| 51  | 20 | 100.0 | 99  | 2 S71520 | M protein type 18   |
| 52  | 20 | 100.0 | 100 | 2 E90355 | hypothetical prote  |
| 53  | 20 | 100.0 | 100 | 2 A99372 | hypothetical prote  |
| 54  | 20 | 100.0 | 101 | 2 S74523 | hypothetical prote  |
| 55  | 20 | 100.0 | 103 | 2 D64450 | conserved hypothet  |
| 56  | 20 | 100.0 | 103 | 2 T40768 | very hypothetical   |
| 57  | 20 | 100.0 | 103 | 2 E86853 | hypothetical prote  |
| 58  | 20 | 100.0 | 103 | 2 H95245 | hypothetical prote  |
| 59  | 20 | 100.0 | 103 | 2 E98110 | hypothetical prote  |
| 60  | 20 | 100.0 | 104 | 2 D42721 | recombination prot  |
| 61  | 20 | 100.0 | 105 | 2 E64343 | hypothetical prote  |
| 62  | 20 | 100.0 | 105 | 2 B70712 | hypothetical prote  |
| 63  | 20 | 100.0 | 106 | 2 C69772 | thioredoxin homolo  |
| 64  | 20 | 100.0 | 107 | 2 A81595 | hypothetical prote  |
| 65  | 20 | 100.0 | 107 | 2 B96906 | hypothetical prote  |
| 66  | 20 | 100.0 | 108 | 2 D90051 | hypothetical prote  |
| 67  | 20 | 100.0 | 108 | 2 E89993 | hypothetical prote  |
| 68  | 20 | 100.0 | 109 | 2 A83265 | conserved hypothet  |
| 69  | 20 | 100.0 | 110 | 1 R6SP2  | acidic ribosomal p  |
| 70  | 20 | 100.0 | 110 | 2 A96907 | hypothetical prote  |
| 71  | 20 | 100.0 | 111 | 2 S10222 | hypothetical prote  |
| 72  | 20 | 100.0 | 111 | 2 C90308 | hypothetical prote  |
| 73  | 20 | 100.0 | 112 | 2 A64434 | hypothetical prote  |
| 74  | 20 | 100.0 | 112 | 2 S75739 | hypothetical prote  |
| 75  | 20 | 100.0 | 112 | 2 AH2211 | hypothetical prote  |
| 76  | 20 | 100.0 | 113 | 2 G72566 | hypothetical prote  |
| 77  | 20 | 100.0 | 114 | 1 JQ2242 | thioredoxin h - Ar  |
| 78  | 20 | 100.0 | 116 | 1 S34611 | nitrogenase (EC 1.  |
| 79  | 20 | 100.0 | 116 | 2 T10739 | thioredoxin - comm  |
| 80  | 20 | 100.0 | 116 | 2 G64056 | arsenate reductase  |
| 81  | 20 | 100.0 | 116 | 2 G64433 | hypothetical prote  |
| 82  | 20 | 100.0 | 116 | 2 A86769 | dihydroneopterin a  |
| 83  | 20 | 100.0 | 117 | 2 S75764 | hypothetical prote  |
| 84  | 20 | 100.0 | 118 | 1 S34812 | thioredoxin h2 - c  |
| 85  | 20 | 100.0 | 118 | 2 T10170 | thioredoxin - cast  |
| 86  | 20 | 100.0 | 118 | 2 I45348 | V118 protein - Afr  |
| 87  | 20 | 100.0 | 118 | 2 C84181 | hypothetical prote  |
| 88  | 20 | 100.0 | 119 | 2 B82782 | hypothetical prote  |
| 89  | 20 | 100.0 | 121 | 1 C69190 | conserved hypothet  |
| 90  | 20 | 100.0 | 121 | 2 AB2314 | ferredoxin-thioeth  |
| 91  | 20 | 100.0 | 121 | 2 S18067 | thyroid hormone re  |
| 92  | 20 | 100.0 | 121 | 2 T31718 | hypothetical prote  |
| 93  | 20 | 100.0 | 121 | 2 T32378 | hypothetical prote  |
| 94  | 20 | 100.0 | 121 | 2 S72496 | transcription acti  |
| 95  | 20 | 100.0 | 121 | 2 S65809 | transcription acti  |
| 96  | 20 | 100.0 | 121 | 2 S65808 | transcription acti  |
| 97  | 20 | 100.0 | 122 | 2 S40152 | thyroid hormone re  |
| 98  | 20 | 100.0 | 122 | 2 AB2199 | hypothetical prote  |
| 99  | 20 | 100.0 | 122 | 2 B70397 | hypothetical prote  |
| 100 | 20 | 100.0 | 123 | 2 JQ0368 | ribosomal protein   |
| 101 | 20 | 100.0 | 124 | 2 S70043 | hypothetical prote  |
| 102 | 20 | 100.0 | 125 | 2 T29941 | hypothetical prote  |

103 20 100.0 126 2 T06861 ribosomal protein  
104 20 100.0 127 1 RDA8YUN ubiquinol-cytochro  
105 20 100.0 127 2 A12120 glycerol-3-phospha  
106 20 100.0 127 1 R32388 hypothetical prote  
107 20 100.0 130 1 R3EC8 ribosomal protein  
108 20 100.0 130 2 JC2280 30S ribosomal chai  
109 20 100.0 130 2 AG1007 30S ribosomal subu  
110 20 100.0 130 2 C91150 30S ribosomal subu  
111 20 100.0 130 2 G85995 ribosomal protein  
112 20 100.0 130 2 H82057 ribosomal protein  
113 20 100.0 130 2 A64094 30S ribosomal prot  
114 20 100.0 130 2 AH0027 ribosomal protein  
115 20 100.0 130 2 A69132 DNA-packaging prot  
116 20 100.0 132 1 JVBFFL probable DNA-packa  
117 20 100.0 132 2 E90900 DNA packaging prot  
118 20 100.0 132 2 D90833 thioredoxin (clone  
119 20 100.0 133 2 S58123 hypothetical prote  
120 20 100.0 133 2 H70646 conserved hypothet  
121 20 100.0 133 2 H82366 FK506-binding prot  
122 20 100.0 134 1 JT0748 4-carboxymuconolac  
123 20 100.0 134 2 B35119 hypothetical prote  
124 20 100.0 134 2 C84385 ribosomal protein  
125 20 100.0 135 2 S48410 hypothetical prote  
126 20 100.0 135 2 D69830 flagellar protein  
127 20 100.0 136 1 B64956 flagellar protein  
128 20 100.0 136 2 H90961 hypothetical prote  
129 20 100.0 136 2 H85809 hypothetical prote  
130 20 100.0 138 1 C64005 hypothetical prote  
131 20 100.0 138 2 JC6308 glia maturation fa  
132 20 100.0 138 2 JC4597 signal transductio  
133 20 100.0 139 2 G69543 conserved hypothet  
134 20 100.0 140 2 C95277 hypothetical prote  
135 20 100.0 141 1 JDBOB glia maturation fa  
136 20 100.0 141 1 S22149 glia maturation fa  
137 20 100.0 141 2 F72778 hypothetical prote  
138 20 100.0 141 2 A96491 hypothetical prote  
139 20 100.0 142 1 PT0410 glia maturation fa  
140 20 100.0 144 2 E71724 hypothetical prote  
141 20 100.0 144 2 A90056 hypothetical prote  
142 20 100.0 144 2 FC7027 aggrutin alpha cha  
143 20 100.0 145 2 F85690 hypothetical prote  
144 20 100.0 145 2 S38235 mucin-like endothe  
145 20 100.0 146 2 A47167 hypothetical prote  
146 20 100.0 146 2 H83244 hypothetical prote  
147 20 100.0 146 2 E88470 protein C28hg.1 [i  
148 20 100.0 146 2 C86187 YUP8H12.12 [import  
149 20 100.0 147 2 D69368 conserved hypothet  
150 20 100.0 147 2 A11030 probable lipoprote

ALIGNMENTS

RESULT 1  
JX0200  
gurmardin - Gymnema sylvestre  
N:Alternate names: sweet-taste-suppressing peptide  
C:Species: Gymnema sylvestre  
C:Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 09-Jul-2004  
C:Accession: JX0200  
R:Kamei, K.; Takano, R.; Miyasaka, A.; Imoto, T.; Hara, S.  
J. Biochem. 111, 109-112, 1992  
A:Title: Amino acid sequence of sweet-taste-suppressing peptide (gurmardin) from the leav  
A:Reference number: JX0200; MUID:92299642; PMID:1607357  
A:Accession: JX0200  
A:Molecule type: protein  
A:Residues: 1-35 <LOC>  
A:Cross-references: UNIPROT:P25810; UNIPARC:UPI000012BE09  
A:Experimental source: leaf  
C:Comment: This protein suppresses sweet taste.  
C:Keywords: pyroglutamic acid; sweet taste  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 100.0%; Score 20; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KDEL 4  
Db 6 KDEL 9  
  
RESULT 2  
C60657  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate 7G8) (frag  
C:Species: Plasmodium falciparum  
C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jun-2000  
C:Accession: C60657  
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.  
Mol. Biochem. Parasitol. 37, 275-280, 1989  
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell  
A:Reference number: A60657; MUID:90114334; PMID:2481827  
A:Accession: C60657  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-38 <LOC>  
A:Cross-references: UNIPARC:UPI0000177F70  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
  
Query Match 100.0%; Score 20; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KDEL 4  
Db 28 KDEL 31  
  
RESULT 3  
B60657  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate T9-98) (fr  
C:Species: Plasmodium falciparum  
C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jul-2004  
C:Accession: B60657  
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.  
Mol. Biochem. Parasitol. 37, 275-280, 1989  
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell  
A:Reference number: A60657; MUID:90114334; PMID:2481827  
A:Accession: B60657  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-38 <LOC>  
A:Cross-references: UNIPROT:Q7M3X1; UNIPARC:UPI0000177F72  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
  
Query Match 100.0%; Score 20; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KDEL 4  
Db 28 KDEL 31

RESULT 4

A38869  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate 427-5) (f  
C:Species: Plasmodium falciparum  
C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jul-2004  
C:Accession: A38869  
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.  
Mol. Biochem. Parasitol. 37, 275-280, 1989  
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell  
A:Reference number: A60657; MUID:90114334; PMID:2481827  
A:Accession: A38869  
A:Status: preliminary; not compared with conceptual translation





Mon Mar 20 08:51:26 2006

RESULT 10  
E96530  
hypothetical protein Fl3F21.16 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: E96530  
R:Theologidis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: E96530  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-54 <STO>  
A:Cross-references: UNIPROT:Q9XIA7; UNIPARC:UPI00000AC31D; GB:AE005173; NID:G5430759; P  
C:Genetics:  
A:Gene: Fl3F21.16  
A:Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
Db 47 KDEL 50

RESULT 11  
A35416  
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.13) II - bovine (fragments)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 09-Jul-2004  
C:Accession: A35416  
R:Austin, C.A.; Barot, H.A.; Margerrison, E.E.C.; Turcatti, G.; Wingfield, P.; Hayes, M.  
Biochem. Biophys. Res. Commun. 170, 763-768, 1990  
A:Title: Structure and partial amino acid sequence of calf thymus DNA topoisomerase II:  
A:Reference number: A35416; MUID:90343796; PMID:1696476  
A:Accession: A35416  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-58 <AUS>  
A:Cross-references: UNIPROT:Q7M3G2; UNIPARC:UPI000017C4F6  
C:Keywords: isomerase

Query Match 100.0%; Score 20; DB 2; Length 58;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
Db 55 KDEL 58

RESULT 12  
AD3018  
conserved hypothetical protein Atu3752 [imported] - Agrobacterium tumefaciens (strain C5  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AD3018  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
e, Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AD3018  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-58 <KUR>  
A:Cross-references: UNIPROT:Q8U9H6; UNIPARC:UPI00000D22FF; GB:AE008689; PIDN:AAL44562.1  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu3752  
A:Map position: linear chromosome

Query Match 100.0%; Score 20; DB 2; Length 58;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
Db 46 KDEL 49

RESULT 13  
AE2387  
hypothetical protein asr4653 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Notes: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AE2387  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AE2387  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-60 <KUR>  
A:Cross-references: UNIPROT:Q8YNB4; UNIPARC:UPI00000CEBDE; GB:BA000019; PIDN:BA876352.1  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: asr4653

Query Match 100.0%; Score 20; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEL 4  
Db 52 KDEL 55

RESULT 14  
D69384  
hypothetical protein AF1076 - Archaeoglobus fulgidus  
C:Species: Archaeoglobus fulgidus  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: D69384  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dods  
Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa  
A:Reference number: A69250; MUID:98049343; PMID:9389475  
A:Accession: D69384  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-62 <KLE>  
A:Cross-references: UNIPROT:O29187; UNIPARC:UPI0000056B66; GB:AE001028; GB:AE0000782; N

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Query Match      100.0%; Score 20; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
      ||||
Db      8 KDEL 11

RESULT 15
copB protein - Escherichia coli plasmid ColV2-K94
C:Species: Escherichia coli
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 30-May-1997
C:Accession: S11883
R:Banerjee, A.; Weber, P.C.; Palchaudhuri, S.
Mol. Gen. Genet. 220, 320-324, 1990
A:Title: Comparison of the CopB systems of plasmids R1 and ColV2-K94: a single base alte
A:Reference number: S11883; MUID:90220506; PMID:2325626
A:Accession: S11883
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <MOL>
A:Cross-references: UNIPARC:UPI00001787B1
C:Genetics:
A:Gene: copB
A:Genome: Plasmid ColV2-K94
C:Superfamily: repA2 protein

Query Match      100.0%; Score 20; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
      ||||
Db      53 KDEL 56

RESULT 16
hypothetical protein asl7289 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120al
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: A12513
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: A12513
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-65 <KUR>
A:Cross-references: UNIPROT:Q8YKK6; UNIPARC:UPI000000CEF75; GB:BA000020; PIDN:BA078373.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl7289
A:Genome: plasmid

Query Match      100.0%; Score 20; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
      ||||
Db      48 KDEL 51

RESULT 17
JU0399
rIIA.1 protein - phage T4
N;Alternate names: gp rIIA.1
```

```
C:Species: phage T4
A:Note: host Escherichia coli
C:Date: 21-Nov-1993 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C:Accession: JU0399
R:Daegelen, P.; Brody, E.
Genetics 125, 237-248, 1990
A:Title: The rIIA gene of bacteriophage T4. I. Its DNA sequence and discovery of a new
A:Reference number: PS0194; MUID:90337270; PMID:2379817
A:Accession: JU0399
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-67 <DAB>
A:Cross-references: UNIPROT:P25186; UNIPARC:UPI000005CAF5; GB:X52686; GB:X00905; NID:G
C:Comment: The protein is a hydrophilic and basic peptide containing alpha-helical str
C:Genetics:
A:Gene: rIIA.1
A:Map position: 2.202-2.403

Query Match      100.0%; Score 20; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
      ||||
Db      52 KDEL 55

RESULT 18
G97737
hypothetical protein RC0303 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97737
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; F
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: G97737
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <KUR>
A:Cross-references: UNIPROT:Q921W7; UNIPARC:UPI000000CBD3B; GB:AE006914; PIDN:AAL02841.1
C:Genetics:
A:Gene: RC0303

Query Match      100.0%; Score 20; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KDEL 4
      ||||
Db      26 KDEL 29

RESULT 19
AC2866
hypothetical protein Atu2357 [imported] - Agrobacterium tumefaciens (strain C58, Dupont
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AC2866
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutuyavin, T.; Levy, R.; Li, M.; McClel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AC2866
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-70 <KUR>
A:Cross-references: UNIPROT:Q8UCX6; UNIPARC:UPI000000DIE8A; GB:AE008688; PIDN:AAL43345.1
```

Mon Mar 20 08:51:26 2006

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Aru2357

A;Map position: circular chromosome

Query Match 100.0%; Score 20; DB 2; Length 70;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4

||||

Db 30 KDEL 33

RESULT 20

D81389 hypothetical protein Cj049c [imported] - Campylobacter jejuni (strain NCTC 11168)

C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C;Accession: D81389

C;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

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R.; Parkhill, J.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

## RESULT 24

holin protein - phage HP1  
C:Species: phage HP1  
C>Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S69531  
R:Exposito, D.; Fitzmaurice, W.P.; Benjamin, R.C.; Goodman, S.D.; Waldman, A.S.; Scocca, Nucleic Acids Res. 24, 2360-2368, 1996  
A>Title: The complete nucleotide sequence of bacteriophage HP1 DNA.  
A:Reference number: S69503; MUID:96279738; PMID:8710508  
A:Accession: S69531  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-78 <ESP>  
A:Cross-references: UNIPROT:P51727; UNIPARC:UPI000012CAD1; EMBL:U24159; NID:G1046235; PMID:8710508  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995  
C:Genetics: hol  
A:Gene: hol

Query Match 100.0%; Score 20; DB 2; Length 78;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4

Db 55 KDEL 58

## RESULT 25

JN0246  
calcium-binding protein, intestinal - human  
N:Alternate names: calbindin D9k; ICBP  
C:Species: Homo sapiens (man)  
C>Date: 17-Aug-1992 #sequence\_revision 06-Dec-1996 #text\_change 09-Jul-2004  
C:Accession: JN0246; S24047; I56435; S21501  
R:Howard, A.; Legon, S.; Spurr, N.K.; Walters, J.R.F. Biochem. Biophys. Res. Commun. 185, 663-669, 1992  
A>Title: Molecular cloning and chromosomal assignment of human calbindin-D9k.  
A:Reference number: JN0246; MUID:92304291; PMID:1610358  
A:Accession: JN0246  
A:Molecule type: mRNA  
A:Residues: 1-79 <HOW>  
A:Cross-references: UNIPROT:P29377; UNIPARC:UPI0000167B2D; EMBL:X65869; NID:G29601; PIDN:JN0246  
A:Experimental source: intestine  
R:Jeung, E.B.; Krisinger, J.; Dann, J.L.; Leung, P.C.K. FEBS Lett. 307, 224-228, 1992  
A>Title: Molecular cloning of the full-length cDNA encoding the human calbindin-D(9k).  
A:Reference number: S24047; MUID:92354716; PMID:1379540  
A:Accession: S24047  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-79 <JEUL>  
A:Cross-references: UNIPARC:UPI0000167B2D; GB:L13220; NID:G291883; PIDN:AAA35638.1; PID:J. Mol. Biol. 235, 1231-1238, 1994  
A>Title: The human calbindin-D9k gene: complete structure and implications on rsdsteroid  
A:Reference number: I56435; MUID:94141916; PMID:8308886  
A:Accession: I56435  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-78, 'S' <JEU2>  
A:Cross-references: UNIPARC:UPI000016A658; GB:L13042; NID:G291881; PIDN:AAA35637.1; PID:J. Mol. Biol. 235, 1231-1238, 1994  
A:Comment: This protein increases calcium absorption by buffering calcium in the cytoplasm  
C:Comment: This protein binds to the regulatory calmodulin binding domain of the plasma  
C:Genetics: hol  
A:Gene: GDB:CALB3  
A:Cross-references: GDB:133780; OMIM:302020  
A:Map position: Xp22.2-Xp22.2  
A:Introns: 45/3  
C:Superfamily: S-100 protein; calmodulin repeat homology  
C:Keywords: acetylated amino end; calcium binding; duplication; EF hand; vitamin D  
F:2-79/Product: calcium-binding protein, intestinal #status predicted <MAY>  
F:5-39/Domain: calmodulin repeat homology <EF1>

## F:45-77/Domain: calmodulin repeat homology &lt;EF2&gt;

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted  
F:18,21,23,26,31/Binding site: calcium, low affinity (Ala, Glu, Asp, Gln, Glu) #status  
F:58,60,62,64,69/Binding site: calcium, high affinity (Asp, Asn, Asp, Glu, Glu) #status:

Query Match 100.0%; Score 20; DB 1; Length 79;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4

Db 29 KDEL 32

## RESULT 26

B90352  
Partial ORF from ISC1778 [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C:Accession: B90352  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chai, J.; Jang, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J. submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: B90352  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-79 <KUR>  
A:Cross-references: UNIPROT:Q97X69; UNIPARC:UPI00000645D2; GB:AE006641; NID:G13815141;  
C:Genetics:  
A:Gene: SS09135

RESULT 28  
AG2544  
hypothetical protein asr7642 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120be  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AG2544  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AG2544  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-79 <KUR>  
A:Cross-references: UNIPROT:Q8ZS70; UNIPARC:UPI00000CCDCG; GB:AP003602; PIDN:BAB77285.1  
C:Genetics:  
A:Gene: asr7642  
A:Genome: plasmid

Query Match 100.0%; Score 20; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KDEL 4  
|||  
DB 37 KDEL 40

RESULT 29  
C69204  
hypothetical protein MTH78 - Methanobacterium thermoautotrophicum (strain Delta H)  
C:Species: Methanobacterium thermoautotrophicum  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: C69204  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional genome  
A:Reference number: A69000; MUID:98037514; PMID:9371463  
A:Accession: C69204  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-80 <MTH>  
A:Cross-references: UNIPROT:O26182; UNIPARC:UPI0000062C23; GB:AE000799; GB:AE000666; NID:11759840  
A:Experimental source: strain Delta H  
C:Genetics:  
A:Gene: MTH78

Query Match 100.0%; Score 20; DB 2; Length 80;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KDEL 4  
|||  
DB 53 KDEL 56

RESULT 30  
S77318  
secretory protein secE - Synechocystis sp. (strain PCC 6803)  
N:Alternate names: protein sel3335  
C:Species: Synechocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S77318  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.  
DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S77318  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-81 <KAN>  
A:Cross-references: UNIPROT:P38382; UNIPARC:UPI00001357A7; EMBL:D90906; GB:AB001339; NID:11759840  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Genetics:  
A:Gene: secE  
A:Start codon: GTG

Query Match 100.0%; Score 20; DB 2; Length 81;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|||  
DB 31 KDEL 34

RESULT 31  
JT0765  
rapid lysis III protein - phage T4  
N:Alternate names: rIII  
C:Species: phage T4  
C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 09-Jul-2004  
C:Accession: JT0765; JU0290; S26171; JQ0526  
R:Raudonikienė, A.; Nivinskas, R.  
Gene 134, 135-136, 1993  
A:Title: The sequences of gene rIII of bacteriophage T4 and its mutants.  
A:Reference number: JT0765; MUID:94063508; PMID:8244025  
A:Accession: JT0765  
A:Molecule type: DNA  
A:Residues: 1-82 <RAU>  
A:Cross-references: UNIPROT:PI7309; UNIPARC:UPI000005CBC1  
R:Raudonikienė, A.; Nivinskas, R.  
Nucleic Acids Res. 18, 4280, 1990  
A:Title: Nucleotide sequence of bacteriophage T4 gene 31 region.  
A:Reference number: JU0290; MUID:90332452; PMID:2377483  
A:Accession: JU0290  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-82 <RA2>  
A:Cross-references: UNIPARC:UPI000005CBC1; EMBL:M37882; NID:9215873; PIDN:AAA32507.1; P1:11759840  
R:Raudonikienė, A.; Nivinskas, R.  
Gene 114, 85-90, 1992  
A:Title: Gene rIII is the nearest downstream neighbour of bacteriophage T4 gene 31.  
A:Reference number: S26167; MUID:92267389; PMID:1587487  
A:Accession: S26171  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-82 <RA3>  
A:Cross-references: UNIPARC:UPI000005CBC1; EMBL:X54536; NID:g15789; PIDN:CAA38406.1; P1:11759840  
R:Prilipov, A.G.; Mesyanzhinov, V.V.; Aebi, U.; Kellenberger, E.  
Nucleic Acids Res. 18, 3635, 1990  
A:Title: Cloning and sequencing of bacteriophage T4 genes between map positions 128.3-129.3  
A:Reference number: JQ0524; MUID:90301484; PMID:2362813  
A:Accession: JQ0526  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-63, 'NLMLLHE', '72', 'QFVTLW' <PRI>  
A:Cross-references: UNIPARC:UPI000016D7D0; EMBL:X17657; NID:g15204; PID:g15208

Query Match 100.0%; Score 20; DB 2; Length 82;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
|||  
DB 57 KDEL 60

```
RESULT 32
D64329
hypothetical protein MJ0235 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: D64329
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: D64329
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-82 <BUL>
A;Cross-references: UNIPROT:Q57687; UNIPARC:UPI00001394CD; GB:U67479; GB:L77117; NID:g15
C;Genetics:
A;Map position: FOR226124-226372

Query Match 100.0%; Score 20; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 36 KDEL 39

RESULT 33
F82891
hypothetical protein UU439 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: F82891
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: F82891
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <GLA>
A;Cross-references: UNIPARC:UPI00000C1C69; GB:AE002140; GB:AF222894; NID:g6899420; PIDN:
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UU439
A;Genetic code: SGC3

Query Match 100.0%; Score 20; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 32 KDEL 35

RESULT 34
E82887
hypothetical protein UU472 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: E82887
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: E82887
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-83 <GLA>
A;Cross-references: UNIPARC:UPI00000C1C80; GB:AE002143; GB:AF222894; NID:g6899457; PIDN:
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UU472
A;Genetic code: SGC3

Query Match 100.0%; Score 20; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 32 KDEL 35

RESULT 35
I40586
hypothetical protein 1 (Tn5401) - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40586
R;Baum, J.A.
J. Bacteriol. 176, 2835-2845, 1994
A;Title: Tn5401, a new class II transposable element from Bacillus thuringiensis.
A;Reference number: I40575; MUID:94245608; PMID:7514590
A;Accession: I40586
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-85 <RES>
A;Cross-references: UNIPROT:Q45701; UNIPARC:UPI00000AF7FA; EMBL:U03554; NID:g495317; P:

Query Match 100.0%; Score 20; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 5 KDEL 8

RESULT 36
T39536
probable involvement in cytochrome oxidase assembly - fission yeast (Schizosaccharomyce
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39536
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
submitted to the EMBL Data Library, February 1998
A;Reference number: Z21862
A;Accession: T39536
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-85 <WOO>
A;Cross-references: UNIPROT:O42921; UNIPARC:UPI000006B7BF; EMBL:AL021748; PIDN:CAA1686
A;Experimental source: strain 972h-; cosmid c16A3
C;Genetics:
A;Gene: SPDB:SPBC16A3.16
A;Map position: 2
A;Introns: 57/3

Query Match 100.0%; Score 20; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 36 KDEL 39

RESULT 37
WMEC5R
replication control protein repA2 - Escherichia coli plasmid R1drrd-19
```

C;Species: Escherichia coli  
C;Date: 29-Jul-1981 #sequence\_revision 29-Jul-1981 #text\_change 09-Jul-2004  
C;Accession: A04484  
R;Strougaard, P.; Molin, S.; Nordstrom, K.; Hansen, F.G.  
Mol. Gen. Genet. 181, 116-122, 1981  
A;Title: The nucleotide sequence of the replication control region of the resistance plasmid pR101  
A;Reference number: A93120; MUID:81172236; PMID:6261081  
A;Accession: A04484  
A;Molecule type: DNA  
A;Residues: 1-86 <STO>  
A;Cross-references: UNIPROT:P03855; UNIPARC:UPI0000000464  
A;Note: This protein is involved in the determination of copy number in gene replication  
C;Genetics:  
A;Genome: plasmid  
C;Superfamily: repA2 protein  
C;Keywords: DNA binding; plasmid copy control; plasmid replication; transcription regulation

Query Match 100.0%; Score 20; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
DB 76 KDEL 79

RESULT 38  
S05557  
hypothetical protein B - phage T4  
C;Species: phage T4  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: S05557  
R;Hahn, S.; Rueger, W.  
Nucleic Acids Res. 17, 6729, 1989  
A;Title: Organization of the bacteriophage T4 genome between map positions 150.745 and 150.745  
A;Reference number: S05555; MUID:69386003; PMID:2674900  
A;Accession: S05557  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-89 <HAN>  
A;Cross-references: UNIPROT:P13320; UNIPARC:UPI0000005CBE1; EMBL:X15818; NID:g15210; PMID:15210

Query Match 100.0%; Score 20; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
DB 47 KDEL 50

RESULT 39  
T04077  
probable ribosomal protein L9 - rice (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T04077  
R;Nakamura, I.; Kameya, N.; Aoki, T.; Tada, T.; Norita, E.; Kanzaki, H.; Uchimiya, H.  
submitted to the EMBL Data Library, August 1994  
A;Description: Partial cDNA sequence of ribosomal protein L9 homolog from rice calli experiment  
A;Reference number: Z15190  
A;Accession: T04077  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-90 <NAK>  
A;Cross-references: UNIPROT:P49210; UNIPARC:UPI000016DEC8; EMBL:D38012; PIDN:BAA07209.1  
A;Experimental source: subsp. Japonica, callus  
C;Superfamily: ribosomal protein L6/L9  
C;Keywords: ribosome

Query Match 100.0%; Score 20; DB 2; Length 90;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
DB 40 KDEL 43

RESULT 40  
AC1030  
hypothetical protein STY4564 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AC1030  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Cronin, A.; Davies, P.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.  
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium  
A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AC1030  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-90 <PAR>  
A;Cross-references: UNIPARC:UPI000005A8A2; GB:AL513382; PIDN:CAD09340.1; PID:g16505340;  
C;Genetics:  
A;Gene: STY4564

Query Match 100.0%; Score 20; DB 2; Length 90;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
DB 13 KDEL 16

RESULT 41  
E59100  
hypothetical protein pX01-77 - Bacillus anthracis virulence plasmid pX01  
C;Species: Bacillus anthracis  
C;Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 09-Jul-2004  
C;Accession: E59100  
R;Okinkaka, R.F.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler, J.; Bacteriol. 181, 6509-6515, 1999  
A;Title: Sequence and organization of pX01, the large Bacillus anthracis plasmid harboring the anthrax toxin genes  
A;Reference number: A59091; MUID:99445483; PMID:10515943  
A;Accession: E59100  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-91 <OKI>  
A;Cross-references: UNIPROT:Q9X347; UNIPARC:UPI000000B07A1; GB:AF065404; NID:g4894216; F  
A;Experimental source: strain Sterne  
C;Genetics:  
A;Gene: pX01-77  
A;Genome: plasmid

Query Match 100.0%; Score 20; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
DB 19 KDEL 22

RESULT 42  
H84264  
hypothetical protein Vng1086c [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: H84264  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,



; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A:Title: Genome sequence of Halobacterium species NRC-1  
A:Reference number: A84160; MUID:20504483; PMID:11016950  
A:Accession: H84264  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-92 <STO>  
A:Cross-references: UNIPROT:Q9HQM9; UNIPARC:UPI00000637EA; GB:AE004437; NID:gi0580634; E  
C:Genetics:  
A:Gene: VNG1086C

Query Match 100.0%; Score 20; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 3 KDEL 6

RESULT 43  
H84296  
hypothetical protein Vng1426h [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: H84296  
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A:Title: Genome sequence of Halobacterium species NRC-1  
A:Reference number: A84160; MUID:20504483; PMID:11016950  
A:Accession: H84296  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-92 <STO>  
A:Cross-references: UNIPROT:Q9HPX7; UNIPARC:UPI00000638AD; GB:AE004437; NID:gi0580928; E  
C:Genetics:  
A:Gene: VNG1426H

Query Match 100.0%; Score 20; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 27 KDEL 30

RESULT 44  
T08319  
conserved hypothetical protein H1232 - Halobacterium sp. (strain NRC-1) plasmid pNRC100  
C:Species: Halobacterium sp.  
A:Variety: strain NRC-1  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
R:Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;  
Genome Res. 8, 1131-1141, 1998  
A:Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or m  
A:Reference number: Z16408; MUID:99063795; PMID:9847077  
A:Accession: T08319  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-93 <DAS>  
A:Cross-references: UNIPROT:O52006; UNIPARC:UPI00000631EA; EMBL:AF016485; NID:g2822278;  
C:Experimental source: strain NRC-1  
C:Genetics:  
A:Gene: HALOSP.H1232  
A:Genome: plasmid pNRC100

Query Match 100.0%; Score 20; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 27 KDEL 30

## RESULT 45

AG2290  
hypothetical protein asr3878 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AG2290  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AG2290  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-93 <KUR>  
A:Cross-references: UNIPROT:Q8YQF3; UNIPARC:UPI00000CE936; GB:BA000019; PIDN:BA075577.  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: asr3878

Query Match 100.0%; Score 20; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 77 KDEL 80

## RESULT 46

S60798  
M protein precursor - Streptococcus pyogenes (serotype M18) (fragment)  
C:Species: Streptococcus pyogenes  
A:Variety: serotype M18  
C:Date: 20-Jul-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S60798  
R:Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.  
Mol. Microbiol. 14, 619-631, 1994  
A:Title: Non-congruent relationships between variation in emm gene sequences and the p  
A:Reference number: S60784; MUID:95198537; PMID:7891551  
A:Accession: S60798  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-94 <WHA>  
A:Cross-references: UNIPROT:O54535; UNIPARC:UPI000017824B; EMBL:U11931  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994  
C:Superfamily: M5 protein

Query Match 100.0%; Score 20; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
|||  
Db 42 KDEL 45

## RESULT 47

G86415  
hypothetical protein F15D2.33 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: G86415  
R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ket, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: G86415  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-94 <STO>  
A;Cross-references: UNIPROT:Q9C7R7; UNIPARC:UPI000009D320; GB:AE005172; NID:gl0092204; F  
C;Genetics:  
A;Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 KDEL 4  
Db 70 KDEL 73

RESULT 48  
S61076  
M protein precursor - Streptococcus pyogenes (serotype M30) (fragment)  
C;Species: Streptococcus pyogenes  
A;Variety: serotype M30  
C;Date: 15-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C;Accession: S61076; S60808  
R;Whitmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.  
submitted to the EMBL Data Library, July 1994  
A;Description: Noncongruent relationships between variation in emml gene sequences and t  
A;Reference number: S61072  
A;Accession: S61076  
A;Molecule type: DNA  
A;Residues: 1-95 <WHA>  
A;Cross-references: UNIPROT:Q54547; UNIPARC:UPI0000178232; EMBL:U11944  
R;Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.  
Mol. Microbiol. 14, 619-631, 1994  
A;Title: Non-congruent relationships between variation in emm gene sequences and the pof  
A;Reference number: S60784; MUID:95198537; PMID:7891551  
A;Accession: S60808  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 19-79 <WHW>  
A;Cross-references: UNIPARC:UPI0000178233; EMBL:U11944  
C;Genetics:  
A;Gene: emm30  
C;Superfamily: M5 protein  
F;1-31/Domain: signal sequence (fragment) #status predicted <SIG>  
F;32-95/Product: M protein (fragment) #status predicted <MAT>

Query Match 100.0%; Score 20; DB 2; Length 95;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 91 KDEL 94

RESULT 49  
F97179  
uncharacterized protein of YOHL family [imported] - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

C;Accession: F97179  
R;Nolling, J.; Brecon, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee  
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: F97179  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-95 <KUR>  
A;Cross-references: UNIPROT:Q97GU7; UNIPARC:UPI000000CA485; GB:AE001437; PIDN:AAK00225.1  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC2268

Query Match 100.0%; Score 20; DB 2; Length 95;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 KDEL 4  
Db 67 KDEL 70

RESULT 50  
ZCBPT9  
gene 55.5 protein - phage T4  
C;Species: phage T4  
A;Note: host Escherichia coli  
C;Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 09-Jul-2004  
C;Accession: B30292  
R;Tomaschewski, J.; Rueger, W.  
Nucleic Acids Res. 15, 3632-3633, 1987  
A;Title: Nucleotide sequence and primary structures of gene products coded for by the T  
A;Reference number: A30291; MUID:87203398; PMID:3575111  
A;Accession: B30292  
A;Molecule type: DNA  
A;Residues: 1-97 <TOM>  
A;Cross-references: UNIPROT:P07079; UNIPARC:UPI0000005CB38; GB:Y00122; NID:gl5346; PIDN  
C;Genetics:  
A;Gene: 55.5  
C;Superfamily: phage T4 gene 55.5 protein

Query Match 100.0%; Score 20; DB 1; Length 97;  
Best Local Similarity 100.0%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 KDEL 4  
Db 53 KDEL 56

Search completed: March 20, 2006, 07:50:41  
Job time : 19 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:49:50 ; Search time 147.5 Seconds

(without alignments)  
19.133 Million cell updates/sec

Title: US-09-673-707-9

Perfect score: 20

Sequence: 1 KDEL 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description  |
|------------|-------|-------------|--------|-------|--------------|
| 1          | 20    | 100.0       | 21     | 2     | Q5ESX0_MOUSE |
| 2          | 20    | 100.0       | 26     | 2     | Q56Z88_ARATH |
| 3          | 20    | 100.0       | 28     | 1     | ORND_PLAOR   |
| 4          | 20    | 100.0       | 34     | 2     | Q41W22_AZOVI |
| 5          | 20    | 100.0       | 35     | 1     | GUR_GYMSY    |
| 6          | 20    | 100.0       | 35     | 2     | Q9S8D1_GYMSY |
| 7          | 20    | 100.0       | 37     | 1     | VPU_HVIZ8    |
| 8          | 20    | 100.0       | 38     | 2     | Q7KYM2_HUMAN |
| 9          | 20    | 100.0       | 38     | 2     | Q7M3X1_PLAFA |
| 10         | 20    | 100.0       | 38     | 2     | Q7M3X5_PLAFA |
| 11         | 20    | 100.0       | 38     | 2     | Q4Z1Z5_PLABE |
| 12         | 20    | 100.0       | 39     | 2     | Q4TI99_TETNG |
| 13         | 20    | 100.0       | 40     | 2     | Q13832_HUMAN |
| 14         | 20    | 100.0       | 40     | 2     | Q13833_HUMAN |
| 15         | 20    | 100.0       | 41     | 2     | Q65527_LACFE |
| 16         | 20    | 100.0       | 41     | 2     | Q6DRV6_STRMU |
| 17         | 20    | 100.0       | 41     | 2     | Q9EQ86_MOUSE |
| 18         | 20    | 100.0       | 42     | 2     | Q9NG47_AEDAL |
| 19         | 20    | 100.0       | 42     | 2     | Q6SF02_9BACT |
| 20         | 20    | 100.0       | 44     | 2     | Q58N49_9CAUD |
| 21         | 20    | 100.0       | 46     | 2     | Q66KA3_DICDI |
| 22         | 20    | 100.0       | 46     | 2     | Q6SSV0_MANSW |
| 23         | 20    | 100.0       | 47     | 2     | Q81BH6_BACCR |
| 24         | 20    | 100.0       | 47     | 2     | Q5Q118_CRIGR |
| 25         | 20    | 100.0       | 48     | 2     | Q9UDJ7_HUMAN |
| 26         | 20    | 100.0       | 49     | 2     | Q8EB07_SHEON |
| 27         | 20    | 100.0       | 50     | 1     | ORNE_PLAOR   |
| 28         | 20    | 100.0       | 50     | 2     | Q8ST38_9NEOP |
| 29         | 20    | 100.0       | 50     | 2     | Q9SVF9_DRYIU |
| 30         | 20    | 100.0       | 50     | 2     | Q50051_MYCLE |
| 31         | 20    | 100.0       | 50     | 2     | Q6RI53_STRPY |

|     |    |       |    |   |              |                    |
|-----|----|-------|----|---|--------------|--------------------|
| 32  | 20 | 100.0 | 50 | 2 | Q8YKY6_ANASP | Q8YKY6 anabaena sp |
| 33  | 20 | 100.0 | 51 | 2 | Q5VUK1_HUMAN | Q5VUK1 homo sapien |
| 34  | 20 | 100.0 | 51 | 2 | Q8T5D0_9NEOP | Q8T5D0 anartia fat |
| 35  | 20 | 100.0 | 51 | 2 | Q8T5E2_9NEOP | Q8T5E2 anartia lvt |
| 36  | 20 | 100.0 | 51 | 2 | Q95VG0_9NEOP | Q95VG0 eueidea vib |
| 37  | 20 | 100.0 | 51 | 2 | Q95VG2_9NEOP | Q95VG2 eueidea ali |
| 38  | 20 | 100.0 | 52 | 1 | ORNC_PLAOR   | P25512 placobdella |
| 39  | 20 | 100.0 | 52 | 2 | Q8T5D1_9NEOP | Q8T5D1 anartia fat |
| 40  | 20 | 100.0 | 52 | 2 | Q8T5D9_9NEOP | Q8T5D9 anartia ama |
| 41  | 20 | 100.0 | 52 | 2 | Q9SPX4_PICAB | Q9SPX4 picea abies |
| 42  | 20 | 100.0 | 52 | 2 | Q65057_PICMA | Q65057 picea maria |
| 43  | 20 | 100.0 | 53 | 2 | Q8T5E1_9NEOP | Q8T5E1 anartia chr |
| 44  | 20 | 100.0 | 53 | 2 | Q30456_HORSE | Q30456 equus cabal |
| 45  | 20 | 100.0 | 53 | 2 | Q30470_HORSE | Q30470 equus cabal |
| 46  | 20 | 100.0 | 53 | 2 | Q30471_HORSE | Q30471 equus cabal |
| 47  | 20 | 100.0 | 53 | 2 | Q30476_HORSE | Q30476 equus cabal |
| 48  | 20 | 100.0 | 53 | 2 | Q9BCX3_HORSE | Q9BCX3 equus cabal |
| 49  | 20 | 100.0 | 53 | 2 | Q9SPX3_PICAB | Q9SPX3 picea abies |
| 50  | 20 | 100.0 | 53 | 2 | Q4MPAS_BACCE | Q4MPAS bacillus ce |
| 51  | 20 | 100.0 | 53 | 2 | Q8KET6_CHLTE | Q8KET6 chlorobium  |
| 52  | 20 | 100.0 | 54 | 1 | TOM6_ARATH   | Q9XIA7 arabidopsis |
| 53  | 20 | 100.0 | 55 | 2 | Q857E1_9CAUD | Q857E1 mycobacteri |
| 54  | 20 | 100.0 | 56 | 2 | Q4MWD1_BACCE | Q4MWD1 bacillus ce |
| 55  | 20 | 100.0 | 57 | 2 | Q9ES41_RAT   | Q9ES41 rattus norv |
| 56  | 20 | 100.0 | 58 | 2 | Q7M3G2_BOVIN | Q7M3G2 bos taurus  |
| 57  | 20 | 100.0 | 58 | 2 | Q8U9H6_AGR75 | Q8U9H6 agrobacteri |
| 58  | 20 | 100.0 | 58 | 2 | Q81W60_BACAN | Q81W60 bacillus an |
| 59  | 20 | 100.0 | 59 | 2 | Q8T5E0_9NEOP | Q8T5E0 anartia chr |
| 60  | 20 | 100.0 | 59 | 2 | Q73FB1_BACCI | Q73FB1 bacillus ce |
| 61  | 20 | 100.0 | 59 | 2 | Q81J55_BACCR | Q81J55 bacillus ce |
| 62  | 20 | 100.0 | 59 | 2 | Q63HA5_BACC2 | Q63HA5 bacillus ce |
| 63  | 20 | 100.0 | 59 | 2 | Q81VU5_BACAN | Q81VU5 bacillus an |
| 64  | 20 | 100.0 | 60 | 1 | Y4653_ANASP  | Q9YNB4 anabaena sp |
| 65  | 20 | 100.0 | 60 | 2 | Q97CI2_THEVO | Q97CI2 thermoplas  |
| 66  | 20 | 100.0 | 60 | 2 | Q7NS55_CHRVO | Q7NS55 thermobacce |
| 67  | 20 | 100.0 | 61 | 2 | Q5JH88_PYRKO | Q5JH88 pyrococcus  |
| 68  | 20 | 100.0 | 61 | 2 | Q81Z37_BACAN | Q81Z37 bacillus an |
| 69  | 20 | 100.0 | 61 | 2 | Q9ADC0_STRCO | Q9ADC0 streptomyce |
| 70  | 20 | 100.0 | 61 | 2 | Q88367_MOUSE | Q88367 mus musculu |
| 71  | 20 | 100.0 | 62 | 1 | Y1076_ARCFU  | Q29187 archaeoglob |
| 72  | 20 | 100.0 | 62 | 2 | Q8JH23_PPERC | Q8JH23 ostracion s |
| 73  | 20 | 100.0 | 62 | 2 | Q91801_XENLA | Q91801 xenopus lae |
| 74  | 20 | 100.0 | 63 | 2 | Q6HP53_BACHK | Q6HP53 bacillus th |
| 75  | 20 | 100.0 | 64 | 1 | RL29_LACPL   | Q88XX8 lactobacill |
| 76  | 20 | 100.0 | 64 | 2 | Q7TBM8_POLIS | Q7TBM8 poliovirus  |
| 77  | 20 | 100.0 | 65 | 2 | Q8T5D2_9NEOP | Q8T5D2 anartia fat |
| 78  | 20 | 100.0 | 65 | 2 | Q8T5D8_9NEOP | Q8T5D8 anartia ama |
| 79  | 20 | 100.0 | 65 | 2 | Q8T5E4_9NEOP | Q8T5E4 anartia ama |
| 80  | 20 | 100.0 | 65 | 2 | Q4ZP77_PSESY | Q4ZP77 pseudomonas |
| 81  | 20 | 100.0 | 65 | 2 | Q8YKK6_ANASP | Q8YKK6 anabaena sp |
| 82  | 20 | 100.0 | 65 | 2 | Q5QU38_IDILO | Q5QU38 idiomarina  |
| 83  | 20 | 100.0 | 66 | 1 | RL29_BARHE   | Q692X3 bartonella  |
| 84  | 20 | 100.0 | 66 | 1 | RL29_BARQU   | Q6fzd0 bartonella  |
| 85  | 20 | 100.0 | 66 | 1 | RL31_GEOKA   | Q5KHU0 geobacillus |
| 86  | 20 | 100.0 | 66 | 2 | Q8T5E6_9NEOP | Q8T5E6 anartia ama |
| 87  | 20 | 100.0 | 66 | 2 | Q7JQ95_BRUMA | Q7JQ95 brugia mala |
| 88  | 20 | 100.0 | 66 | 2 | Q4KH40_PSEF5 | Q4KH40 pseudomonas |
| 89  | 20 | 100.0 | 66 | 2 | Q88N42_PSEPK | Q88N42 pseudomonas |
| 90  | 20 | 100.0 | 67 | 1 | Y00A_BPT4    | P25186 bacterioph  |
| 91  | 20 | 100.0 | 67 | 2 | Q5Z699_CRYNE | Q5Z699 cryptococcu |
| 92  | 20 | 100.0 | 67 | 2 | Q7VPH6_HAEDU | Q7VPH6 haemophilus |
| 93  | 20 | 100.0 | 67 | 2 | Q81C76_BACCR | Q81C76 bacillus ce |
| 94  | 20 | 100.0 | 67 | 2 | Q8KCE6_CHLTE | Q8KCE6 chlorobium  |
| 95  | 20 | 100.0 | 68 | 2 | Q8T5E3_9NEOP | Q8T5E3 anartia lvt |
| 96  | 20 | 100.0 | 68 | 2 | Q8T5E5_9NEOP | Q8T5E5 anartia ama |
| 97  | 20 | 100.0 | 68 | 2 | Q9TWU7_ASCSU | Q9TWU7 ascaris suu |
| 98  | 20 | 100.0 | 68 | 2 | Q4YZF3_PLABE | Q4YZF3 plasmodium  |
| 99  | 20 | 100.0 | 68 | 2 | Q92IW7_RICCN | Q92IW7 rickettsia  |
| 100 | 20 | 100.0 | 68 | 2 | Q67546_9VIRU | Q67546 garlic comm |
| 101 | 20 | 100.0 | 69 | 1 | SSPI_BACSK   | Q8WEJ3 bacillus cl |
| 102 | 20 | 100.0 | 69 | 2 | Q8MZK7_PLAFA | Q8MZK7 plasmodium  |
| 103 | 20 | 100.0 | 69 | 2 | Q5CJQ6_CRYHO | Q5CJQ6 cryptospori |
| 104 | 20 | 100.0 | 69 | 2 | Q8T5D6_9NEOP | Q8T5D6 anartia ama |

|                       |  |      |        |              |  |
|-----------------------|--|------|--------|--------------|--|
| 105                   | Q5F5F9_NEIG1   | 69   | 2      | Q5F5F9_NEIG1 | Q5f5f9 neisseria g                                 |
| 106                   | Q7VCX2_PROWA   | 69   | 2      | Q7VCX2_PROWA | Q7vcx2 prochloroco                                 |
| 107                   | Q8XNS4_CLOPE   | 69   | 2      | Q8XNS4_CLOPE | Q8xns4 clostridium                                 |
| 108                   | Q4MK34_BACE  | 70   | 2      | Q4MK34_BACE  | Q4mk34 bacillus ce                                 |
| 109                   | Q8UCX6_AGRF5   | 70   | 2      | Q8UCX6_AGRF5 | Q8ucx6 agrobacteri                                 |
| 110                   | Q4YXK9_PLABE   | 71   | 2      | Q4YXK9_PLABE | Q4yxk9 plasmodium                                  |
| 111                   | Q4HNS5_CAMLA   | 71   | 2      | Q4HNS5_CAMLA | Q4hns5 campylobact                                 |
| 112                   | Q5HW18_CAMJR   | 71   | 2      | Q5HW18_CAMJR | Q5hw18 campylobact                                 |
| 113                   | Q9PI59_CAMJE   | 71   | 2      | Q9PI59_CAMJE | Q9pi59 campylobacte                                |
| 114                   | Q7NSV8_CHRVO   | 71   | 2      | Q7NSV8_CHRVO | Q7nsv8 chromobacte                                 |
| 115                   | Q9PUA7_ELEQC   | 71   | 2      | Q9PUA7_ELEQC | Q9pu7 eleutheroda                                  |
| 116                   | Q4TFS9_TETNG   | 71   | 2      | Q4TFS9_TETNG | Q4tfs9 tetraodon n                                 |
| 117                   | Q8TSD3_9NEOP   | 72   | 2      | Q8TSD3_9NEOP | Q8tsd3 junonia eva                                 |
| 118                   | Q5F8C2_NEIG1   | 72   | 2      | Q5F8C2_NEIG1 | Q5f8c2 neisseria g                                 |
| 119                   | Q9JRB9_NEINA   | 72   | 2      | Q9JRB9_NEINA | Q9jrb9 neisseria m                                 |
| 120                   | Q7DDI2_NEIMB   | 72   | 2      | Q7DDI2_NEIMB | Q7ddi2 neisseria m                                 |
| 121                   | Q5L842_BACFN   | 73   | 2      | Q5L842_BACFN | Q5l842 bacteroides                                 |
| 122                   | Q5HTB0_CAMJR   | 73   | 2      | Q5HTB0_CAMJR | Q5htb0 campylobact                                 |
| 123                   | Q64NB9_BACFR   | 73   | 2      | Q64NB9_BACFR | Q64nb9 bacteroides                                 |
| 124                   | Q8A444_BACTN   | 73   | 2      | Q8A444_BACTN | Q8a444 bacteroides                                 |
| 125                   | Q6MAC9_PARUM   | 73   | 2      | Q6MAC9_PARUM | Q6mac9 parachlamyd                                 |
| 126                   | Q6IVP9_MOUSE   | 73   | 2      | Q6IVP9_MOUSE | Q6ivf9 mus musculu                                 |
| 127                   | Q42249_ATH   | 74   | 1      | TLP_OCEIH    | Q8et84 oceanobacil                                 |
| 128                   | Q42249_ATH   | 74   | 2      | Q42249_ATH   | Q42249 arabidopsi                                  |
| 129                   | Q4HHB5_CAMCO   | 74   | 2      | Q4HHB5_CAMCO | Q4hhb5 campylobact                                 |
| 130                   | Q7URG1_RHOBA   | 74   | 2      | Q7URG1_RHOBA | Q7urg1 rhodospirell                                |
| 131                   | Q6YWA6_ORYSA   | 75   | 2      | Q6YWA6_ORYSA | Q6ywa6 oryza sativ                                 |
| 132                   | Q7HNZ5_PYLII   | 75   | 2      | Q7HNZ5_PYLII | Q7hnz5 pylaiella l                                 |
| 133                   | Q94223_9PHAE   | 75   | 2      | Q94223_9PHAE | Q94223 laminaria d                                 |
| 134                   | Q9TA12_CAFRO   | 75   | 2      | Q9TA12_CAFRO | Q9ta12 caferteria r                                |
| 135                   | Q60625_METCA   | 75   | 2      | Q60625_METCA | Q60625 methylococc                                 |
| 136                   | Q8KBW4_CHLTE   | 75   | 2      | Q8KBW4_CHLTE | Q8kbw4 chlorobium                                  |
| 137                   | Q066_HALSA   | 76   | 1      | Q066_HALSA   | Q8hsu8 halobacteri                                 |
| 138                   | Q7RH55_FLAYO   | 76   | 2      | Q7RH55_FLAYO | Q7rh55 plasmodium                                  |
| 139                   | Q89TC7_BRAJA   | 76   | 2      | Q89TC7_BRAJA | Q89tc7 bradyrhizob                                 |
| 140                   | Q26211_METTH   | 77   | 2      | Q26211_METTH | Q26211 methanobact                                 |
| 141                   | Q9HHD8_HALSA   | 77   | 2      | Q9HHD8_HALSA | Q9hhd8 halobacteri                                 |
| 142                   | Q5WAD5_BACSK   | 77   | 2      | Q5WAD5_BACSK | Q5wad5 bacillus cl                                 |
| 143                   | Q838A1_ENTFA   | 77   | 2      | Q838A1_ENTFA | Q838a1 enterococcu                                 |
| 144                   | Q5Z265_LEGPH   | 77   | 2      | Q5Z265_LEGPH | Q5z265 legionella                                  |
| 145                   | Q1EX7S_NOCFA   | 78   | 1      | EX7S_NOCFA   | Qyq91 nocardia fa                                  |
| 146                   | HOLI_BPHP1   | 78   | 1      | HOLI_BPHP1   | P51727 bacterioph                                  |
| 147                   | S100G_HUMAN  | 78   | 1      | S100G_HUMAN  | P29377 homo sapien                                 |
| 148                   | Q5JHJ2_PVRKO   | 78   | 2      | Q5JHJ2_PVRKO | Q5jhj2 pyrococcus                                  |
| 149                   | Q8N4C5_HUMAN   | 78   | 2      | Q8N4C5_HUMAN | Q8n4c5 homo sapien                                 |
| 150                   | Q94MY7_9CAUD   | 78   | 2      | Q94MY7_9CAUD | Q94my7 haemophilus                                 |
| ALIGNMENTS            |  |      |        |              |  |
| RESULT 1              |  |      |        |              |  |
| Q9ESX0_MOUSE          | Q9ESX0_MOUSE PRELIMINARY;  | PRT; | 21 AA. |              |  |
| ID                    | Q9ESX0   |      |        |              |  |
| AC                    | Q9ESX0   |      |        |              |  |
| DT                    | 01-MAR-2001 (TRENBLrel. 16, Created)                                   |      |        |              |  |
| DT                    | 01-MAR-2001 (TRENBLrel. 16, Last sequence update)                      |      |        |              |  |
| DT                    | 01-OCT-2003 (TRENBLrel. 25, Last annotation update)                    |      |        |              |  |
| DE                    | Gephyrin (Fragment)  |      |        |              |  |
| GN                    | Name=Gphn; Synonym=gephyrin;   |      |        |              |  |
| OS                    | Mus musculus (Mouse)   |      |        |              |  |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |      |        |              |  |
| OC                    | Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  |      |        |              |  |
| OC                    | Muridae; Murinae; Mus.   |      |        |              |  |
| OX                    | NCBI_TaxID=10090;  |      |        |              |  |
| RN                    | [1]  |      |        |              |  |
| RP                    | NUCLEOTIDE SEQUENCE.   |      |        |              |  |
| RX                    | MEDLINE=20420367; PubMed=10963686; DOI=10.1073/pnas.97.18.10266;       |      |        |              |  |
| RA                    | Ramming M., Kins S., Werner N., Hermann A., Betz H., Kirsch J.;        |      |        |              |  |
| RT                    | "Diversity and phylogeny of Gephyrin: tissue-specific splice variants, |      |        |              |  |
| RT                    | gene structure, and sequence similarities to molybdenum cofactor-      |      |        |              |  |
| RT                    | synthesizing and cytoskeleton-associated proteins."                    |      |        |              |  |
| RL                    | Proc. Natl. Acad. Sci. U.S.A. 97:10266-10271(2000).                    |      |        |              |  |
| RESULT 2              |  |      |        |              |  |
| Q56Z88_ATH            | Q56Z88_ATH PRELIMINARY;  | PRT; | 26 AA. |              |  |
| ID                    | Q56Z88   |      |        |              |  |
| AC                    | Q56Z88   |      |        |              |  |
| DT                    | 10-MAY-2005 (TRENBLrel. 30, Created)                                   |      |        |              |  |
| DT                    | 10-MAY-2005 (TRENBLrel. 30, Last sequence update)                      |      |        |              |  |
| DT                    | 10-MAY-2005 (TRENBLrel. 30, Last annotation update)                    |      |        |              |  |
| DE                    | Putative thioredoxin (Fragment)  |      |        |              |  |
| GN                    | Name=Atig77510;  |      |        |              |  |
| OS                    | Arabidopsis thaliana (Mouse-ear cress).                                |      |        |              |  |
| OC                    | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;     |      |        |              |  |
| OC                    | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;   |      |        |              |  |
| OC                    | eurosid II; Brassicales; Brassicaceae; Arabidopsi                      |      |        |              |  |
| OX                    | NCBI_TaxID=3702;   |      |        |              |  |
| RN                    | [1]  |      |        |              |  |
| RP                    | NUCLEOTIDE SEQUENCE.   |      |        |              |  |
| RA                    | Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,        |      |        |              |  |
| RA                    | Naruaka M., Shin-i T., Nakegawa M., Sakamoto N., Oishi K., Kohara Y.,  |      |        |              |  |
| RA                    | Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,   |      |        |              |  |
| RA                    | Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,               |      |        |              |  |
| RA                    | Hayashizaki Y., Shinozaki K.;  |      |        |              |  |
| RT                    | "Large-scale analysis of RIKEN Arabidopsis full-length (RAPL) cDNAs."  |      |        |              |  |
| RL                    | Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.                |      |        |              |  |
| DR                    | EMBL; AK221081; BAD94922.1; -; mRNA.                                   |      |        |              |  |
| FT                    | NON_TER  |      |        |              |  |
| SQ                    | SEQUENCE 26 AA; 2859 MW; 239F28BA553191C2 CRC64;                       |      |        |              |  |
| Query Match           |  |      |        |              | 100.0%; Score 20; DB 2; Length 26;                 |
| Best Local Similarity |  |      |        |              | 100.0%; Pred. No. 1.2e+03;                         |
| Matches               |  |      |        |              | 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy                    | 1 KDEL 4   |      |        |              |  |
| Db                    | 9 KDEL 12  |      |        |              |  |
| RESULT 3              |  |      |        |              |  |
| ORND_PLAOR            | ORND_PLAOR STANDARD;   | PRT; | 28 AA. |              |  |
| ID                    | ORND_PLAOR   |      |        |              |  |
| AC                    | P25513;  |      |        |              |  |
| DT                    | 01-MAY-1992 (Rel. 22, Created)   |      |        |              |  |
| DT                    | 01-MAY-1992 (Rel. 22, Last sequence update)                            |      |        |              |  |
| DT                    | 05-JUL-2004 (Rel. 44, Last annotation update)                          |      |        |              |  |
| DE                    | Ornatin D (Fragment)   |      |        |              |  |
| OS                    | Placodella ornata (Turtle leech).                                      |      |        |              |  |
| OC                    | Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;       |      |        |              |  |
| OC                    | Rhynchobdellida; Glossiphoniidae; Placobdella.                         |      |        |              |  |
| OX                    | NCBI_TaxID=6415;   |      |        |              |  |
| RN                    | [1]  |      |        |              |  |
| RP                    | PROTEIN SEQUENCE.  |      |        |              |  |
| RX                    | MEDLINE=92111479; PubMed=1765068;                                      |      |        |              |  |
| RA                    | Mazur P., Henzel W.J., Seymour J.L., Lazarus R.A.;                     |      |        |              |  |
| RT                    | "Ornatin: potent glycoprotein IIB-IIIA antagonists and platelet        |      |        |              |  |
| RT                    | aggregation inhibitors from the leech Placobdella ornata."             |      |        |              |  |
| RL                    | Eur. J. Biochem. 202:1073-1082(1991).                                  |      |        |              |  |

CC -!- FUNCTION: Potent inhibitor of fibrinogen interaction with platelet  
 CC receptors expressed on glycoprotein IIB-IIIA complex. May prevent  
 CC blood from clotting during either feeding and/or storage of  
 CC ingested blood.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the ornatin family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC InterPro: IPR002463; Ornatin.  
 CC Pfam: PF02088; Ornatin; 1.  
 CC PRINTS: PR01184; ORNATIN.  
 CC ProDom: PD012062; Ornatin; 1.  
 CC Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.  
 KW NON\_TER 28  
 FT SEQUENCE 28 AA; 3361 MW; CFC38951F91337C2 CRC64;  
 SQ  
 Query Match 100.0%; Score 20; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KDEL 4  
 Db 7 KDEL 10  
 RESULT 4  
 Q41WL2 AZOVI  
 ID Q41WL2 AZOVI PRELIMINARY; PRT; 34 AA.  
 AC Q41WL2;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=AvindRAFT\_2561;  
 OS Azotobacter vinelandii AvOP.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 CC Pseudomonadaceae; Azotobacter.  
 OX NCBI\_TaxID=322710;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AvOP;  
 RG US DOE Joint Genome Institute (JGI-PGF);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,  
 RA Hammon N., Israni S., Pitluck S., Richardson P.;  
 RT "Sequencing of the draft genome assembly of Azotobacter vinelandii  
 RT AvOP.";  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AvOP;  
 RG US DOE Joint Genome Institute (JGI-ORNL);  
 RA Larimer F., Land M.;  
 RT "Annotation of the draft genome assembly of Azotobacter vinelandii  
 RT AvOP.";  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AvOP;  
 RG US DOE Joint Genome Institute (JGI-PGF);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,  
 RA Hammon N., Israni S., Pitluck S., Richardson P.;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; AAAU03000007; EAM05212.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 34 AA; 3855 MW; BAOE98F64340ABB9 CRC64;  
 Query Match 100.0%; Score 20; DB 2; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KDEL 4  
 Db 26 KDEL 29  
 RESULT 5  
 GUR\_GYMSY  
 ID GUR\_GYMSY STANDARD; PRT; 35 AA.  
 AC P25810;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Gurmarin (Sweet-taste-suppressing peptide).  
 OS Gymnema sylvestre (Gurmar).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 CC asterids; lamiids; Gentianales; Apocynaceae; Periplocoideae; Gymnema.  
 OX NCBI\_TaxID=4068;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Leaf;  
 RX MEDLINE=92299642; PubMed=1607357;  
 RA Kamei K., Takano R., Miyasaka A., Imoto T., Hara S.;  
 RT "Amino acid sequence of sweet-taste-suppressing peptide (gurmarin)  
 RT from the leaves of Gymnema sylvestre.";  
 RL J. Biochem. 111:109-112(1992).  
 RN [2]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=95307084; PubMed=7787425;  
 RA Arai K., Ishima R., Morikawa S., Miyasaka A., Imoto T., Yoshimura S.,  
 RA Almoto S., Akasaka K.;  
 RT "Three-dimensional structure of gurmarin, a sweet taste-suppressing  
 RT polypeptide.";  
 RL J. Biomol. NMR 5:297-305(1995).  
 RN [3]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=99421659; PubMed=10491100;  
 RA Fletcher J.I., Dingley A.J., Smith R., Connor M., Christie M.J.,  
 RA King G.F.;  
 RT "High-resolution solution structure of gurmarin, a sweet-taste-  
 RT suppressing plant polypeptide.";  
 RL Eur. J. Biochem. 264:525-533(1999).  
 CC -!- FUNCTION: Suppresses strongly the sweet taste responses in the rat  
 CC with high specificity to sucrose, glucose, glycine, and saccharin.  
 CC This effect is reversible, but complete recovery of the suppressed  
 CC responses required at least 3h. Gurmarin showed no effect or only  
 CC a very weak effect on the sweet taste sensation in humans.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC PIR: JX0200; JX0200.  
 CC PDB: 1C4E; NMR; A=1-35.  
 CC PDB: 1GUR; NMR; @=1-35.  
 CC InterPro: IPR010485; Gurmarin.  
 CC Pfam: PF06410; Gurmarin; 1.  
 KW 3D-structure; Direct protein sequencing; Pyrrolidone carboxylic acid;  
 KW Taste-modifying protein.  
 FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
 FT DISULFID 3 18

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FT DISULFID 10 23
FT DISULFID 17 33
FT TURN 12 15
FT STRAND 24 27
FT TURN 28 29
FT STRAND 30 32
SQ SEQUENCE 35 AA; 4232 MW; 661BD6FBAF504CB6 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 6 KDEL 9

RESULT 6
Q9S8D1_GYMSY PRELIMINARY; PRT; 35 AA.
AC Q9S8D1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GURMARIN-SWEETNESS-suppressing polypeptide.
OS Gymnema sylvestre (Gurmar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Gentianales; Apocynaceae; Periplocoideae; Gymnema.
OX NCBI_TaxID=4068;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96068945; PubMed=8534991;
RA Ota M., Ariyoshi Y.;
RT "Location of the disulfide bonds of the sweetness-suppressing
RL polypeptide gurmarin."
RL Biosci. Biotechnol. Biochem. 59:1956-1957(1995).
DR HSP; P25810; IGR.
DR InterPro; IPR010485; Gurmarin.
DR Pfam; PF06410; Gurmarin; 1.
SQ SEQUENCE 35 AA; 4233 MW; 661BCAB6E904CB6 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 6 KDEL 9

RESULT 7
VPU_HV128
ID_VPU_HV128 STANDARD; PRT; 37 AA.
AC P08607;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE VPU protein (U ORF protein) (Fragment).
GN Name=VPU;
OS Human immunodeficiency virus type 1 (isolate Z-84) (HIV-1).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11681;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RX MEDLINE=88281278; PubMed=3395517;
RA Younso J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian isolate
RT of HIV-1."
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -!- FUNCTION: Acts in the degradation of CD4 in the endoplasmic
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CC reticulum and in the enhancement of virion release from the plasma
CC membrane of infected cells.
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- MISCELLANEOUS: The Z-84 isolate was taken from a 54 year-old
CC Zairean male.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; J03653; AAA44683.1; -; Genomic_RNA.
CC HSP; P19554; 1VPU.
CC HIV; J03653; VPUSJY1.
CC InterPro; IPR008187; Vpu.
CC InterPro; IPR009032; Vpu_cyt.
CC Pfam; PF00558; Vpu; 1.
CC AIDS; Transmembrane.
CC NON_TER 1
CC SEQUENCE 37 AA; 4131 MW; 00EA53CA27D09509 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 17 KDEL 20

RESULT 8
Q7KYM2_HUMAN PRELIMINARY; PRT; 38 AA.
ID Q7KYM2_HUMAN PRELIMINARY; PRT; 38 AA.
AC Q7KYM2;
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Titin protein (Fragment).
GN Name=titin;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart muscle;
RX MEDLINE=95119041; PubMed=7819249;
RA Musco G., Tziatzos C., Schuck P., Pastore A.;
RT "Dissecting titin into its structural motifs: identification of an
RT alpha helix near the N-terminus."
RL Biochemistry 34:553-561(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart muscle;
RA Labeit S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBSJ databases.
DR EMBL; X83270; CAA58243.1; -; mRNA.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA; 4562 MW; B792A11CAAE2F248 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 13 KDEL 16

RESULT 9
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O7M3X1 PLAF6A
ID O7M3X1 PLAF6A PRELIMINARY; PRT; 38 AA.
AC O7M3X1;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Circumsporozoite protein (Fragments).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=90114334; PubMed=2481827; DOI=10.1016/0166-6851(89)90159-X;
RA Lockyer M.J., Marsh K., Newbold C.I.;
RT "Wild isolates of Plasmodium falciparum show extensive polymorphism in
RT T cell epitopes of the circumsporozoite protein.";
RL Mol. Biochem. Parasitol. 37:275-280(1989).
DR PIR; B60657; B60657.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA; 4301 MW; D51BC1C086B6BD94 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDEL 4
Db 28 KDEL 31

RESULT 10
O7M3X5 PLAF6A
ID O7M3X5 PLAF6A PRELIMINARY; PRT; 38 AA.
AC O7M3X5;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Circumsporozoite protein (Fragments).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=90114334; PubMed=2481827; DOI=10.1016/0166-6851(89)90159-X;
RA Lockyer M.J., Marsh K., Newbold C.I.;
RT "Wild isolates of Plasmodium falciparum show extensive polymorphism in
RT T cell epitopes of the circumsporozoite protein.";
RL Mol. Biochem. Parasitol. 37:275-280(1989).
DR PIR; A38869; A38869.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA; 4287 MW; CEB7BC5D6E3BD94 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDEL 4
Db 28 KDEL 31

RESULT 11
O4Z1Z5 PLABE
ID O4Z1Z5 PLABE PRELIMINARY; PRT; 38 AA.
AC O4Z1Z5;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB102634.00.0;
OS Plasmodium berghei.
```

```
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAI01001046; CAH95692.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 38
SQ SEQUENCE 38 AA; 4660 MW; F07E2408947C15DA CRC64;

Query Match 100.0%; Score 20; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KDEL 4
Db 13 KDEL 16

RESULT 12
O4TI89 TETNG
ID O4TI89 TETNG PRELIMINARY; PRT; 39 AA.
AC O4TI89;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome undetermined SCAF2327, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0000079001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Aichouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (PDB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01002327; CAP87393.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4418 MW; E33A6CD2FA262A6B CRC64;
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|                       |  |         |                    |                  |                                 |  |  |
|-----------------------|--|---------|--------------------|------------------|---------------------------------|--|--|
| Query Match           |  | 100.0%; | Score 20;          | DB 2;            | Length 40;                      |  |  |
| Best Local Similarity |  | 100.0%; | Pred. No. 1.8e+03; |                  |                                 |  |  |
| Matches               |  | 4;      | Conservative       | 0;               | Mismatches 0; Indels 0; Gaps 0; |  |  |
| QY                    | 1 KDEL 4   |         |                    |                  |                                 |  |  |
| Db                    | 23 KDEL 26   |         |                    |                  |                                 |  |  |
| RESULT 15             |  |         |                    |                  |                                 |  |  |
| ID                    | O06527_LACFE PRELIMINARY;  | PRT;    | 41 AA.             |                  |                                 |  |  |
| AC                    | O06527;  |         |                    |                  |                                 |  |  |
| DT                    | 01-JUL-1997 (TrEMBLrel. 04, Created)                                 |         |                    |                  |                                 |  |  |
| DT                    | 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)                    |         |                    |                  |                                 |  |  |
| DT                    | 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)                  |         |                    |                  |                                 |  |  |
| DE                    | Cystathionine gamma-lyase homolog (Fragment).                        |         |                    |                  |                                 |  |  |
| OS                    | Lactobacillus fermentum.   |         |                    |                  |                                 |  |  |
| OC                    | Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;             |         |                    |                  |                                 |  |  |
| OC                    | Lactobacillus.   |         |                    |                  |                                 |  |  |
| OX                    | NCBI_TaxID=1613;   |         |                    |                  |                                 |  |  |
| RN                    | [1]  |         |                    |                  |                                 |  |  |
| RP                    | NUCLEOTIDE SEQUENCE.   |         |                    |                  |                                 |  |  |
| RC                    | STRAIN=BR11;   |         |                    |                  |                                 |  |  |
| RX                    | MEDLINE=97294473; PubMed=9150229;                                    |         |                    |                  |                                 |  |  |
| RA                    | Turner M.S., Timms P., Hafner L.M., Giffard P.M.;                    |         |                    |                  |                                 |  |  |
| RT                    | "Identification and characterization of a basic cell surface-located |         |                    |                  |                                 |  |  |
| RT                    | protein from Lactobacillus fermentum BR11.";                         |         |                    |                  |                                 |  |  |
| RL                    | J. Bacteriol. 179:3310-3316(1997).                                   |         |                    |                  |                                 |  |  |
| RP                    | [2]  |         |                    |                  |                                 |  |  |
| RN                    | NUCLEOTIDE SEQUENCE.   |         |                    |                  |                                 |  |  |
| RC                    | STRAIN=BR11;   |         |                    |                  |                                 |  |  |
| RX                    | MEDLINE=99194729;  |         |                    |                  |                                 |  |  |
| RA                    | Turner M.S., Woodberry T., Hafner L.M., Giffard P.M.;                |         |                    |                  |                                 |  |  |
| RT                    | "The bspA locus of Lactobacillus fermentum BR11 encodes an L-cystine |         |                    |                  |                                 |  |  |
| RT                    | uptake system.";   |         |                    |                  |                                 |  |  |
| RL                    | J. Bacteriol. 181:2192-2198(1999).                                   |         |                    |                  |                                 |  |  |
| DR                    | EMBL; U97348; AAC45329.1; -; Genomic DNA.                            |         |                    |                  |                                 |  |  |
| DR                    | HSSP; O15564; 1E5E.  |         |                    |                  |                                 |  |  |
| DR                    | GO; GO:0016829; F:lyase activity; IEA.                               |         |                    |                  |                                 |  |  |
| DR                    | GO; GO:0006520; P:amino acid metabolism; IEA.                        |         |                    |                  |                                 |  |  |
| DR                    | InterPro; IPR000277; Cys_Met_Meta_PP.                                |         |                    |                  |                                 |  |  |
| DR                    | Pfam; PF01053; Cys_Met_Meta_PP; 1.                                   |         |                    |                  |                                 |  |  |
| KW                    | Lyase.   |         |                    |                  |                                 |  |  |
| FT                    | NON TER  | 1       |                    |                  |                                 |  |  |
| SQ                    | SEQUENCE   | 41 AA;  | 4647 MW;           | 7875F22817910FB7 | CRC64;                          |  |  |
| Query Match           |  |         |                    |                  |                                 |  |  |
| Best Local Similarity |  | 100.0%; | Score 20;          | DB 2;            | Length 41;                      |  |  |
| Matches               |  | 4;      | Conservative       | 0;               | Mismatches 0; Indels 0; Gaps 0; |  |  |
| QY                    | 1 KDEL 4   |         |                    |                  |                                 |  |  |
| Db                    | 13 KDEL 16   |         |                    |                  |                                 |  |  |
| RESULT 16             |  |         |                    |                  |                                 |  |  |
| ID                    | Q8DRV6_STRMU PRELIMINARY;  | PRT;    | 41 AA.             |                  |                                 |  |  |
| AC                    | Q8DRV6;  |         |                    |                  |                                 |  |  |
| DT                    | 01-MAR-2003 (TrEMBLrel. 23, Created)                                 |         |                    |                  |                                 |  |  |
| DT                    | 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)                    |         |                    |                  |                                 |  |  |
| DT                    | 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)                  |         |                    |                  |                                 |  |  |
| DE                    | Hypothetical protein SMU.2105.                                       |         |                    |                  |                                 |  |  |
| GN                    | OrderedLocusNames=SMU.2105;  |         |                    |                  |                                 |  |  |
| OS                    | Streptococcus mutans.  |         |                    |                  |                                 |  |  |
| OC                    | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;             |         |                    |                  |                                 |  |  |
| OC                    | Streptococcus.   |         |                    |                  |                                 |  |  |
| OX                    | NCBI_TaxID=1309;   |         |                    |                  |                                 |  |  |
| RN                    | [1]  |         |                    |                  |                                 |  |  |
| RP                    | NUCLEOTIDE SEQUENCE.   |         |                    |                  |                                 |  |  |
| RC                    | STRAIN=UAI59 / ATCC 700610 / Serotype C;                             |         |                    |                  |                                 |  |  |
| RX                    | MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;       |         |                    |                  |                                 |  |  |

|                       |  |         |                    |                  |                                 |  |  |
|-----------------------|--|---------|--------------------|------------------|---------------------------------|--|--|
| Query Match           |  | 100.0%; | Score 20;          | DB 2;            | Length 39;                      |  |  |
| Best Local Similarity |  | 100.0%; | Pred. No. 1.8e+03; |                  |                                 |  |  |
| Matches               |  | 4;      | Conservative       | 0;               | Mismatches 0; Indels 0; Gaps 0; |  |  |
| QY                    | 1 KDEL 4   |         |                    |                  |                                 |  |  |
| Db                    | 36 KDEL 39   |         |                    |                  |                                 |  |  |
| RESULT 13             |  |         |                    |                  |                                 |  |  |
| ID                    | Q13832_HUMAN PRELIMINARY;  | PRT;    | 40 AA.             |                  |                                 |  |  |
| AC                    | Q13832;  |         |                    |                  |                                 |  |  |
| DT                    | 01-NOV-1996 (TrEMBLrel. 01, Created)                                   |         |                    |                  |                                 |  |  |
| DT                    | 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)                      |         |                    |                  |                                 |  |  |
| DT                    | 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)                    |         |                    |                  |                                 |  |  |
| DE                    | B2 bradykinin receptor basal promoter, allele BP-58-C (Fragment).      |         |                    |                  |                                 |  |  |
| OS                    | Homo sapiens (Human).  |         |                    |                  |                                 |  |  |
| OC                    | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;                |         |                    |                  |                                 |  |  |
| OC                    | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; |         |                    |                  |                                 |  |  |
| OC                    | Homo.  |         |                    |                  |                                 |  |  |
| OX                    | NCBI_TaxID=9606;   |         |                    |                  |                                 |  |  |
| RN                    | [1]  |         |                    |                  |                                 |  |  |
| RP                    | NUCLEOTIDE SEQUENCE.   |         |                    |                  |                                 |  |  |
| RX                    | MEDLINE=96209920; PubMed=8655154; DOI=10.1007/s004390050117;           |         |                    |                  |                                 |  |  |
| RA                    | Braun A., Maier E., Kammerer S., Mueller B., Roscher A.A.;             |         |                    |                  |                                 |  |  |
| RT                    | "A novel sequence polymorphism in the promoter region of the human     |         |                    |                  |                                 |  |  |
| RT                    | bradykinin B2-receptor gene.";   |         |                    |                  |                                 |  |  |
| RL                    | Hum. Genet. 97:688-689(1996).  |         |                    |                  |                                 |  |  |
| DR                    | EMBL; X91663; CAA62851.1; -; Genomic DNA.                              |         |                    |                  |                                 |  |  |
| DR                    | GO; GO:0004872; F:receptor activity; IEA.                              |         |                    |                  |                                 |  |  |
| KW                    | Receptor.  |         |                    |                  |                                 |  |  |
| FT                    | NON TER  | 1       |                    |                  |                                 |  |  |
| FT                    | NON TER  | 40      |                    |                  |                                 |  |  |
| SQ                    | SEQUENCE   | 40 AA;  | 4140 MW;           | 3908E9AD371EF4A5 | CRC64;                          |  |  |
| Query Match           |  |         |                    |                  |                                 |  |  |
| Best Local Similarity |  | 100.0%; | Score 20;          | DB 2;            | Length 40;                      |  |  |
| Matches               |  | 4;      | Conservative       | 0;               | Mismatches 0; Indels 0; Gaps 0; |  |  |
| QY                    | 1 KDEL 4   |         |                    |                  |                                 |  |  |
| Db                    | 23 KDEL 26   |         |                    |                  |                                 |  |  |
| RESULT 14             |  |         |                    |                  |                                 |  |  |
| ID                    | Q13833_HUMAN PRELIMINARY;  | PRT;    | 40 AA.             |                  |                                 |  |  |
| AC                    | Q13833;  |         |                    |                  |                                 |  |  |
| DT                    | 01-NOV-1996 (TrEMBLrel. 01, Created)                                   |         |                    |                  |                                 |  |  |
| DT                    | 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)                      |         |                    |                  |                                 |  |  |
| DT                    | 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)                    |         |                    |                  |                                 |  |  |
| DE                    | B2 bradykinin receptor basal promoter, allele BP-58-T (Fragment).      |         |                    |                  |                                 |  |  |
| OS                    | Homo sapiens (Human).  |         |                    |                  |                                 |  |  |
| OC                    | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;                |         |                    |                  |                                 |  |  |
| OC                    | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; |         |                    |                  |                                 |  |  |
| OC                    | Homo.  |         |                    |                  |                                 |  |  |
| OX                    | NCBI_TaxID=9606;   |         |                    |                  |                                 |  |  |
| RN                    | [1]  |         |                    |                  |                                 |  |  |
| RP                    | NUCLEOTIDE SEQUENCE.   |         |                    |                  |                                 |  |  |
| RX                    | MEDLINE=96209920; PubMed=8655154; DOI=10.1007/s004390050117;           |         |                    |                  |                                 |  |  |
| RA                    | Braun A., Maier E., Kammerer S., Mueller B., Roscher A.A.;             |         |                    |                  |                                 |  |  |
| RT                    | "A novel sequence polymorphism in the promoter region of the human     |         |                    |                  |                                 |  |  |
| RT                    | bradykinin B2-receptor gene.";   |         |                    |                  |                                 |  |  |
| RL                    | Hum. Genet. 97:688-689(1996).  |         |                    |                  |                                 |  |  |
| DR                    | EMBL; X91664; CAA62852.1; -; Genomic DNA.                              |         |                    |                  |                                 |  |  |
| DR                    | GO; GO:0004872; F:receptor activity; IEA.                              |         |                    |                  |                                 |  |  |
| KW                    | Receptor.  |         |                    |                  |                                 |  |  |
| FT                    | NON TER  | 1       |                    |                  |                                 |  |  |
| FT                    | NON TER  | 40      |                    |                  |                                 |  |  |
| SQ                    | SEQUENCE   | 40 AA;  | 4153 MW;           | 1408E9AD371EE17F | CRC64;                          |  |  |



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RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RA Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
DR EMBL; AE015032; AAN59699.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 41 AA; 4849 MW; CD8F7DC062B6D60B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 5 KDEL 8

RESULT 17
Q9EQE6_MOUSE
ID Q9EQE6_MOUSE PRELIMINARY; PRT; 41 AA.
AC Q9EQE6_
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE General transcription factor II-I repeat domain protein 1
DE (Fragment)
GN Name=Gtf2lrd1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SV;
RX MEDLINE=21250999; PubMed=11352562; DOI=10.1006/geno.2001.6507;
RA Durkin M.E., Keck-Waggoner C.L., Popescu N.C., Thorgeirsson S.S.;
RT "Integration of a c-myc transgene results in disruption of the mouse
RT Gtf2lrd1 gene, the homologue of the human GTF2LRD1 gene hemizyously
RT deleted in Williams-Beuren syndrome.";
RL Genomics 73:20-27 (2001).
DR EMBL; AF257477; AAG44656.1; -; Genomic DNA.
DR MGI; MGI:1861942; Gtf2lrd1.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0003700; F:transcription factor activity; IDA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.
FT NON TER 41
SQ SEQUENCE 41 AA; 4482 MW; D7E29ECA570059DC CRC64;

Query Match 100.0%; Score 20; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 27 KDEL 30

RESULT 18
Q9NG47_AEDAL
ID Q9NG47_AEDAL PRELIMINARY; PRT; 42 AA.
AC Q9NG47_
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal S5 protein (Fragment).
OS Aedes albopictus (Forest day mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Culicinae; Culicini; Aedes; Stegomyia.
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OX NCBI_TaxID=7160;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang F.F., Zhao T.T., Li D.D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF263471; AAF73440.1; -; mRNA.
DR GO; GO:0015935; C:small ribosomal subunit; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000235; Ribosomal S7.
DR InterPro; IPR005716; Ribosomal_S7e/a.
DR Pfam; PF00177; Ribosomal_S7; 1.
DR TIGRFAMs; TIGR01028; S7_S5_E_A; 1.
FT NON TER 1
SQ SEQUENCE 42 AA; 4711 MW; CE1FE5123B5053A2 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 31 KDEL 34

RESULT 19
Q6SFQ2_9BACT
ID Q6SFQ2_9BACT PRELIMINARY; PRT; 42 AA.
AC Q6SFQ2_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
DE ORFNames=BBAC000-36A07.5;
GN uncultured bacterium 580.
OC Bacteria; environmental samples.
OX NCBI_TaxID=257400;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA DeLong E.F.;
RT "Monterey Bay Coastal Ocean Microbial Observatory environmental clone
RT sequencing.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong E.F.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY458647; AAR38160.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 42 AA; 5136 MW; 26A3A4736779A936 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 24 KDEL 27

RESULT 20
Q58N49_9CAUD
ID Q58N49_9CAUD PRELIMINARY; PRT; 44 AA.
AC Q58N49_
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PSSP7_009;
OS Cyanophage P-SSP7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=268748;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RX PubMed=15828858; DOI=10.1371/journal.pbio.0030144;
RA Sullivan M.B., Coleman M.L., Weigle P., Rohwer F., Chisholm S.W.;
RT "Three prochlorococcus cyanophage genomes: signature features and
RT ecological interpretations.";
RL PLoS Biol. 3:E144-E144(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindell D., Sullivan M.B., Johnson Z.I., Tolonen A.C., Rohwer F.,
RA Chisholm S.W.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY939843; AAX44189.1; -, Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 44 AA; 5189 MW; 57C219AD9FAFD4F7 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 28+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 23 KDEL 26

RESULT 21
Q86KA3_DICDI PRELIMINARY; PRT; 46 AA.
AC Q86KA3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DDB0167608;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
RA April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., Van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Lounsged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shauly G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.P., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";

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RL Nature 0:0-0(2005).
DR EMBL; AC116956; AAO51164.1; -, Genomic_DNA.
DR EMBL; AAF10100027; EAL70094.1; -, Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 46 AA; 5295 MW; 90B4DD2FFD66E424 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 26 KDEL 29

RESULT 22
Q65SV0_MNSM PRELIMINARY; PRT; 46 AA.
AC Q65SV0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=MS1353;
OS Mannheimia succiniciproducens (strain MBEL55E). Pasteurellales;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OX Pasteurellaceae; Mannheimia.
OC NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens.";
RN Nat. Biotechnol. 22:1275-1281(2004).
DR EMBL; AE016827; AAU37960.1; -, Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 46 AA; 5633 MW; 08EF7F4B232074B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4
Db 9 KDEL 12

RESULT 23
Q81BH6_BACCR PRELIMINARY; PRT; 47 AA.
AC Q81BH6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=BC3181;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin V., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).

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DR EMBL; AB017008; AAP10123.1; -, Genomic\_DNA.  
DR InterPro; IPR006542; Cons\_hypoth1655.  
DR Pfam; PF06486; DUF1093; 1.

KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 47 AA; 5565 MW; D36072B5A6AFA0A4 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
Db 33 KDEL 36

## RESULT 24

Q5Q1L8 CRIGR PRELIMINARY; PRT; 47 AA.  
AC Q5Q1L8;

DT 01-FEB-2005 (TREMBlrel. 29, Created)  
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
DE Putative ER-resident protein ERdj5 (Fragment).  
OS Cricetulus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Cricetinae; Cricetulus.  
OX NCBI\_TaxID=10029;  
RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Chen P., Harcum S.W.;

RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY788841; AAV69868.1; -, mRNA.

DR InterPro; IPR000886; ER target S.

DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.

FT NON\_TER 1

SQ SEQUENCE 47 AA; 5607 MW; C3DBF0A6325A21E1 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
Db 44 KDEL 47

## RESULT 25

Q9UDJ7 HUMAN

ID Q9UDJ7 HUMAN PRELIMINARY; PRT; 48 AA.  
AC Q9UDJ7;

DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2004 (TREMBlrel. 26, Last annotation update)  
DE Nucleolar shuttle protein B-23=38 kDa major NOS-binding protein (Fragments).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.

OX NCBI\_TaxID=9606;  
RN [1]

RP PROTEIN SEQUENCE.

EX MEDLINE=93300776; PubMed=8314759;

RA Adachi Y., Copeland T.D., Hatanaka M., Oroszlan S.;

RT "Nucleolar targeting signal of Rex protein of human T-cell leukemia

virus type I specifically binds to nucleolar shuttle protein B-23.";

RL J. Biol. Chem. 268:13930-13934 (1993).

FT NON\_TER 1

FT NON\_CONS 18 19

FT NON\_CONS 33 34

FT NON\_TER 48 48

SQ SEQUENCE 48 AA; 4783 MW; 5D73D533BD386A9E CRC64;

Query Match 100.0%; Score 20; DB 2; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
Db 5 KDEL 8

## RESULT 26

Q8EB07 SHEON

ID Q8EB07 SHEON PRELIMINARY; PRT; 49 AA.  
AC Q8EB07;

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Hypothetical protein SO3729.

GN OrderedLocustNames=SO3729;

OS Shewanella oneidensis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Oceanellales; Shewanella.

OX NCBI\_TaxID=70863;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=MR-1;

RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,

RA Read T.D., Eisen J.A., Seshadri R., Ward N.B., Methe B.A.,

RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,

RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,

RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,

RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,

RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,

RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,

RA Venter J.C., Neilson K.H., Fraser C.M.;

RT "Genome sequence of the dissimilatory metal ion-reducing bacterium

Shewanella oneidensis.";

RL Nat. Biotechnol. 20:1118-1123 (2002).

DR EMBL; AE015806; AAN56713.1; -, Genomic\_DNA.

DR TIGR; SO3729; -.

KW Complete proteome.

SQ SEQUENCE 49 AA; 5340 MW; 7ABE848EAD0FFA80 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4  
Db 31 KDEL 34

## RESULT 27

ORNE PLAOR

ID ORNE PLAOR STANDARD; PRT; 50 AA.  
AC P25514;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Ornatin E.

OS Placobdella ornata (Turtle leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;

OC Rhynchobdellida; Glossiphoniidae; Placobdella.

OX NCBI\_TaxID=6415;

RN [1]

RP PROTEIN SEQUENCE.

EX MEDLINE=92111479; PubMed=1765068;

RA Mazur P., Henzel W.J., Seymour J.L., Lazarus R.A.;

RT "Ornatin: potent glycoprotein IIB-IIIA antagonists and platelet

aggregation inhibitors from the leech Placobdella ornata.";

RL Eur. J. Biochem. 202:1073-1082 (1991).

CC !- FUNCTION: Potent inhibitor of fibrinogen interaction with platelet

CC receptors expressed on glycoprotein IIB-IIIA complex. May prevent  
 CC blood from clotting during either feeding and/or storage of  
 CC ingested blood.

CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC removed.

CC PIR: S19624; S19624.  
 DR InterPro: IPR002463; Ornatin.  
 DR Pfam: PF02088; Ornatin; 1.  
 DR PRINTS: PR01184; ORNATIN.  
 DR ProDom: PD012062; Ornatin; 1.  
 KW Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.  
 FT MOTIF 42 44  
 FT Cell attachment site.  
 SQ SEQUENCE 50 AA; 5728 MW; 6B8408EB1E001B92 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
 Db 7 KDEL 10

RESULT 28  
 Q8ST38\_QNEOP PRELIMINARY; PRT; 50 AA.  
 ID Q8ST38;  
 AC Q8ST38;  
 DT 01-JUN-2002 (TRENBLrel. 21, Created)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)  
 DE Triosephosphate isomerase (Fragment).  
 OS Anartia fatima.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Nymphalidae; Anartia.  
 OC NCBI\_TaxID=145889;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22359425; PubMed=12470937; DOI=10.1016/S1055-7903(02)00291-9;  
 RA Blum M.J., Bermingham E., Dasmahapatra K.;  
 RT "A molecular phylogeny of the neotropical butterfly genus Anartia  
 (Lepidoptera: Nymphalidae).";  
 RL Mol. Phylogenet. Evol. 26:46-55(2003).  
 DR EMBL; AY038684; AAM03332.1; -; Genomic DNA.  
 DR EMBL; AY038685; AAM03333.1; -; Genomic DNA.  
 DR HSSP; P00940; 1TPH.  
 DR SMR; Q8ST38; 1-47.  
 DR GO; GO:0016853; F:isomerase activity; IEA.  
 DR GO; GO:0004807; F:triose-phosphate isomerase activity; IEA.  
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
 DR GO; GO:0006094; P:gluconeogenesis; IEA.  
 DR GO; GO:0006096; P:glycolysis; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.  
 DR InterPro; IPR000652; Triophos\_ismrse.  
 DR Pfam; PF00121; TIM; 1.  
 DR ProDom; PD001005; Triophos\_ismrse; 1.  
 DR NON\_TER 1  
 FT NON\_TER 50  
 SQ SEQUENCE 50 AA; 5450 MW; F985EA898F5A3BAF CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
 Db 7 KDEL 10

RESULT 30  
 Q50051\_MYCLE PRELIMINARY; PRT; 50 AA.  
 ID Q50051;  
 AC Q50051;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DE U2266p.  
 OS Mycobacterium leprae.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OC NCBI\_TaxID=1769;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

Query Match 100.0%; Score 20; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
 Db 3 KDEL 6

Qy 1 KDEL 4  
 Db 2 KDEL 5

RESULT 29  
 Q95VF9\_DRYU PRELIMINARY; PRT; 50 AA.  
 ID Q95VF9;  
 AC Q95VF9;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Triosephosphate isomerase (Fragment).  
 GN Name=Tpi;  
 OS Dryas iulia (Julia butterfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Dryas.  
 OC NCBI\_TaxID=33453;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22337200; PubMed=12446809;  
 RA Beltran M., Jiggins C.D., Bull V., Linares M., Mallet J.,  
 RA McMillan W.O., Bermingham E.;  
 RT "Phylogenetic discordance at the species boundary: comparative gene  
 RT genealogies among rapidly radiating heliconius butterflies.";  
 RL Mol. Biol. Evol. 19:2176-2190(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Beltran M.S., Jiggins C.D., Bull V., McMillan O., Bermingham E.,  
 RA Mallet J., Linares M.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF413797; AAL08558.1; -; Genomic DNA.  
 DR HSSP; P00940; 1TPH.  
 DR SMR; Q95VF9; 1-48.  
 DR GO; GO:0016853; F:isomerase activity; IEA.  
 DR GO; GO:0004807; F:triose-phosphate isomerase activity; IEA.  
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
 DR GO; GO:0006094; P:gluconeogenesis; IEA.  
 DR GO; GO:0006096; P:glycolysis; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.  
 DR InterPro; IPR000652; Triophos\_ismrse.  
 DR Pfam; PF00121; TIM; 1.  
 DR ProDom; PD001005; Triophos\_ismrse; 1.  
 DR NON\_TER 1  
 FT NON\_TER 50  
 SQ SEQUENCE 50 AA; 5394 MW; AF3E2F54436BAFF8 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
 Db 3 KDEL 6

RESULT 30  
 Q50051\_MYCLE PRELIMINARY; PRT; 50 AA.  
 ID Q50051;  
 AC Q50051;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DE U2266p.  
 OS Mycobacterium leprae.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OC NCBI\_TaxID=1769;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

Query Match 100.0%; Score 20; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
 Db 3 KDEL 6

RA Smith D.R.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Robison K.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U15182; AAA62966.1; -; Genomic\_DNA.  
SQ SEQUENCE 50 AA; 5563 MW; 5B5A4419AD5DD6C2 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 41 KDEL 44

## RESULT 31

Q6RI53\_STRPY  
ID Q6RI53\_STRPY PRELIMINARY; PRT; 50 AA.  
AC Q6RI53;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE M protein (Fragment).  
GN Name=emm;  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1314;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15071004; DOI=10.1126/JCM.42.4.1559-1563.2004;  
RA Hasenbein M.E., Warner J.E., Lambert K.G., Cole S.E., Onderdonk A.B.,  
RA McAdam A.J.;  
RT "Detection of multiple macrolide- and lincosamide-resistant strains of  
RT Streptococcus pyogenes from patients in the Boston area."  
RL J. Clin. Microbiol. 42:1559-1563(2004).  
DR EMBL; AY497033; AAR89487.1; -; Genomic\_DNA.  
FT NON\_TER 1 50  
FT NON\_TER 50 50  
SQ SEQUENCE 50 AA; 5828 MW; F3F49D82A588BFDC CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 11 KDEL 14

## RESULT 32

Q8YK6\_ANASP  
ID Q8YK6\_ANASP PRELIMINARY; PRT; 50 AA.  
AC Q8YK6;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Transposase.  
GN OrderedLocusNames=asr7152;  
OS Anabaena sp. (strain PCC 7120).  
OG Plasmid pCC7120alpha.  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
OX NCBI\_TaxID=103690;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21595285; PubMed=11759840;  
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,

RA Yasuda M., Tabata S.;  
RT "Complete genomic sequence of the filamentous nitrogen-fixing  
RT cyanobacterium Anabaena sp. strain PCC 7120."  
RL DNA Res. 8:205-213(2001).  
DR EMBL; BA000020; BAB78236.1; -; Genomic\_DNA.  
DR PIR; AH2496; AH2496.  
SQ Complete proteome; Plasmid.  
KW SEQUENCE 50 AA; 5761 MW; EE163ACA7E5C489B CRC64;

Query Match 100.0%; Score 20; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 8 KDEL 11

## RESULT 33

Q5VUK1\_HUMAN  
ID Q5VUK1\_HUMAN PRELIMINARY; PRT; 51 AA.  
AC Q5VUK1;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Novel protein (Fragment).  
GN Name=RP11-290P14.1; ORFNames=RP11-290P14.1-010;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Peck A.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL589763; CAH72046.1; -; Genomic\_DNA.  
FT NON\_TER 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 51 AA; 5737 MW; 9D2FB367916CE45A CRC64;

Query Match 100.0%; Score 20; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEL 4  
Db 21 KDEL 24

## RESULT 34

Q8T5D0\_9NEOP  
ID Q8T5D0\_9NEOP PRELIMINARY; PRT; 51 AA.  
AC Q8T5D0;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Triosephosphate isomerase (Fragment).  
OS Anartia fatima.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Papilionoidea; Nymphalidae; Nymphalinae; Anartia.  
OX NCBI\_TaxID=145889;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22359425; PubMed=12470937; DOI=10.1016/S1055-7903(02)00291-9;  
RA Blum M.J., Birmingham E., Dagmahapatra K.;  
RT "A molecular phylogeny of the neotropical butterfly genus Anartia  
RT (Lepidoptera: Nymphalidae)."  
RL Mol. Phylogenet. Evol. 26:46-55(2003).  
DR EMBL; AY038691; AAM03323.1; -; Genomic\_DNA.  
DR HSSP; P00940; 1TFH.  
DR SMK; Q8T5D0; 1-48.  
DR GO; GO:0016853; F:isomerase activity; IEA.

DR GO:0004807; F:triose-phosphate isomerase activity; IEA.  
DR GO:0008152; P:metabolism; IEA.  
DR InterPro: IPR000652; Triophos\_ismrse.  
DR Pfam: PF00121; TIM; 1.  
KW Isomerase.  
FT NON\_TER 1 1  
FT NON\_TER 51 51  
SQ SEQUENCE 51 AA; 5523 MW; E1E59B6F54436BAF CRC64;  
  
Query Match 100.0%; Score 20; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KDEL 4  
DB 3 KDEL 6  
  
RESULT 35  
Q8T5E2\_9NEOP  
ID Q8T5E2\_9NEOP PRELIMINARY; PRT; 51 AA.  
AC Q8T5E2;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Triosephosphate isomerase (Fragment).  
OS Anartia lytrea.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Papilionoidea; Nymphalidae; Nymphalinae; Anartia.  
OC NCBI\_TaxID=165847;  
OX [1]  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=22359425; PubMed=12470937; DOI=10.1016/S1055-7903(02)00291-9;  
RX Blum M.J., Bermingham E., Dasgahapatra K.,  
RT "A molecular phylogeny of the neotropical butterfly genus Anartia  
(Lepidoptera: Nymphalidae)."  
RL Mol. Phylogenet. Evol. 26:46-55 (2003).  
DR EMBL: AY038677; AAM03325.1; -; Genomic\_DNA.  
DR HSSP: P00940; 1TPH.  
DR SMR: Q8T5E2; 2-46.  
DR GO:0016853; F:isomerase activity; IEA.  
DR GO:0004807; F:triose-phosphate isomerase activity; IEA.  
DR GO:0008152; P:metabolism; IEA.  
DR InterPro: IPR000652; Triophos\_ismrse.  
DR Pfam: PF00121; TIM; 1.  
KW Isomerase.  
FT NON\_TER 1 1  
FT NON\_TER 51 51  
SQ SEQUENCE 51 AA; 5531 MW; 55D759F281E44EEA CRC64;  
  
Query Match 100.0%; Score 20; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KDEL 4  
DB 1 KDEL 4  
  
RESULT 36  
Q95VG0\_9NEOP  
ID Q95VG0\_9NEOP PRELIMINARY; PRT; 51 AA.  
AC Q95VG0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Triosephosphate isomerase (Fragment).  
GN Name=Tpi;  
OS Eueides vibilia.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Eueides.

OX NCBI\_TaxID=101930;  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=22337200; PubMed=12446809;  
RX Beltran M., Jiggins C.D., Bull V., Linares M., Mallet J.,  
RA McMillan W.O., Bermingham E.; the species boundary: comparative gene  
RT "Phylogenetic discordance at the species boundary: comparative gene  
RL genealogies among rapidly radiating heliconius butterflies.";  
Mol. Biol. Evol. 19:2176-2190(2002).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RP Beltran M.S., Jiggins C.D., Bull V., McMillan O., Bermingham E.,  
RA Mallet J., Linares M.;  
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AF413796; AAL08557.1; -; Genomic\_DNA.  
DR HSSP: P00940; 1TPH.  
DR SMR: Q95VG0; 1-48.  
DR GO:0016853; F:isomerase activity; IEA.  
DR GO:0004807; F:triose-phosphate isomerase activity; IEA.  
DR GO:0008152; P:metabolism; IEA.  
DR InterPro: IPR000652; Triophos\_ismrse.  
DR Pfam: PF00121; TIM; 1.  
KW Isomerase.  
FT NON\_TER 1 1  
FT NON\_TER 51 51  
SQ SEQUENCE 51 AA; 5523 MW; F98584DEFF436BAF CRC64;  
  
Query Match 100.0%; Score 20; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KDEL 4  
DB 3 KDEL 6  
  
RESULT 37  
Q95VG2\_9NEOP  
ID Q95VG2\_9NEOP PRELIMINARY; PRT; 51 AA.  
AC Q95VG2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Triosephosphate isomerase (Fragment).  
GN Name=Tpi;  
OS Eueides aliphera.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Eueides.  
OC NCBI\_TaxID=33449;  
OX [1]  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=22337200; PubMed=12446809;  
RX Beltran M., Jiggins C.D., Bull V., Linares M., Mallet J.,  
RA McMillan W.O., Bermingham E.;  
RT "Phylogenetic discordance at the species boundary: comparative gene  
RL genealogies among rapidly radiating heliconius butterflies.";  
Mol. Biol. Evol. 19:2176-2190(2002).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RP Beltran M.S., Jiggins C.D., Bull V., McMillan O., Bermingham E.,  
RA Mallet J., Linares M.;  
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AF413794; AAL08555.1; -; Genomic\_DNA.  
DR HSSP: P00940; 1TPH.  
DR SMR: Q95VG2; 1-48.  
DR GO:0016853; F:isomerase activity; IEA.  
DR GO:0004807; F:triose-phosphate isomerase activity; IEA.  
DR GO:0008152; P:metabolism; IEA.  
DR InterPro: IPR000652; Triophos\_ismrse.  
DR Pfam: PF00121; TIM; 1.  
KW Isomerase.  
FT NON\_TER 1 1  
FT NON\_TER 51 51

```

FT  NON TER      51      51
SQ  SEQUENCE 51 AA; 5509 MW;  F9815FFEFF436BAF  CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KDEL 4
Db  3 KDEL 6

RESULT 38
ORNC PLAOR
ID  ORNC PLAOR      STANDARD;      PRT;      52 AA.
AC  P25512;
DT  01-MAY-1992 (Rel. 22, Created)
DT  01-MAY-1992 (Rel. 22, Last sequence update)
DT  10-MAY-2005 (Rel. 47, Last annotation update)
DE  Ornatin C.
OS  Placobdella ornata (Turtle leech).
OC  Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC  Rhynchobdellida; Glossiphoniidae; Placobdella.
OX  NCBI_TaxID=6415;
RN  [1]
RP  PROTEIN SEQUENCE.
RX  MEDLINE=92111479; PubMed=1765068;
RA  Mazur P., Henzel W.J., Seymour J.L., Lazarus R.A.;
RT  "Ornatins: potent glycoprotein IIB-IIIa antagonists and platelet
RT  aggregation inhibitors from the leech Placobdella ornata.";
RL  Eur. J. Biochem. 202:1073-1082(1991).
CC  -!- FUNCTION: Potent inhibitor of fibrinogen interaction with platelet
CC  receptors expressed on glycoprotein IIB-IIIa complex. May prevent
CC  blood from clotting during either feeding and/or storage of
CC  ingested blood.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the ornatin family.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  PIR; S19623;
DR  InterPro: IPR002463; Ornatin.
DR  Pfam; PF02088; Ornatin; 1.
DR  PRINTS; PR01184; ORNATIN.
DR  ProDom; PD012062; Ornatin; 1.
DR  KEGG; B04844; Ornatin; 1.
KW  Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.
FT  MOTIF 42 44      Cell attachment site.
SQ  SEQUENCE 52 AA; 5845 MW;  BA55CA7408EF4F09  CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KDEL 4
Db  7 KDEL 10

RESULT 39
Q8T5D1_9NEOP
ID  Q8T5D1_9NEOP PRELIMINARY;      PRT;      52 AA.
AC  Q8T5D1;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Triosephosphate isomerase (Fragment).
OS  Anartia fatima.
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

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OC  Papilionoidea; Nymphalidae; Nymphalinae; Anartia.
OX  NCBI_TaxID=145889;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22359425; PubMed=12470937; DOI=10.1016/S1055-7903(02)00291-9;
RA  Blum M.J., Bermingham E., Dasmahapatra K.;
RT  "A molecular phylogeny of the neotropical butterfly genus Anartia
RT  (Lepidoptera: Nymphalidae).";
RL  Mol. Phylogenet. Evol. 26:46-55(2003).
DR  EMBL; AY038690; AAM03322.1; -; Genomic_DNA.
DR  HSSP; P00940; 1TPH.
DR  SMR; Q8T5D1; 2-49.
DR  GO; GO:0016853; F:isomerase activity; IEA.
DR  GO; GO:0004807; F:triose-phosphate isomerase activity; IEA.
DR  GO; GO:0008152; P:metabolism; IEA.
DR  InterPro: IPR000652; Triophos_ismrse.
DR  Pfam; PF00121; TIM; 1.
KW  isomerase.
FT  NON TER      1      1
FT  NON TER      52      52
SQ  SEQUENCE 52 AA; 5620 MW;  F9859E17CF2EA5EF  CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KDEL 4
Db  4 KDEL 7

RESULT 40
Q8T5D9_9NEOP
ID  Q8T5D9_9NEOP PRELIMINARY;      PRT;      52 AA.
AC  Q8T5D9;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Triosephosphate isomerase (Fragment).
OS  Anartia amathea.
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC  Papilionoidea; Nymphalidae; Nymphalinae; Anartia.
OX  NCBI_TaxID=145890;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22359425; PubMed=12470937; DOI=10.1016/S1055-7903(02)00291-9;
RA  Blum M.J., Bermingham E., Dasmahapatra K.;
RT  "A molecular phylogeny of the neotropical butterfly genus Anartia
RT  (Lepidoptera: Nymphalidae).";
RL  Mol. Phylogenet. Evol. 26:46-55(2003).
DR  EMBL; AY038680; AAM03328.1; -; Genomic_DNA.
DR  HSSP; P00940; 1TPH.
DR  SMR; Q8T5D9; 1-48.
DR  GO; GO:0016853; F:isomerase activity; IEA.
DR  GO; GO:0004807; F:triose-phosphate isomerase activity; IEA.
DR  GO; GO:0008152; P:metabolism; IEA.
DR  InterPro: IPR000652; Triophos_ismrse.
DR  Pfam; PF00121; TIM; 1.
KW  isomerase.
FT  NON TER      1      1
FT  NON TER      52      52
SQ  SEQUENCE 52 AA; 5620 MW;  8759859E6F54436B  CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KDEL 4
Db  3 KDEL 6

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RESULT 41
QSPX4_PICAB
ID QSPX4_PICAB PRELIMINARY; PRT; 52 AA.
AC QSPX4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative 60S ribosomal protein L31 (Fragment).
GN Names: S42;
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1];
NUCLEOTIDE SEQUENCE.
RP MEDLINE=99436016; PubMed=10504420;
RA Perry D.J., Isabel N., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes: the amount and
RT nature of variation revealed in norway spruce.";
RL Heredity 83:239-248(1999)
DR EMBL; AF127445; AAC02462.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000054; Ribosomal_L31e.
DR Pfam; PF01198; Ribosomal_L31e; 1.
KW Ribosomal protein.
FT NON TER 1
SQ SEQUENCE 52 AA; 5968 MW; 76842A0D745F72D7 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 23 KDEL 26

RESULT 42
O65057_PICMA
ID O65057_PICMA PRELIMINARY; PRT; 52 AA.
AC O65057;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative ER-targeted protein (Fragment).
GN Name=Sb19;
OS Picea mariana (Black spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3335;
RN [1];
NUCLEOTIDE SEQUENCE.
RP MEDLINE=98278823; PubMed=9611216;
RA Perry D.J., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes: development,
RT characterization and analysis of linkage in black spruce.";
RL Genetics 149:1089-1098(1998).
DR EMBL; AF051215; AAC32119.1; -; mRNA.
DR InterPro; IPR000886; ER_target_S.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 52 AA; 6012 MW; A3AFE2C63F8B4791 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 49 KDEL 52

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RESULT 43
OBTSE1_9NEOP
ID OBTSE1_9NEOP PRELIMINARY; PRT; 53 AA.
AC OBTSE1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Triosephosphate isomerase (Fragment).
OS Anartia chrysopoelea.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Nymphalinae; Anartia.
OX NCBI_TaxID=165849;
RN [1];
NUCLEOTIDE SEQUENCE.
RP MEDLINE=22359425; PubMed=12470937; DOI=10.1016/S1055-7903(02)00291-9;
RA Blum M.J., Bermingham E., Dasmahapatra K.;
RT "A molecular phylogeny of the neotropical butterfly genus Anartia
RT (Lepidoptera: Nymphalidae).";
RL Mol. Phylogenet. Evol. 26:46-55(2003).
DR EMBL; AX038678; AAM03326.1; -; Genomic_DNA.
DR HSP; P00940; ITPH.
DR SMR; OBTSE1; 1-48.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0004807; F:triose-phosphate isomerase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000652; Triophos_ismase.
DR Pfam; PF00121; TIM; 1.
KW Isomerase.
FT NON TER 1
SQ SEQUENCE 53 AA; 5718 MW; 22D759859B5F5443 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
Db 3 KDEL 6

RESULT 44
Q30456_HORSE
ID Q30456_HORSE PRELIMINARY; PRT; 53 AA.
AC Q30456;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC ELA-DQbeta cell surface glycoprotein (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1];
NUCLEOTIDE SEQUENCE.
RP TISSUE=Blood;
RC MEDLINE=93370708; PubMed=8363103;
RA Szalai G., Bailey E., Gerber H., Lazary S.;
RT "DNA sequence analysis of serologically detected ELA class II
RT haplotypes at the equine DQ beta locus.";
RL Anim. Genet. 24:187-190(1993).
DR EMBL; L08739; AAA30933.1; -; Genomic_DNA.
DR SMR; Q30456; 1-53.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.

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DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 53
SQ SEQUENCE 53 AA; 6341 MW; 88884EF9415FC6E3 CRC64;

Query Match      100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      45 KDEL 48

RESULT 45
Q30470 HORSE
ID Q30470 HORSE PRELIMINARY; PRT; 53 AA.
AC Q30470;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC ELA-DQbeta cell surface glycoprotein (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Szalai G., Bailey E., Gerber H., Lazary S.;
RT "DNA sequence analysis of serologically detected ELA class II
haplotypes at the equine DQ beta locus."
RL Anim. Genet. 24:187-190(1993).
DR EMBL; L08740; AAA30935.1; -; Genomic_DNA.
DR SMR; Q30470; 1-53.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 53
SQ SEQUENCE 53 AA; 6326 MW; 88885ABA615FC6E3 CRC64;

Query Match      100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      45 KDEL 48

RESULT 47
Q30476 HORSE
ID Q30476 HORSE PRELIMINARY; PRT; 53 AA.
AC Q30476;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC ELA-DQbeta cell surface glycoprotein (fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Szalai G., Bailey E., Gerber H., Lazary S.;
RT "DNA sequence analysis of serologically detected ELA class II
haplotypes at the equine DQ beta locus."
RL Anim. Genet. 24:187-190(1993).
DR EMBL; L08747; AAA30941.1; -; Genomic_DNA.
DR SMR; Q30476; 1-53.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 53
SQ SEQUENCE 53 AA; 6309 MW; 88885AA9415FC6E3 CRC64;

Query Match      100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEL 4
Db      45 KDEL 48

RESULT 46
Q30471 HORSE
ID Q30471 HORSE PRELIMINARY; PRT; 53 AA.
AC Q30471;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC ELA-DQbeta cell surface glycoprotein (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;

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DR GO: 0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR00054; Ribosomal_L31le.
DR Pfam; PF01198; Ribosomal_L31le; 1.
KW Ribosomal protein.
FT NON_TER 1
SQ SEQUENCE 53 AA; 6025 MW; 01842A0D00B9A9CE CRC64;

Query Match 100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 24 KDEL 27

RESULT 50
Q4MPA5_BACCE
ID Q4MPA5_BACCE PRELIMINARY; PRT; 53 AA.
AC Q4MPA5;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Alpha/beta hydrolase
ORFNames=BCE_G9241.2817;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -i- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAEK01000019; EAL14002.1; -; Genomic_DNA.
DR KW Hydrolase.
SQ SEQUENCE 53 AA; 6525 MW; D5B74F6551F7970 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 5 KDEL 8

Search completed: March 20, 2006, 07:57:21
Job time : 154.5 secs

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QY 1 KDEL 4
DB 45 KDEL 48

RESULT 48
Q9BCX3_HORSE
ID Q9BCX3_HORSE PRELIMINARY; PRT; 53 AA.
AC Q9BCX3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=ELA-DQB;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
NUCLEOTIDE SEQUENCE.
RP MEDLINE=22027051; PubMed=12030922;
RA Horin P., Matiasovic J.;
RT "A second locus and new alleles in the major histocompatibility
RT complex class II (ELA-DQB) region in the horse.";
RL Anim. Genet. 33:196-200(2002).
DR EMBL; AF348966; AAK29638.1; -; mRNA.
DR GO: 0016021; C:integral to membrane; IEA.
DR GO: 0016020; C:membrane; IEA.
DR GO: 00045012; F:MHC class II receptor activity; IEA.
DR GO: 00019884; P:antigen presentation, exogenous antigen; IEA.
DR GO: 00019886; P:antigen processing, exogenous antigen via M. .; IEA.
DR GO: 0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta_N.
DR Pfam; PF00969; MHC_II_beta_1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 53
SQ SEQUENCE 53 AA; 6380 MW; 8EDCC47AE79061B7 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEL 4
DB 45 KDEL 48

RESULT 49
Q9SPX3_PICAB
ID Q9SPX3_PICAB PRELIMINARY; PRT; 53 AA.
AC Q9SPX3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Putative 60S ribosomal protein L31 (Fragment).
GN Name=Sb42;
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1]
NUCLEOTIDE SEQUENCE.
RP MEDLINE=99436016; PubMed=10504420;
RA Perry D.J., Isabel N., Bouquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes: the amount and
RT nature of variation revealed in norway spruce.";
RL Hereditas 83:239-248(1999).
DR EMBL; AF127446; AAF02463.1; -; Genomic_DNA.
DR GO: 0005622; C:intracellular; IEA.
DR GO: 0005840; C:ribosome; IEA.
DR GO: 0003735; F:structural constituent of ribosome; IEA.

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